

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 20, 2006, 07:28:19 ; Search time 270.726 Seconds
(without alignments)
1213.978 Million cell updates/sec

Title: US-10-687-035-1
Perfect score: 3945
Sequence: 1 AAQARRARRTKLFTTHRSSV.....QKLISEDLMNMTGHHHHH 748

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A Geneseq_21.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3945	100.0	748	8	ADS94302
2	3904.5	99.0	809	8	ADS94303
3	3663	92.9	833	3	AB12554 Human ova
4	3663	92.9	833	5	ABP30898
5	3663	92.9	833	7	ADA08542
6	3663	92.9	833	7	ADP08885
7	3663	92.9	833	7	ADG46172
8	3663	92.9	833	3	AB12552 Human ova
9	3663	92.9	833	3	AB12552 Human ova
10	3663	92.9	914	4	ABP30968
11	3663	92.9	914	5	ABP30896
12	3663	92.9	914	5	ADU01425
13	3663	92.9	914	5	ADZ41689
14	3663	92.9	914	5	ADA08631
15	3663	92.9	914	7	ADA08465
16	3663	92.9	914	7	ADP08974
17	3663	92.9	914	7	ADP08808
18	3663	92.9	914	7	ADG46095
19	3663	92.9	914	8	ADN40451
20	3663	92.9	914	8	ADN40451
21	3663	92.9	914	9	ADN40451
22	3663	92.9	914	9	ADN40451
23	3658	92.7	1889	6	ABP30899
24	3658	92.7	1890	5	ABG96381

98 1345 34.1 318 5 ABP31025
99 1345 34.1 318 7 ADA08747
100 1345 34.1 318 7 ADF09090

ABP31025 Amino aci
ADA08747 Human O77
ADF09090 Secreted

ALIGNMENTS

RESULT 1
ADS94302

XX AC ADS94302 standard; protein; 748 AA.

XX AC ADS94302;

XX DT 02-DEC-2004 (first entry)

XX DE CA 125/O772P 3-repeat amino acid sequence SEQ ID NO:1.

XX KW antibody; antigen-binding antibody fragment;

XX KW cell-associated CA 125/O772P; monoclonal antibody; cytostatic;
XX KW immunostimulant; mediator of lysis; tumour; cell proliferative disorder;
XX KW cancer; cervical cancer; uterine cancer; breast cancer; lung cancer;
XX KW ovarian cancer.

XX OS Synthetic.

XX FN WO2004035537-A2.

XX PD 29-APR-2004.

XX PP 15-OCT-2003; 2003WO-US032945.

XX PR 16-OCT-2002; 2002US-0418828P.

XX PR 10-JUL-2003; 2003US-0485986P.

XX PA (EURO-) EUROCELTIQUE SA.

XX PI Albione EF, Soltis DA;

XX DR WPI; 2004-357171/33.

XX PT Novel isolated antibody, or antigen-binding antibody fragment binding
XX PT with cell-associated CA 125/O772P polypeptide relative to shed CA
XX PT 125/O772P polypeptide, useful for ameliorating cervical or ovarian cancer.

XX PS Example; SEQ ID NO 1; 153pp; English.

XX CC The present invention describes an isolated antibody, or an antigen-
XX CC binding antibody fragment (I), that preferentially binds cell-associated
XX CC CA 125/O772P polypeptide relative to shed CA 125/O772 polypeptide. Also
XX CC described: (1) a monoclonal antibody (II) produced by hybridoma 4E7; (2)
XX CC a monoclonal antibody that competes with binding of (II); (3) a hybridoma
XX CC as deposited in (II); (4) an isolated nucleic acid molecule (III)
XX CC comprising a nucleotide sequence that encodes a variable chain region of
XX CC (I); (5) a pharmaceutical composition comprising an antibody or an
XX CC antigen-binding antibody fragment that preferentially binds cell-
XX CC associated CA 125/O772P polypeptide relative to shed CA 125/O772P
XX CC polypeptide, and a carrier; (6) a pharmaceutical composition comprising a
XX CC monoclonal antibody or an antigen-binding monoclonal antibody fragment
XX CC that preferentially binds cell-associated CA 125/O772P polypeptide
XX CC relative to shed CA 125/O772P polypeptide, and a carrier; (7) an article
XX CC of manufacture (IV) comprising packaging material and a composition
XX CC comprising an antibody, or an antigen-binding antibody fragment that
XX CC preferentially binds cell-associated CA 125/O772P relative to shed CA
XX CC 125/O772P, and a carrier contained within the packaging material, and
XX CC composition in a form suitable for administration to a subject; (8) a
XX CC fusion polypeptide (V) comprising an antibody, or an antigen-binding
XX CC antibody fragment, which preferentially binds cell-associated CA
XX CC 125/O772P relative to shed CA 125/O772P operably linked to a heterologous
XX CC agent; (9) ameliorating (M1) a symptom of a CA 125/O772P-related disorder
XX CC; (10) a monoclonal antibody (VI) chosen from 325.1, 621.1, 633.1, 654.1,
XX CC 725.1, 8G9, 7F10, 8A1, 8AC3, 15C9, 8B5, 7G10, 16C7, 7C6, 7H1, 16H9,
XX CC 7A11, 4E7, 117.1, 368.1, 446.1, 501.1, and 776.1 or its antigen-binding

CC antibody fragment; (11) an antibody or antigen binding antibody fragment
CC that competes with (VI); and (12) a pharmaceutical composition comprising
CC (VI) and a carrier. (I) has cytostatic activity, and can be used as an
CC immunostimulant and a mediator of lysis of positive tumour cell. (I) is
CC useful for ameliorating a symptom of a CA 125/O77P-related disorder which
CC is a cell proliferative disorder such as cancer, cervical or uterine
CC cancer, breast or lung cancer or ovarian cancer. (V) is useful
CC diagnostically for monitoring the development or progression of cancer or
CC tumour as part of clinical testing procedure. The present sequence
CC represents the CA 125/O772P 3-repeat amino acid sequence, which is used
CC in the exemplification of the present invention.

XX SQ Sequence 748 AA;

Query Match 100.0%; Score 3945; DB 8; Length 748;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 748; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAQARRARRTKLFTHRSSVSTTSTPGTPVYLGASKTPASIFGPSAASHLLILFTLNFT 60

DB 1 AAQARRARRTKLFTHRSSVSTTSTPGTPVYLGASKTPASIFGPSAASHLLILFTLNFT 60

QY 61 ITNLYEENWMPGSRKFNFTTTERVLQGLLRPLFKNTSVGPLYSGCRLTLRPEKDGATGV 120

DB 61 ITNLYEENWMPGSRKFNFTTTERVLQGLLRPLFKNTSVGPLYSGCRLTLRPEKDGATGV 120

QY 121 DAICTHRPDPGCLDREQLYELSQLTHSITELGPYTLDRDSLTYNGFTHRSSVPTTST 180

DB 121 DAICTHRPDPGCLDREQLYELSQLTHSITELGPYTLDRDSLTYNGFTHRSSVPTTST 180

QY 181 GVWSEEPFTLNFTINNLRYNMDMGQPGSLKFNFTDNVMKHLSPFLFORSSLGARYTCRV 240

DB 181 GVWSEEPFTLNFTINNLRYNMDMGQPGSLKFNFTDNVMKHLSPFLFORSSLGARYTCRV 240

QY 241 IALRSVKNAGAEIVRDLICTYLQPLSGPLIKQVHFELHSQOHTGITLPGYSLDKSLYL 300

DB 241 IALRSVKNAGAEIVRDLICTYLQPLSGPLIKQVHFELHSQOHTGITLPGYSLDKSLYL 300

QY 301 NGYNECPDEPPTTPKPAATFLPPLSEATTAMGVHLKATLTNFTISNLQSPDMGKGSAT 360

DB 301 NGYNECPDEPPTTPKPAATFLPPLSEATTAMGVHLKATLTNFTISNLQSPDMGKGSAT 360

QY 361 FNSTEGVQLHLLRPLFKQKSMGPFYLGCLISLRPEKDGATGVDTTCTYHPDPVPGCLD 420

DB 361 FNSTEGVQLHLLRPLFKQKSMGPFYLGCLISLRPEKDGATGVDTTCTYHPDPVPGCLD 420

QY 421 IQQLYWELSQLTHGVTOLGPFVLDRLDSLFINGVAPQNLISIRGEYQINPHIVNNLSNPD 480

DB 421 IQQLYWELSQLTHGVTOLGPFVLDRLDSLFINGVAPQNLISIRGEYQINPHIVNNLSNPD 480

QY 481 TSSEYITLLRDIDQKVTLTKGSQLHDTFRCLVTNLTMDSVLTVKALPSSNLDPSLVE 540

DB 481 TSSEYITLLRDIDQKVTLTKGSQLHDTFRCLVTNLTMDSVLTVKALPSSNLDPSLVE 540

QY 541 QVFLDKTLNLSFHWLGSYQLVDIHVTMESVSVQPTSSSTQHFYLFNFTITNLPYSQDK 600

DB 541 QVFLDKTLNLSFHWLGSYQLVDIHVTMESVSVQPTSSSTQHFYLFNFTITNLPYSQDK 600

QY 601 AQPCTTNYQRNKRNIEDALNQLFNNSISKYSFSCQVSTFRSVNRRHHTGVDSLNCNPSPL 660

DB 601 AQPCTTNYQRNKRNIEDALNQLFNNSISKYSFSCQVSTFRSVNRRHHTGVDSLNCNPSPL 660

QY 661 ARRVDRAVIEEFLRMTRNGTQLQNFITLDRSSVLVDGYSNRPNPLTGNADIOHSGGRS 720

DB 661 ARRVDRAVIEEFLRMTRNGTQLQNFITLDRSSVLVDGYSNRPNPLTGNADIOHSGGRS 720

QY 721 SLEGPREFQKLISEEDLNMTGHHHHH 748

DB 721 SLEGPREFQKLISEEDLNMTGHHHHH 748

RESULT 2
ADS94303

AD	ADS94303 standard; protein; 809 AA.
XX	
AC	ADS94303;
XX	
DT	02-DEC-2004 (first entry)
XX	
DE	CA 125/0772P 3-repeat TM amino acid sequence SEQ ID NO:2.
XX	
KW	antibody; antigen-binding antibody fragment;
KW	cell-associated CA 125/0772P; monoclonal antibody; cytostatic;
KW	immunostimulant; mediator of lysis; tumour; cell proliferative disorder;
KW	cancer; cervical cancer; uterine cancer; breast cancer; lung cancer;
KW	ovarian cancer.
XX	
OS	Synthetic.
OS	
WO	WO2004035537-A2.
PN	
PD	29-APR-2004.
XX	
XX	15-OCT-2003; 2003WO-US032945.
XX	
PR	16-OCT-2002; 2002US-0418828P.
PR	10-JUL-2003; 2003US-0485988P.
XX	
PA	(EURO-) EUROCELTIQUE SA.
XX	
DA	Albone EF, Soltis DA;
PI	
DR	WPI; 2004-357171/33.
XX	
PT	Novel isolated antibody, or antigen-binding antibody fragment binding
PT	with cell-associated CA 125/0772P polypeptide relative to shed CA
PT	125/0772 polypeptide, useful for ameliorating cervical or ovarian cancer.
PS	Example; SEQ ID NO 2; 153pp; English.
XX	
CC	The present invention describes an isolated antibody, or an antigen-
CC	binding antibody fragment (I), that preferentially binds cell-associated
CC	CA 125/0772P polypeptide relative to shed CA 125/0772 polypeptide. Also
CC	described: (1) a monoclonal antibody (II) produced by hybridoma #E7; (2)
CC	a monoclonal antibody that competes with binding of (II); (3) a myridoma
CC	as deposited in (III); (4) an isolated nucleic acid molecule (III)
CC	comprising a nucleotide sequence that encodes a variable chain region of
CC	(I); (5) a pharmaceutical composition comprising an antibody or an
CC	antigen-binding antibody fragment that preferentially binds cell-
CC	associated CA 125/0772P polypeptide relative to shed CA 125/0772P
CC	polypeptide, and a carrier; (6) a pharmaceutical composition comprising a
CC	monoclonal antibody or an antigen-binding monoclonal antibody fragment
CC	that preferentially binds cell-associated CA 125/0772P polypeptide
CC	relative to shed CA 125/0772P polypeptide, and a carrier; (7) an article
CC	of manufacture (IV) comprising packaging material and a composition
CC	comprising an antibody, or an antigen-binding antibody fragment that
CC	preferentially binds cell-associated CA 125/0772P relative to shed CA
CC	125/0772P, and a carrier contained within the packaging material, and
CC	a composition in a form suitable for administration to a subject; (8) a
CC	fusion polypeptide (V) comprising an antibody, or an antigen-binding
CC	antibody fragment, which preferentially binds cell-associated CA
CC	125/0772P relative to shed CA 125/0772P operably linked to a heterologous
CC	agent; (9) ameliorating (MI) a symptom of a CA 125/0772P-related disorder
CC	; (10) a monoclonal antibody (VI) chosen from 325.1, 621.1, 633.1, 654.1,
CC	725.1, 8G9, 7F10, 8A1, 8AC3, 15C9, 8E3, 8B5, 7G10, 16C7, 7C6, 7H1, 16H9,
CC	7A11, 4E7, 117.1, 368.1, 446.1, 501.1, and 776.1 or its antigen-binding
CC	antibody fragment; (11) an antibody or antigen binding antibody fragment
CC	that competes with (VI); and (12) a pharmaceutical composition comprising
CC	(VI) and a carrier. (I) has cytostatic activity, and can be used as an
CC	immunostimulant and a mediator of lysis of positive tumour cell. (I) is
CC	useful for ameliorating a symptom of a CA 125/0772P-related disorder which
CC	is a cell proliferative disorder such as cancer, cervical or uterine
CC	cancer, breast or lung cancer or ovarian cancer. (V) is useful
CC	diagnostically for monitoring the development or progression of cancer or
CC	tumour as part of clinical testing procedure. The present sequence
CC	represents the CA 125/0772P 3-repeat TM amino acid sequence, which is

CC used in the exemplification of the present invention.

xx
SQ Sequence 809 AA:

Query Match	99.0%	Score 3904.5	DB 8	Length 809
Best Local Similarity	92.5%	Pred. No. 0		

1 AAQPARRRRTKLFTHRSSVSTSTPGTPTVYLGASKTPASIFGPSAASHLLILFLLNFT '60 QY

61 ITNLRYEENWPGSRKFNTTERTVLOGLLRPLFKNTSVGPLYSGCRLTLRLRPEKDGEATGV 12

121 DATCTTHRPDPPTGGGIDRBOIYIEISQITHTSTIEIGPYTIDRDSIYVNGFTHRSSVPTTST 18

101 CUNISCEPPEPPI NPTTNAT PYMA NMCDPCCI YENTTNTNTMTHT I CBI EDPBCCI CAPVTCCPIV 24

QY
101 QVVEEEF I LNE I NNDA INP MOQESSTAFN I IDNVNNHLS FEF QRSSLEGA I 19CRV 29

241 TAYNOR, J. A. 1964. The effect of the rate of growth on the rate of development of the larva of the European spruce sawfly, *Pristiphora excelsa* (L.). *Entomol. exp. appl.* 8: 1-10.

QY 241 TALKSVANGAEIRVDLLCII LQFSLSGFLFKV FHELSQVINGIIRKLPISLDDNDSTLIL 30

[illegible]

301 NGYNEPGPDBPPTTTPKPPATTFLLPPLSEBATTAMGIHKLITLNF.TISNLQISFDMGKGSAT 36

QUESTION

QY 361 FNSIEGVLQHLLRPLFQKSSMGFFYLGCCILSTRPEKDGAAIGVDITCTYHFDVPVGGLD 42

1. The first step in the process is to identify the problem or issue that needs to be addressed. This involves gathering information and understanding the context of the problem.

421 IQQLYWELSQLTHGVTQLGFVWLBDRDSLFIINGYAPQNL SIRGEYQINFIHVNWNLSPDF 48
QY

Qy 481 TSSEYITLLRDIQDKVTTLTKGSQLHDTFRFCCLVTNLTMDSVLTVTKALFSSNLDPSLVE 54

Qy 541 QVFLDKTLNASFWLGSTYQLVDIHVTEMESVYQPTSSSSSTQHFLNFTITNLPSQDK 600
Qy

Qy 601 A QPGTTNYQRNKRNIEDALNQLFRNSSIKSYFSDCQVSTFRSVPNRHHTGVDSL CNFSPL 66

[illegible]

QY 661 ARVDRVAIYEEFLRMTNRGTQLQNFTLDRSSVLVDGYSPNRNEPLTG-----700

DD 86I ARKVDRAVATIEBFERKMIKNGIQVLQNF ILDRSSVLVDGISFNKNBFLLGNSSDUFFWAVILI 72

Qy 709 -----NSADIQHSGGR 719

DB /21 GLAGLGLTCTLCGVLVTTTRRRRKEGEYNVQ

720 SSLEGRPEQKLI SEEDLN MHTGHHHH 748 QY

RESULT 3

AAB12554

ID AAB12554 standard; protein; 833 AA.

AC AAB12554;

XX
ED
07-NOV-2000 (F) 14:00

XXI

DE Human ovarian carcinoma antigen O772P protein SEQ ID NO:389.
XX
KW Human; ovarian carcinoma; ovarian cancer; therapy; diagnosis;
KW tumour antigen; identification; cytostatic; gene therapy; vaccine.
XX
OS Homo sapiens.
XX
PN W0200036107-A2.
XX
XX 22-JUN-2000.
XX
XX 17-DEC-1999; 99WO-US030270.
XX
XX 17-DEC-1998; 98US-00215681.
PR 17-DEC-1998; 98US-00216003.
PR 23-JUN-1999; 99US-00338933.
PR 24-SEP-1999; 99US-00404879.
XX
XX (CORI-) CORIXA CORP.
XX
XX Mitcham JL, King GE, Algate PA, Frudakis TN;
XX
XX WPI; 2000-431589/37.
DR N-PSDB; AAA70075.
XX
XX Immunogenic portion of an ovarian carcinoma protein and the nucleic acid
PT encoding it, useful for the diagnosis, prevention and treatment of
PT cancer, preferably ovarian cancer.
XX
XX Example 2; Page 200-203; 299pp; English.
XX
XX The present invention describes an isolated polypeptide comprising an
CC immunogenic portion of an ovarian carcinoma protein (or its variants).
CC Ovarian carcinoma proteins, and polynucleotides encoding them, have
CC cytostatic activity and can be used in gene therapy and vaccines. Ovarian
CC carcinoma polypeptides, nucleic acids, antibodies and vaccines are useful
CC for the prevention, diagnosis and treatment of cancer, preferably ovarian
CC cancer. AAA69691 to AAA70077 and AAB12552 to AAB12557 represent human
CC ovarian carcinoma polynucleotides and proteins used in the
CC exemplification of the present invention
XX
XX Sequence 833 AA;
SQ
Query Match 92.9%; Score 3663; DB 3; Length 833;
Best Local Similarity 99.9%; Pred. No. 2.2e-315;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
14 FTHRSSVSTSTPGTPTVYLGASKTPTASIFGSPSAASHLLILFTLNFTITNLRYEENWPG 73
78 FTHRSSVSTSTPGTPTVYLGASKTPTASIFGSPSAASHLLILFTLNFTITNLRYEENWPG 137
74 SRKPNTERVLQGLLRPLPKNTSVGPVLYSGCRLTLRLPEKDGATGVDAICTHRPDPGTP 133
138 SRKPNTERVLQGLLRPLPKNTSVGPVLYSGCRLTLRLPEKDGATGVDAICTHRPDPGTP 197
134 GLDREQLYLELSQTHSTELGPTLDRDSLYVNGFTHRSSVPTSTGVWSEEPFTLNFT 193
198 GLDREQLYLELSQTHSTELGPTLDRDSLYVNGFTHRSSVPTSTGVWSEEPFTLNFT 257
194 INNRYMADMQPGLSKFNITDVMKLLPLFORSSIGARYTCGRVIALRSVKNGAETR 253
258 INNRYMADMQPGLSKFNITDVMKLLPLFORSSIGARYTCGRVIALRSVKNGAETR 317
254 VDLCTYLQPLSGPLPKQVHFELSQTHGTRGYSYLDKSLYLNGYNPEGDPBPPT 313
318 VDLCTYLQPLSGPLPKQVHFELSQTHGTRGYSYLDKSLYLNGYNPEGDPBPPT 377
314 TPKPATTFPLPLSEATTAMGWHKTLTNFTISNLYQSPDMKGSATFNSTEGVLQHLR 373
378 TPKPATTFPLPLSEATTAMGWHKTLTNFTISNLYQSPDMKGSATFNSTEGVLQHLR 437
374 PLFKQSSMGPFYLGCOLISLRPEKGAATGVDTTCTYHPDPVPGGLDIQQLYWELSQLTH 433

Db 438 PLFKQSSMGPFYLGCOLISLRPEKGAATGVDTTCTYHPDPVPGGLDIQQLYWELSQLTH 497
Qy 434 GVTQLGFYVLDRLDSLFINGYAPQNLISIRGEYQINFIHVNWNLNPNPDTSEYITLLRDIQ 493
Db 498 GVTQLGFYVLDRLDSLFINGYAPQNLISIRGEYQINFIHVNWNLNPNPDTSEYITLLRDIQ 557
Qy 494 DKVTTLTKGSQLHDTFRFCLVTNLTWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASPH 553
Db 558 DKVTTLTKGSQLHDTFRFCLVTNLTWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASPH 617
Qy 554 WLGSYQLVDIHVTENESSYQPTSSSTQHFVNLFTITNLPSYODKAQPGTTNYQNRK 613
Db 618 WLGSYQLVDIHVTENESSYQPTSSSTQHFVNLFTITNLPSYODKAQPGTTNYQNRK 677
Qy 614 NIEDALNQLFRNSSIKSYFSDCOVSTFRSVNRRHHTGVDSLCNFSPLARRVDRVAIYE 673
Db 678 NIEDALNQLFRNSSIKSYFSDCOVSTFRSVNRRHHTGVDSLCNFSPLARRVDRVAIYE 737
Qy 674 LRMRNGTQLQNFLLDRSSVLDVGYSPNRNEPLTGNS 710
Db 738 LRMRNGTQLQNFLLDRSSVLDVGYSPNRNEPLTGNS 774
RESULT 4
ABP30898
ID ABP30898 standard; protein; 833 AA.
AC ABP30898;
XX
DT 02-JUL-2002 (first entry)
XX
DE 0772P clone 21003.
XX
KW Human; immunostimulant; cytostatic; cancer; ovarian carcinoma.
XX
OS Homo sapiens.
XX
PN W0200206317-A2.
XX
PD 24-JAN-2002.
XX
PF 17-JUL-2001; 2001WO-US022635.
XX
PR 17-JUL-2000; 2000US-00617747.
PR 10-AUG-2000; 2000US-00636801.
PR 20-SEP-2000; 2000US-00667857.
PR 04-APR-2001; 2001US-00827271.
PR 18-JUN-2001; 2001US-00884441.
XX
XX (CORI-) CORIXA CORP.
XX
XX Mitcham JL, King GE, Algate PA, Pling SP, Retter MW, Fanger GR;
XX Reed SG, Vedvick TS, Carter D, Hill P, Albone E;
XX
XX WPI; 2002-164781/21.
XX
XX N-PSDB; ABN72969.
XX
XX Polypeptides comprising an immunogenic portion of an ovarian carcinoma
PT protein or its variants, useful for stimulating an immune response in a
PT patient and treating ovarian cancer.
XX
XX Example 2; Page 316-318; 408pp; English.
XX
XX This invention relates to polypeptides comprising an immunogenic portion
CC of an ovarian carcinoma protein which acts as an immunostimulant and is
CC cytostatic. The polypeptides, polynucleotides, antibodies, fusion
CC proteins, T cell populations and antigen presenting cells that express
CC the polypeptides are useful for stimulating an immune response in a
CC patient and treating ovarian cancer. This sequence represents protein
CC related to the invention
XX
XX Sequence 833 AA;

Query Match		92.9%;	Score 3663;	DB 5;	Length 833;
Best Local Similarity		99.9%;	Pred. No. 2.2e-315;		
Matches 696;		Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	14	FTHRSSVSTSTPGTPTVYLGA	KTPASIFGPSAASHLLILFTLNFTITNLYEENWPG	73	
DB	78	FTHRSSVSTSTPGTPTVYLGA	KTPASIFGPSAASHLLILFTLNFTITNLYEENWPG	137	
QY	74	SRKFNTERVLOGLLRPLFKNT	SVGLYSGCRITLLRPEKDGATGVDAICTHRDPDTPG	133	
DB	138	SRKFNTERVLOGLLRPLFKNT	SVGLYSGCRITLLRPEKDGATGVDAICTHRDPDTPG	197	
QY	134	GLDREQLYLELSQTHSITEL	GPYTLDRDSLXVNGFTHRSSVPTTSTGVVSEEPFLNFT	193	
DB	198	GLDREQLYLELSQTHSITEL	GPYTLDRDSLXVNGFTHRSSVPTTSTGVVSEEPFLNFT	257	
QY	194	INNLRYMADMGQPSGLKFN	ITDNVMKHLISPLFQSSLGARYTGCRIALRSVKNGAETR	253	
DB	258	INNLRYMADMGQPSGLKFN	ITDNVMKHLISPLFQSSLGARYTGCRIALRSVKNGAETR	317	
QY	254	VLLCTYLOPLSGPLPIKQV	FHELISOOTHGITRLGPYSLDKDSLXVNGFTHRSSVPTTSTGVVSEEPFLNFT	313	
DB	318	VLLCTYLOPLSGPLPIKQV	FHELISOOTHGITRLGPYSLDKDSLXVNGFTHRSSVPTTSTGVVSEEPFLNFT	377	
QY	314	TPKPATTELPPLSEATTAM	GYHLKTLTNFTISNLQYSPDMGKGSATFNSTEGVLOHLR	373	
DB	378	TPKPATTELPPLSEATTAM	GYHLKTLTNFTISNLQYSPDMGKGSATFNSTEGVLOHLR	437	
QY	374	PLFQKSSMGPFYLGCOLIS	LRPEKDGATGVDTTCTYHPDPVPGGLDIOQLYWELSQLTH	433	
DB	438	PLFQKSSMGPFYLGCOLIS	LRPEKDGATGVDTTCTYHPDPVPGGLDIOQLYWELSQLTH	497	
QY	434	GVTOLGFVLDRLDSLFING	YAPQNLSIRGEYQINPHIVNMNLSNPDPTSSSEYITLLRDIO	493	
DB	498	GVTOLGFVLDRLDSLFING	YAPQNLSIRGEYQINPHIVNMNLSNPDPTSSSEYITLLRDIO	557	
QY	494	DKVTLYKGSQHLDTFR	CLVTNLTMDSVLVTVKALFSSNLDPSLVEQVFLDKTINASFH	553	
DB	558	DKVTLYKGSQHLDTFR	CLVTNLTMDSVLVTVKALFSSNLDPSLVEQVFLDKTINASFH	617	
QY	554	WLGSTYQLVDIHVT	EMSSVYQPTSSSSTQHFYLNFTITNLPSQDKAQPGTNYQNRK	613	
DB	618	WLGSTYQLVDIHVT	EMSSVYQPTSSSSTQHFYLNFTITNLPSQDKAQPGTNYQNRK	677	
QY	614	NIEDALNQLFNSSIK	SVESDCOVSTERSVPNRHHTGVDSICNPSPLARRVDRVAIYEEF	673	
DB	678	NIEDALNQLFNSSIK	SVESDCOVSTERSVPNRHHTGVDSICNPSPLARRVDRVAIYEEF	737	
QY	674	LEWTRNGTQLQNFTL	DRSSVLVDGYSVNNRNEPLTGN	710	
DB	738	LEWTRNGTQLQNFTL	DRSSVLVDGYSVNNRNEPLTGN	774	
RESULT 5					
ID	ADA08542				
XX	ADA08542	standard; protein; 833 AA.			
AC	ADA08542;				
DT	06-NOV-2003	(first entry)			
XX	Human ovarian carcinoma antigen O772P #2.				
XX	human; gene therapy; ovarian cancer; cancer.				
OS	Homo sapiens.				
XX	US2003091580-A1.				
PN	15-MAY-2003.				
XX	17-JUL-2001; 2001US-00907969.				
PD					
XX					
PF					
XX					
18-JUN-2001; 2001US-00884441.					
PA	(MITC/) MITCHAM J L.				
PA	(KING/) KING G E.				
PA	(ALGA/) ALGATE P A.				
PA	(FLIN/) FLING S P.				
PA	(RETT/) RETTER M W.				
PA	(FANG/) FANGER G R.				
PA	(REED/) REED S G.				
PA	(VEDV/) VEDVICK T S.				
PA	(CART/) CARTER D.				
PA	(HILL/) HILL P.				
PA	(ALBO/) ALBONE E.				
XX					
PI	Mitcham JL, King GE, Algate PA, Fling SP, Retter MW, Fanger GR, Reed SG, Vedvick TS, Carter D, Hill P, Albone E, WPI; 2003-532352/50.				
XX					
XX	New isolated O772P polypeptides and polynucleotides, useful in gene therapy, particularly for treating or diagnosing cancer, e.g. ovarian cancer.				
PT					
PT					
XX					
PS	Example 2; SEQ ID NO 389; 371pp; English.				
XX					
CC	The invention relates to an isolated O772P polypeptide, which has the structure fully defined in the specification. The composition containing the polypeptides, polynucleotides, fusion proteins, antibodies, T-cells or antigen presenting cells are useful for stimulating an immune response and treating ovarian cancer. Detecting the presence of the polynucleotides and polypeptides is useful for diagnosing cancer. Ovarian carcinoma cDNAs and protein cDNAs were identified using microarray technology. The present sequence represents a human ovarian carcinoma antigen.				
CC					
XX					
SQ	Sequence 833 AA;				
Query Match		92.9%;	Score 3663;	DB 7;	Length 833;
Best Local Similarity		99.9%;	Pred. No. 2.2e-315;		
Matches 696;		Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	14	FTHRSSVSTSTPGTPTVYLGA	KTPASIFGPSAASHLLILFTLNFTITNLYEENWPG	73	
DB	78	FTHRSSVSTSTPGTPTVYLGA	KTPASIFGPSAASHLLILFTLNFTITNLYEENWPG	137	
QY	74	SRKFNTERVLOGLLRPLFKNT	SVGLYSGCRITLLRPEKDGATGVDAICTHRDPDTPG	133	
DB	138	SRKFNTERVLOGLLRPLFKNT	SVGLYSGCRITLLRPEKDGATGVDAICTHRDPDTPG	197	
QY	134	GLDREQLYLELSQTHSITEL	GPYTLDRDSLXVNGFTHRSSVPTTSTGVVSEEPFLNFT	193	
DB	198	GLDREQLYLELSQTHSITEL	GPYTLDRDSLXVNGFTHRSSVPTTSTGVVSEEPFLNFT	257	
QY	194	INNLRYMADMGQPSGLKFN	ITDNVMKHLISPLFQSSLGARYTGCRIALRSVKNGAETR	253	
DB	258	INNLRYMADMGQPSGLKFN	ITDNVMKHLISPLFQSSLGARYTGCRIALRSVKNGAETR	317	
QY	254	VLLCTYLOPLSGPLPIKQV	FHELISOOTHGITRLGPYSLDKDSLXVNGFTHRSSVPTTSTGVVSEEPFLNFT	313	
DB	318	VLLCTYLOPLSGPLPIKQV	FHELISOOTHGITRLGPYSLDKDSLXVNGFTHRSSVPTTSTGVVSEEPFLNFT	377	
QY	314	TPKPATTELPPLSEATTAM	GYHLKTLTNFTISNLQYSPDMGKGSATFNSTEGVLOHLR	373	
DB	378	TPKPATTELPPLSEATTAM	GYHLKTLTNFTISNLQYSPDMGKGSATFNSTEGVLOHLR	437	
QY	374	PLFQKSSMGPFYLGCOLIS	LRPEKDGATGVDTTCTYHPDPVPGGLDIOQLYWELSQLTH	433	
DB	438	PLFQKSSMGPFYLGCOLIS	LRPEKDGATGVDTTCTYHPDPVPGGLDIOQLYWELSQLTH	497	
QY	374	PLFQKSSMGPFYLGCOLIS	LRPEKDGATGVDTTCTYHPDPVPGGLDIOQLYWELSQLTH	433	
DB	438	PLFQKSSMGPFYLGCOLIS	LRPEKDGATGVDTTCTYHPDPVPGGLDIOQLYWELSQLTH	497	
QY	434	GVTOLGFVLDRLDSLFING	YAPQNLSIRGEYQINPHIVNMNLSNPDPTSSSEYITLLRDIO	493	
DB	498	GVTOLGFVLDRLDSLFING	YAPQNLSIRGEYQINPHIVNMNLSNPDPTSSSEYITLLRDIO	557	

samples, and therefore which patients may be in need of restorative therapy. The host cell may also be used as antigens in the production of antibodies against (ii) and in assays to identify modulators of (ii)'s expression and activity. The anti-(ii) antibodies, agonists and antagonists may be used to regulate expression and activity and as diagnostic agents for detecting the presence of (ii) in samples (e.g. by immunoassay). This sequence represents a secreted ovarian carcinoma antigen.

XX SQ Sequence 833 AA;
Query Match 92.9%; Score 3663; DB 7; Length 833;
Best Local Similarity 99.9%; Pred. No. 2.2e-315;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
14 FTHRSSVSTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLFTINLYEENMWPG 73
138 SRKFNTERVLOGLLRPLFKNTSVGLYSGCLTLTLRPEKGEATGVDAICTHRPPTGP 137
74 SRKFNTERVLOGLLRPLFKNTSVGLYSGCLTLTLRPEKGEATGVDAICTHRPPTGP 133
134 GLDREQLYLELSQTHSITELGPTLDRDLSLVNGFTHRSSVPTTSTGVVSEEPFTLNFT 193
198 GLDREQLYLELSQTHSITELGPTLDRDLSLVNGFTHRSSVPTTSTGVVSEEPFTLNFT 257
194 INNLRYMDWQPGSLKFNITDNVMKHLSPPLQSRSLGARYTGCVRVIALRSVNGAETR 253
258 INNLRYMDWQPGSLKFNITDNVMKHLSPPLQSRSLGARYTGCVRVIALRSVNGAETR 317
254 VDILCTYLOPLSGPLPIKOVFHELSSQTHGITELGPTSLDKSLVNGNEPDEPPT 313
318 VDILCTYLOPLSGPLPIKOVFHELSSQTHGITELGPTSLDKSLVNGNEPDEPPT 377
314 TPXPATTFPLPSEATTAMGYHLKTLTLNFTINLQYSPDMGKGSATFNSTEGVLOHLR 373
378 TPXPATTFPLPSEATTAMGYHLKTLTLNFTINLQYSPDMGKGSATFNSTEGVLOHLR 437
374 PLFOKSMGPFYLGCCQLISLRPEKDGATGVTCTVHPDPVPGGLDIQQLYWELSQLTH 433
438 PLFOKSMGPFYLGCCQLISLRPEKDGATGVTCTVHPDPVPGGLDIQQLYWELSQLTH 497
434 GVTQLGPFVLDRLSLFNGVAPQNLSTIRGEYQINFHVNNLSNPDPSTSSVITLLRDIQ 493
498 GVTQLGPFVLDRLSLFNGVAPQNLSTIRGEYQINFHVNNLSNPDPSTSSVITLLRDIQ 557
494 DKVTTLKGSQHLHDFRCLVNTLMTDSVLVTKALFSSNLDPSLVEQVFLDKTLNASFH 553
558 DKVTTLKGSQHLHDFRCLVNTLMTDSVLVTKALFSSNLDPSLVEQVFLDKTLNASFH 617
554 WLGSTYQLVDIHVTEMESSVYQPTSSSTQHFYLNFTITNLPYSODKAPGTTNYQRKR 613
618 WLGSTYQLVDIHVTEMESSVYQPTSSSTQHFYLNFTITNLPYSODKAPGTTNYQRKR 677
614 NIEDALNQLFRNSSIKSYFSDCQVSTFRSPNRRHTGVDSLNCNFSPLARRVDRVAIYEEF 673
678 NIEDALNQLFRNSSIKSYFSDCQVSTFRSPNRRHTGVDSLNCNFSPLARRVDRVAIYEEF 737
674 LMRTRNGTQLQNFTLDRSSVLVDGYSPNRRNEPLTGNS 710
738 LMRTRNGTQLQNFTLDRSSVLVDGYSPNRRNEPLTGNS 774

RESULT 7
ADG46172

ID ADG46172 standard; protein; 833 AA.

XX AC ADG46172;

XX DT 26-FEB-2004 (first entry)

XX DE Human ovarian carcinoma polypeptide #3.

QY 494 DKVTTLKGSQHLHDFRCLVNTLMTDSVLVTKALFSSNLDPSLVEQVFLDKTLNASFH 553
DB 558 DKVTTLKGSQHLHDFRCLVNTLMTDSVLVTKALFSSNLDPSLVEQVFLDKTLNASFH 617
QY 554 WLGSTYQLVDIHVTEMESSVYQPTSSSTQHFYLNFTITNLPYSODKAPGTTNYQRKR 613
DB 618 WLGSTYQLVDIHVTEMESSVYQPTSSSTQHFYLNFTITNLPYSODKAPGTTNYQRKR 677
QY 614 NIEDALNQLFRNSSIKSYFSDCQVSTFRSPNRRHTGVDSLNCNFSPLARRVDRVAIYEEF 673
DB 678 NIEDALNQLFRNSSIKSYFSDCQVSTFRSPNRRHTGVDSLNCNFSPLARRVDRVAIYEEF 737
QY 674 LMRTRNGTQLQNFTLDRSSVLVDGYSPNRRNEPLTGNS 710
DB 738 LMRTRNGTQLQNFTLDRSSVLVDGYSPNRRNEPLTGNS 774

RESULT 6

ID ADF08885
ADP08885 standard; protein; 833 AA.

XX AC ADF08885;

XX DT 12-FEB-2004 (first entry)

XX DE Secreted ovarian carcinoma antigen seqid 389.

XX KW gene therapy; protein therapy; vaccine; antibody inhibition;

XX KW breast cancer; restorative therapy; diagnostic agent; immunoassay;

XX KW secreted ovarian carcinoma antigen.

XX OS Homo sapiens.

XX PN US2003124140-A1.

XX PD 03-JUL-2003.

XX PF 17-JUL-2002; 2002US-00198053.

XX PR 17-DEC-1998; 98US-00215681.

XX PR 17-DEC-1998; 98US-00216003.

XX PR 23-JUN-1999; 99US-00338933.

XX PR 24-SEP-1999; 99US-00404879.

XX PR 17-JUL-2000; 2000US-00617747.

XX PR 10-AUG-2000; 2000US-00636801.

XX PR 20-SEP-2000; 2000US-00667857.

XX PR 04-APR-2001; 2001US-00827271.

XX PR 18-JUN-2001; 2001US-00884441.

XX PR 17-JUL-2001; 2001US-00907969.

XX PA (CORI-) CORIXA CORP.

XX PI Bangur CS, Retter MW, Fanger GR, Hill P;

XX WPI; 2003-897152/82.

XX DR N-PSDB; ADF08882.

XX PT Oncogenic nucleic acids useful for the prevention, diagnosis and treatment of breast cancer.

XX PS Example 2; SEQ ID NO 389; 399pp; English.

XX CC The invention describes nucleic acids (I) and the polypeptides (II) they encode. The nucleic acids (I) may be used for preventing, diagnosing and treating diseases related to their aberrant expression i.e. breast cancers. For example, (I) and (II) may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (II) by expressing inactive proteins or to supplement the patients own production of (II). Additionally, (I) may be used to produce (II), by inserting (I) into a host cell and culturing the cell to express the protein (II). (I) And its complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in

XX Human; ovarian carcinoma; O8E; ovarian cancer; secreted tumour antigen;
 KW cytostatic; O772P.
 XX
 OS Homo sapiens.
 XX
 PN US2003165504-A1.
 XX
 PD 04-SEP-2003.
 XX
 PF 04-APR-2001; 2001US-00827271.
 XX
 PR 17-DEC-1998; 98US-00215681.
 PR 17-DEC-1998; 98US-00216003.
 PR 23-JUN-1999; 99US-00338933.
 PR 24-SEP-1999; 99US-00404879.
 PR 17-JUL-2000; 2000US-00617747.
 PR 10-AUG-2000; 2000US-00636801.
 PR 20-SEP-2000; 2000US-00667857.
 XX
 PA (RETT/) RETTER M W.
 PA (FANG/) FANGER G R.
 XX
 PI Retter MW, Fanger GR;
 XX
 XX WPI; 2003-898035/82.
 DR
 XX
 XX New isolated O8E or O772P polypeptides, useful for diagnosing,
 PT preventing, treating and monitoring cancer, e.g. ovarian cancer,
 PT stimulating the immune response in patient.
 PT
 XX
 PS Claim 5; SEQ ID NO 389; 290pp; English.
 CC
 CC The invention relates to human ovarian carcinoma polypeptides, designated
 CC O8E or O772P, and the polynucleotides encoding them. The invention also
 CC relates to methods for inhibiting the development of cancer, e.g. ovarian
 CC cancer in a patient, methods for stimulating and/or expanding T cells and
 CC methods for identifying secreted tumour antigens. The polypeptides,
 CC compositions, antibodies to the polypeptides and methods are useful for
 CC diagnosing, preventing, treating and monitoring cancer, e.g. ovarian
 CC cancer. The composition is particularly useful for stimulating an immune
 CC response in patient. This sequence represents a human ovarian carcinoma
 CC polypeptide of the invention.
 XX
 SQ Sequence 833 AA;
 Query Match 92.9%; Score 3663; DB 7; Length 833;
 Best Local Similarity 99.9%; Pred. No. 2.2e-315;
 Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 14 FTHRSSVSTTSTPGTPTVYLGASKTPASIFGSPASASHLLILFTLFTITNLYENMMPG 73
 78 FTHRSSVSTTSTPGTPTVYLGASKTPASIFGSPASASHLLILFTLFTITNLYENMMPG 137
 74 SKKFTTERTVQLGLRLPKNSTVGLVSGCRLTLRLPEKGEATGDAICTHRPDPTGP 133
 138 SRKFTTERTVQLGLRLPKNSTVGLVSGCRLTLRLPEKGEATGDAICTHRPDPTGP 197
 134 GLDRQLVLELSQTHSITELGPYTLDRDSLXNGFTHRSSVPTTSTGVSEPTINFT 193
 198 GLDRQLVLELSQTHSITELGPYTLDRDSLXNGFTHRSSVPTTSTGVSEPTINFT 257
 194 INNLYMADMGQPGSLKFNITDNVKKHLLSPLFQSSILGARYTGCVRVIALRSVKNGAETR 253
 258 INNLYMADMGQPGSLKFNITDNVKKHLLSPLFQSSILGARYTGCVRVIALRSVKNGAETR 317
 254 VDLCTYQLPSGGLPIKQVPHLSQQTHGTRIGPYSLDKDSLXLYNGYNEPGDEPPT 313
 318 VDLCTYQLPSGGLPIKQVPHLSQQTHGTRIGPYSLDKDSLXLYNGYNEPGDEPPT 377
 314 TPKPATTELPPLSEATTAMGHLKTLTNTFTISNLYQSPDMCKGSAATNSTEGVLOHLRL 373
 378 TPKPATTELPPLSEATTAMGHLKTLTNTFTISNLYQSPDMCKGSAATNSTEGVLOHLRL 437

QY 374 PLFQKSSMGPFYLGCOLISLRPEKGAATGVDTCTTTHPDPVGPGLDIQOLYWELSOLTH 433
 DB 438 PLFQKSSMGPFYLGCOLISLRPEKGAATGVDTCTTTHPDPVGPGLDIQOLYWELSOLTH 497
 QY 434 GVTQLGFFVLDLDRSLFINGYAPQNLISIRGEYQINFIHVNMLSNPDPTSEYITLLRDIQ 493
 DB 498 GVTQLGFFVLDLDRSLFINGYAPQNLISIRGEYQINFIHVNMLSNPDPTSEYITLLRDIQ 557
 QY 494 DKVTTYLKGSQLHDTFRCLVTNLTWDSVLVTVKALFSSNLDPSSLVQVFLDKTLNASFH 553
 DB 558 DKVTTYLKGSQLHDTFRCLVTNLTWDSVLVTVKALFSSNLDPSSLVQVFLDKTLNASFH 617
 QY 554 WLGSSTYQLVDIHVTEMESSYQPTSSSTQHFYLNFTITNLYPSQDKAOPGTTNYQRNKR 613
 DB 618 WLGSSTYQLVDIHVTEMESSYQPTSSSTQHFYLNFTITNLYPSQDKAOPGTTNYQRNKR 677
 QY 614 NIEDALNQLFRNSSIKSYFSDQVSTFRSVPNRHHTGVDSLGNFSPPLARRVDRVAIYEEF 673
 DB 678 NIEDALNQLFRNSSIKSYFSDQVSTFRSVPNRHHTGVDSLGNFSPPLARRVDRVAIYEEF 737
 QY 674 LRWTRNGTOLQNTLDRSSVLVDGYSPNREPLTGNS 710
 DB 738 LRWTRNGTOLQNTLDRSSVLVDGYSPNREPLTGNS 774
 RESULT 8
 ADX17768
 ID ADX17768 standard; protein; 833 AA.
 XX
 AC ADX17768;
 XX
 DT 21-APR-2005 (first entry)
 XX
 DE Human ovarian carcinoma antigen cDNA O772P clone 21003 encoded protein.
 XX
 KW diagnosis; cytostatic; immunostimulant; gene therapy; tumor;
 KW ovarian tumor; cancer; carcinoma; antigen.
 XX
 OS Homo sapiens.
 XX
 PN US2005031634-A1.
 XX
 PD 10-FEB-2005.
 XX
 PF 02-JUN-2004; 2004US-00860790.
 XX
 PR 17-DEC-1998; 98US-00216003.
 PR 23-JUN-1999; 99US-00338933.
 PR 24-SEP-1999; 99US-00404879.
 PR 17-JUL-2000; 2000US-00617747.
 PR 10-AUG-2000; 2000US-00636801.
 PR 20-SEP-2000; 2000US-00667857.
 PR 04-APR-2001; 2001US-00827271.
 PR 18-JUN-2001; 2001US-00894441.
 PR 17-JUL-2001; 2001US-00907969.
 PR 17-JUL-2002; 2002US-00198053.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Bangur CS, Retter MW, Fanger GR, Hill P;
 XX
 XX WPI; 2005-151645/16.
 XX
 PT New ovarian carcinoma polynucleotides, preferably cDNAs, useful for
 PT diagnosing, preventing and treating diseases, such as ovarian cancer, and
 PT for eliciting humoral and/or cellular immune response.
 XX
 PS Example 2; SEQ ID NO 389; 398pp; English.
 XX
 CC The invention relates to an isolated polynucleotide comprising a sequence
 CC of, a sequence hybridizing under highly stringent conditions to, or
 CC having at least 75, or 90% identity to a 849 or 1399 bp, fully defined in

CC the specification, its complement or degenerate variants, or a sequence
CC of at least 20 contiguous residues of the 849 or 1399 bp sequence. The
CC polynucleotides and polypeptides are useful for diagnosing, preventing
CC and treating diseases, such as ovarian cancer, and for eliciting humoral
CC and/or cellular immune response. This sequence corresponds to an ovarian
CC carcinoma antigen protein of the invention.

XX	Sequence 833 AA;	
XX	Query Match	92.9%; Score 3663; DB 9; Length 833;
XX	Best Local Similarity	99.9%; Pred. No. 2.2e-315;
XX	Matches	696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	14	FTHRSSVSTSTPGTPTVYLGASKTPASIFGSAASHLLILFTLNFTINLYEENWPG 73
DB	78	FTHRSSVSTSTPGTPTVYLGASKTPASIFGSAASHLLILFTLNFTINLYEENWPG 137
QY	74	SRKFNTERVLOGLLRPLFNTSVGLYSGCRLTLRPEKGEATGVDAICTHRPDPTGP 133
DB	138	SRKFNTERVLOGLLRPLFNTSVGLYSGCRLTLRPEKGEATGVDAICTHRPDPTGP 197
QY	134	GLDREQLYLELSQTHSITELGPTTLDRDLSLVNGFTHRSSVPTTGTGVVSEEPFLNFT 193
DB	198	GLDREQLYLELSQTHSITELGPTTLDRDLSLVNGFTHRSSVPTTGTGVVSEEPFLNFT 257
QY	194	INNLRYMADMGQPSLKFNTIDNMVKHLLSPFORSLGARYTGCRIALRSVKNGAETR 253
DB	258	INNLRYMADMGQPSLKFNTIDNMVKHLLSPFORSLGARYTGCRIALRSVKNGAETR 317
QY	254	VDLLCTYLQPLSGPGLPIKQVHELSSQTHGTRGLPYSLDKDLSVLYNGNEPDEPPT 313
DB	318	VDLLCTYLQPLSGPGLPIKQVHELSSQTHGTRGLPYSLDKDLSVLYNGNEPDEPPT 377
QY	314	TPKPATTFPLPSEATTAMGVHLKTLTLNFTINLYQSPDMGKGSATFNSTEGVLQHLR 373
DB	378	TPKPATTFPLPSEATTAMGVHLKTLTLNFTINLYQSPDMGKGSATFNSTEGVLQHLR 437
QY	374	PLFKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTTHPDVPGGLDIQOLYWELSOLTH 433
DB	438	PLFKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTTHPDVPGGLDIQOLYWELSOLTH 497
QY	434	GVTOLGFVLDRLDSLFNGVAPQNLISIRGEYQINFIHVNWNLSNPDPTSSSEYITLLRDIQ 493
DB	498	GVTOLGFVLDRLDSLFNGVAPQNLISIRGEYQINFIHVNWNLSNPDPTSSSEYITLLRDIQ 557
QY	494	DKVTTLYKGSQLDHDFRCLVTNLTMDSVLTVKALFSSNLDPSLVEQVFLDKTINASFH 553
DB	558	DKVTTLYKGSQLDHDFRCLVTNLTMDSVLTVKALFSSNLDPSLVEQVFLDKTINASFH 617
QY	554	WLGSTYQLVDIHVTMESVVOPTSSSTQHFYLNFTINLYPSQDKAOPGTTNVRNKR 613
DB	618	WLGSTYQLVDIHVTMESVVOPTSSSTQHFYLNFTINLYPSQDKAOPGTTNVRNKR 677
QY	614	NIEDALNQLFNSSIKSFSDQVSTFRSVPNRHHTGVDSLCNFSPLARRVDRVAIYEEF 673
DB	678	NIEDALNQLFNSSIKSFSDQVSTFRSVPNRHHTGVDSLCNFSPLARRVDRVAIYEEF 737
QY	674	LRMTNRTGQLQNFTLDRSSVLVDGYSNPNRBLTGN 710
DB	738	LRMTNRTGQLQNFTLDRSSVLVDGYSNPNRBLTGN 774

RESULT 9
ID AAB12552
XX AAB12552 standard; protein; 914 AA.
XX AAB12552;
AC AAB12552;
XX
XX 07-NOV-2000 (first entry)
XX Human ovarian carcinoma antigen O772P protein SEQ ID NO:312.
XX Human; ovarian carcinoma; ovarian cancer; therapy; diagnosis;
XX

tumour antigen; identification; cytostatic; gene therapy; vaccine.
Homo sapiens.
WO200036107-A2.
22-JUN-2000.
17-DEC-1999; 99WO-US0302070.
17-DEC-1998; 98US-00215681.
17-DEC-1998; 98US-00216003.
23-JUN-1999; 99US-00338933.
24-SEP-1999; 99US-00404879.
(CORI-) CORIXA CORP.
Mitcham JL, King GE, Algate PA, Frudakis TN;
WPI; 2000-431589/37.
N-PSDB; AAA70001.
Immunogenic portion of an ovarian carcinoma protein and the nucleic acid
encoding it, useful for the diagnosis, prevention and treatment of
cancer, preferably ovarian cancer.

Example 2; Page 172-174; 299pp; English.

The present invention describes an isolated polypeptide comprising an
immunogenic portion of an ovarian carcinoma protein (or its variant).
Ovarian carcinoma proteins, and polynucleotides encoding them, have
cytostatic activity and can be used in gene therapy and vaccines. Ovarian
carcinoma polypeptides, nucleic acids, antibodies and vaccines are useful
for the prevention, diagnosis and treatment of cancer, preferably ovarian
cancer. AAA9691 to AAA70077 and AAB12552 to AAB12557 represent human
ovarian carcinoma polynucleotides and proteins used in the
exemplification of the present invention

Sequence 914 AA;

Query Match	92.9%;	Score 3663;	DB 3;	Length 914;
Best Local Similarity	99.9%;	Pred. No. 2.2e-315;		
Matches	696;	Conservative 0;	Mismatches 1;	Indels 0; Gaps 0;
QY	14	FTHRSSVSTSTPGTPTVYLGASKTPASIFGSAASHLLILFTLNFTINLYEENWPG	73	
DB	159	FTHRSSVSTSTPGTPTVYLGASKTPASIFGSAASHLLILFTLNFTINLYEENWPG	218	
QY	74	SRKFNTERVLOGLLRPLFNTSVGLYSGCRLTLRPEKGEATGVDAICTHRPDPTGP	133	
DB	219	SRKFNTERVLOGLLRPLFNTSVGLYSGCRLTLRPEKGEATGVDAICTHRPDPTGP	278	
QY	134	GLDREQLYLELSQTHSITELGPTTLDRDLSLVNGFTHRSSVPTTGTGVVSEEPFLNFT	193	
DB	279	GLDREQLYLELSQTHSITELGPTTLDRDLSLVNGFTHRSSVPTTGTGVVSEEPFLNFT	338	
QY	194	INNLRYMADMGQPSLKFNTIDNMVKHLLSPFORSLGARYTGCRIALRSVKNGAETR	253	
DB	339	INNLRYMADMGQPSLKFNTIDNMVKHLLSPFORSLGARYTGCRIALRSVKNGAETR	398	
QY	254	VDLLCTYLQPLSGPGLPIKQVHELSSQTHGTRGLPYSLDKDLSVLYNGNEPDEPPT	313	
DB	399	VDLLCTYLQPLSGPGLPIKQVHELSSQTHGTRGLPYSLDKDLSVLYNGNEPDEPPT	458	
QY	314	TPKPATTFPLPSEATTAMGVHLKTLTLNFTINLYQSPDMGKGSATFNSTEGVLQHLR	373	
DB	459	TPKPATTFPLPSEATTAMGVHLKTLTLNFTINLYQSPDMGKGSATFNSTEGVLQHLR	518	
QY	374	PLFKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTTHPDVPGGLDIQOLYWELSOLTH	433	
DB	519	PLFKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTTHPDVPGGLDIQOLYWELSOLTH	578	
QY	434	GVTOLGFVLDRLDSLFNGVAPQNLISIRGEYQINFIHVNWNLSNPDPTSSSEYITLLRDIQ	493	

Db 579 GVTQLGQYVLDRLSLFNGYAPQNLIRGEYQINFIHVNWNLSPDPPTSSEYITLLRDIQ 638
 Qy 494 DKVTLLYKGSQQLHDTFRFCLVNTLTMDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFH 553
 Db 639 DKVTLLYKGSQQLHDTFRFCLVNTLTMDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFH 698
 Qy 554 WLGSYQLVDIHVTEMESSVYQPTSSSTQHFLNFTITNLPSYQDKAQPGTTNYQRNKR 613
 Db 699 WLGSYQLVDIHVTEMESSVYQPTSSSTQHFLNFTITNLPSYQDKAQPGTTNYQRNKR 758
 Qy 614 NIEDALNQLFRNSIKSYFSDCOVSTFRSPNRHHTGVDSLGNFSPPLARRVDRVAIYEEF 673
 Db 759 NIEDALNQLFRNSIKSYFSDCOVSTFRSPNRHHTGVDSLGNFSPPLARRVDRVAIYEEF 818
 Qy 674 LRMRNGTQLQNFLLDRSSVLVDGYSNRPNEPLTGN 710
 Db 819 LRMRNGTQLQNFLLDRSSVLVDGYSNRPNEPLTGN 855

RESULT 10
 AAB99203
 ID AAB99203 standard; protein; 914 AA.
 XX
 AC AAB99203;
 XX
 DT 04-SEP-2001 (first entry)
 XX
 DE Human ovarian tumour-derived antigen O772P.
 XX
 KW Cytostatic; human; breast tumour protein; breast cancer; ovarian tumour;
 antigen; O772P.
 XX
 OS Homo sapiens.
 XX
 PN WO200140269-A2.
 XX
 PD 07-JUN-2001.
 XX
 PF 29-NOV-2000; 2000WO-US032520.
 XX
 PR 30-NOV-1999; 99US-00451651.
 PR 22-FEB-2000; 2000US-00510662.
 PR 10-MAR-2000; 2000US-00523586.
 PR 07-APR-2000; 2000US-00545068.
 PR 15-MAY-2000; 2000US-00571025.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Dillon DC, Day CH, Jiang Y, Houghton RL, Mitcham JL, Wang A;
 WPI; 2001-356154/37.
 DR N-PSDB; AAH55680.
 XX
 PT Breast tumor polypeptides and the nucleic acids that encode them, useful
 for the prevention, diagnosis and treatment of breast cancer.
 XX
 PS Example 3; Page 187-188; 221pp; English.
 XX
 CC The present invention relates to human breast tumour protein coding
 sequences (see AAH55479-AAH55513, AAH55517-AAH55679 and AAH55682-
 CC AAH55762). The breast tumour protein DNA sequences may be used in the
 CC prevention, diagnosis and treatment of diseases associated with
 CC inappropriate expression of the breast tumour protein e.g. breast cancer.
 CC The present sequence is a human ovarian tumour-derived antigen, which was
 CC used in an example from the present invention

XX
 SQ Sequence 914 AA;
 Query Match 92.9%; Score 3663; DB 4; Length 914;
 Best Local Similarity 99.9%; Pred. No. 2.5e-315;
 Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 14 FTHRSSVSTSTPGTPTVYLGASKTPASIFGSPAASHLLILFTLNFTITNLRYEENWMPG 73
 Db 159 FTHRSSVSTSTPGTPTVYLGASKTPASIFGSPAASHLLILFTLNFTITNLRYEENWMPG 218
 Qy 74 SRKPNTTTERVLOGLLRPLPKNTSVGLYSQCRLLTLLRPEKGEATGVDAICTHRPDTGTP 133
 Db 219 SRKPNTTTERVLOGLLRPLPKNTSVGLYSQCRLLTLLRPEKGEATGVDAICTHRPDTGTP 278
 Qy 134 GLDREQLYLELSQLTHTSITELGPVTLDRDLSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 193
 Db 279 GLDREQLYLELSQLTHTSITELGPVTLDRDLSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 338
 Qy 194 INNLRYMADMGQPGSLKFNITDNMKHLLSPLRQSSLGARYTGCRRVIALRSVXQGAETR 253
 Db 339 INNLRYMADMGQPGSLKFNITDNMKHLLSPLRQSSLGARYTGCRRVIALRSVXQGAETR 398
 Qy 254 VDLCTYLOPLSGPGLPIKQVFHELSSQTHGITELGPYSLDKDSLVLNGYNEGPDPDPPT 313
 Db 399 VDLCTYLOPLSGPGLPIKQVFHELSSQTHGITELGPYSLDKDSLVLNGYNEGPDPDPPT 458
 Qy 314 TPKPATTFPLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLOHLR 373
 Db 459 TPKPATTFPLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLOHLR 518
 Qy 374 PLPQKSSMGPFYLGCOLISLRPEKGAATGVDTCTTTHPDPVGPGLDIQOLYWELSQLT 433
 Db 519 PLPQKSSMGPFYLGCOLISLRPEKGAATGVDTCTTTHPDPVGPGLDIQOLYWELSQLT 578
 Qy 434 GVTQLGQYVLDRLSLFNGYAPQNLIRGEYQINFIHVNWNLSPDPPTSSEYITLLRDIQ 493
 Db 579 GVTQLGQYVLDRLSLFNGYAPQNLIRGEYQINFIHVNWNLSPDPPTSSEYITLLRDIQ 638
 Qy 494 DKVTLLYKGSQQLHDTFRFCLVNTLTMDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFH 553
 Db 639 DKVTLLYKGSQQLHDTFRFCLVNTLTMDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFH 698
 Qy 554 WLGSYQLVDIHVTEMESSVYQPTSSSTQHFLNFTITNLPSYQDKAQPGTTNYQRNKR 613
 Db 699 WLGSYQLVDIHVTEMESSVYQPTSSSTQHFLNFTITNLPSYQDKAQPGTTNYQRNKR 758
 Qy 614 NIEDALNQLFRNSIKSYFSDCOVSTFRSPNRHHTGVDSLGNFSPPLARRVDRVAIYEEF 673
 Db 759 NIEDALNQLFRNSIKSYFSDCOVSTFRSPNRHHTGVDSLGNFSPPLARRVDRVAIYEEF 818
 Qy 674 LRMRNGTQLQNFLLDRSSVLVDGYSNRPNEPLTGN 710
 Db 819 LRMRNGTQLQNFLLDRSSVLVDGYSNRPNEPLTGN 855

RESULT 11
 ABP30968
 ID ABP30968 standard; protein; 914 AA.
 XX
 AC ABP30968;
 XX
 DT 02-JUL-2002 (first entry)
 XX
 DE Hypothetical protein sequence for clone 0772P.
 XX
 KW Human; immunostimulant; cytostatic; cancer; ovarian carcinoma.
 XX
 OS Homo sapiens.
 XX
 PN WO200206317-A2.
 XX
 PD 24-JAN-2002.
 XX
 PF 17-JUL-2001; 2001WO-US022635.
 XX
 PR 17-JUL-2000; 2000US-00617747.
 PR 10-AUG-2000; 2000US-00636801.
 PR 20-SEP-2000; 2000US-00667857.
 PR 04-APR-2001; 2001US-00827271.

```
PR 18-JUN-2001; 2001US-00884441.
XX (CORI-) CORIXA CORP.
XX Mitcham JL, King GE, Algate PA, Fling SP, Retter MW, Fanger GR;
XX Reed SG, Vedvick TS, Carter D, Hill P, Albone E;
XX WPI; 2002-164781/21.
DR N-PSDB; ABN72974.
XX Polypeptides comprising an immunogenic portion of an ovarian carcinoma
PT protein or its variants, useful for stimulating an immune response in a
PT patient and treating ovarian cancer.
XX Disclosure; Page 350-352; 408pp; English.
XX This invention relates to polypeptides comprising an immunogenic portion
CC of an ovarian carcinoma protein which acts as an immunostimulant and is
CC cytotatic. The polypeptides, polynucleotides, antibodies, fusion
CC proteins, T cell populations and antigen presenting cells that express
CC the polypeptides are useful for stimulating an immune response in a
CC patient and treating ovarian cancer. This sequence represents protein
CC related to the invention
XX
XX SQ Sequence 914 AA;
Query Match 92.9%; Score 3663; DB 5; Length 914;
Best Local Similarity 99.9%; Pred. No. 2.5e-315;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 14 FTHRSSVSTTSTPGTPTVYLKASITPASIFGPAASHLLILFTLNTLNRYEENMWP 73
DB 159 FTHRSSVSTTSTPGTPTVYLKASITPASIFGPAASHLLILFTLNTLNRYEENMWP 218
QY 74 SRKFNTERVQLGLRLPLFKNTSVGLYSGCRLTLRLPEKDGATGVDAICTHRPDP 133
DB 219 SRKFNTERVQLGLRLPLFKNTSVGLYSGCRLTLRLPEKDGATGVDAICTHRPDP 278
QY 134 GLDRQLYLELSQTHSITELGPTLDRDSLRYNGFTHRSSVPTTSTGVVSEEPFLNFT 193
DB 279 GLDRQLYLELSQTHSITELGPTLDRDSLRYNGFTHRSSVPTTSTGVVSEEPFLNFT 338
QY 194 INNLRVYMDMGPQGLSKFNITDNNVHLLSPFORSSIGARYTCRVIARSVKNGAETR 253
DB 339 INNLRVYMDMGPQGLSKFNITDNNVHLLSPFORSSIGARYTCRVIARSVKNGAETR 398
QY 254 VDLICTVLOPLSGPLPIKQVHLSQTHGITRLGYSVLDKSLYNGYNEPDPDPPT 313
DB 399 VDLCTVLOPLSGPLPIKQVHLSQTHGITRLGYSVLDKSLYNGYNEPDPDPPT 458
QY 314 TPKPATTFPLPSEATTAMGYHLKTLTLNFTISNLQYSPDMGKSATFNSTEGVLQHLR 373
DB 459 TPKPATTFPLPSEATTAMGYHLKTLTLNFTISNLQYSPDMGKSATFNSTEGVLQHLR 518
QY 374 PLFQKSMGPFYLGQCLISLPEKDGATGVDTTCTHDPDPVGLDITQQLYWELSQLTH 433
DB 519 PLFQKSMGPFYLGQCLISLPEKDGATGVDTTCTHDPDPVGLDITQQLYWELSQLTH 578
QY 434 GTVQLGFTVLDRLSLFINGYAPONLSIRGEVQINPHIVNWLNSNPDPTSSEVITLRLDIQ 493
DB 579 GTVQLGFTVLDRLSLFINGYAPONLSIRGEVQINPHIVNWLNSNPDPTSSEVITLRLDIQ 638
QY 494 DKVTLLYKGSQSLHDFRCLVNTLMDSVLTVKALFSSNLDPSLVEQVFLDKTLNASFH 553
DB 639 DKVTLLYKGSQSLHDFRCLVNTLMDSVLTVKALFSSNLDPSLVEQVFLDKTLNASFH 698
QY 554 WLGSYQLVDIHVTEMSSSVQPTSSSTQHLYNFTITNLPYSQDKAQPGTNTYQRNKR 613
DB 699 WLGSYQLVDIHVTEMSSSVQPTSSSTQHLYNFTITNLPYSQDKAQPGTNTYQRNKR 758
QY 614 NIEDALNQLFRNSSIKSYFSDQVSTFRVNRHHTGVDSLNCNFSPLARRVDRVAIYEEF 673
DB 759 NIEDALNQLFRNSSIKSYFSDQVSTFRVNRHHTGVDSLNCNFSPLARRVDRVAIYEEF 818
```

```
QY 674 LEWTRNGTOLQNFILDRSSVLVDGYSPNREPLTGN 710
DB 819 LEWTRNGTOLQNFILDRSSVLVDGYSPNREPLTGN 855
RESULT 12
ABP30896
ID ABP30896 standard; protein; 914 AA.
XX
XX AC ABP30896;
XX 02-JUL-2002 (first entry)
XX 0772P protein.
XX Human; immunostimulant; cytostatic; cancer; ovarian carcinoma.
XX KW Homo sapiens.
XX OS Homo sapiens.
XX PN W0200206317-A2.
XX PD 24-JAN-2002.
XX PF 17-JUL-2001; 2001WO-US022635.
XX PR 17-JUL-2000; 2000US-00617747.
XX PR 10-AUG-2000; 2000US-00636801.
XX PR 20-SEP-2000; 2000US-00667857.
XX PR 04-APR-2001; 2001US-00827271.
XX PR 18-JUN-2001; 2001US-00884441.
XX (CORI-) CORIXA CORP.
XX Mitcham JL, King GE, Algate PA, Fling SP, Retter MW, Fanger GR;
XX Reed SG, Vedvick TS, Carter D, Hill P, Albone E;
XX WPI; 2002-164781/21.
XX N-PSDB; ABN72895.
XX Polypeptides comprising an immunogenic portion of an ovarian carcinoma
PT protein or its variants, useful for stimulating an immune response in a
PT patient and treating ovarian cancer.
XX Example 2; Page 291; 408pp; English.
XX This invention relates to polypeptides comprising an immunogenic portion
CC of an ovarian carcinoma protein which acts as an immunostimulant and is
CC cytotatic. The polypeptides, polynucleotides, antibodies, fusion
CC proteins, T cell populations and antigen presenting cells that express
CC the polypeptides are useful for stimulating an immune response in a
CC patient and treating ovarian cancer. This sequence represents protein
CC related to the invention
XX
XX SQ Sequence 914 AA;
Query Match 92.9%; Score 3663; DB 5; Length 914;
Best Local Similarity 99.9%; Pred. No. 2.5e-315;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 14 FTHRSSVSTTSTPGTPTVYLKASITPASIFGPAASHLLILFTLNTLNRYEENMWP 73
DB 159 FTHRSSVSTTSTPGTPTVYLKASITPASIFGPAASHLLILFTLNTLNRYEENMWP 218
QY 74 SRKFNTERVQLGLRLPLFKNTSVGLYSGCRLTLRLPEKDGATGVDAICTHRPDP 133
DB 219 SRKFNTERVQLGLRLPLFKNTSVGLYSGCRLTLRLPEKDGATGVDAICTHRPDP 278
QY 134 GLDRQLYLELSQTHSITELGPTLDRDSLRYNGFTHRSSVPTTSTGVVSEEPFLNFT 193
DB 279 GLDRQLYLELSQTHSITELGPTLDRDSLRYNGFTHRSSVPTTSTGVVSEEPFLNFT 338
QY 194 INNLRVYMDMGPQGLSKFNITDNNVHLLSPFORSSIGARYTCRVIARSVKNGAETR 253
```


Db 339 INNLRYMADMGQPSGLKFNITDNVMKHLSPFQSSSLGARYTGCRVIALRSVKNAGETR 398
QY 254 VDLCTYQLPSLPGPIKQVHFELSOOTHGIRLGPYSLDKDSLYLNGVNBEPGPBPPT 313
Db 399 VDLCTYQLPSLPGPIKQVHFELSOOTHGIRLGPYSLDKDSLYLNGVNBEPGPBPPT 458
QY 314 TPKPATTFLPPLSEATTAMGYHLKTLTNTFTISNLQYSPDMGKGSATFNSGVLQHLR 373
Db 459 TPKPATTFLPPLSEATTAMGYHLKTLTNTFTISNLQYSPDMGKGSATFNSGVLQHLR 518
QY 374 PLFQKSSMGPPYLGCCILSRPEKGAATGVDCTTCTHYHDPVCPGLDIOQLYWELSQLTH 433
Db 519 PLFQKSSMGPPYLGCCILSRPEKGAATGVDCTTCTHYHDPVCPGLDIOQLYWELSQLTH 578
QY 434 GVTQLGFVYLDRLDSLFNGVAPQNLISIRGEYQINFNHIVNWNLSNPDPPTSEYITLLRDQ 493
Db 579 GVTQLGFVYLDRLDSLFNGVAPQNLISIRGEYQINFNHIVNWNLSNPDPPTSEYITLLRDQ 638
QY 494 DKVTTLVKGSLQHDTRFCLVNTLMTDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFH 553
Db 639 DKVTTLVKGSLQHDTRFCLVNTLMTDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFH 698
QY 554 WLGSTYQLVDIHVTEMESSYQPTSSSTQHFYLNFTITNLVPSQKAPGTTNYQNRK 613
Db 699 WLGSTYQLVDIHVTEMESSYQPTSSSTQHFYLNFTITNLVPSQKAPGTTNYQNRK 758
QY 614 NIEDALNQLFRNSIISYSDCOVSTFRSVPNRHRTGVDSLCNPSPLARRVDRVAIYEEF 673
Db 759 NIEDALNQLFRNSIISYSDCOVSTFRSVPNRHRTGVDSLCNPSPLARRVDRVAIYEEF 818
QY 674 LRMRNGTQLQNFTRDSSVLDVGYSPNRNEPLTGNS 710
Db 819 LRMRNGTQLQNFTRDSSVLDVGYSPNRNEPLTGNS 855
RESULT 13
ID ADU01425
XX ADU01425 standard; protein; 914 AA.
XX ADU01425;
XX
DT 30-DEC-2004 (first entry)
XX
DE Breast cancer associated polypeptide seqid 206.
XX
KW cytostatic; gene therapy; vaccine; breast cancer; cancer; tumour;
KW immune response; O8E; vaccine.
XX
OS Homo sapiens.
XX
PN US2002081609-A1.
XX
PD 27-JUN-2002.
XX
PF 20-JUL-2001; 2001US-00910689.
XX
PR 10-NOV-1999; 99US-00451651.
PR 22-FEB-2000; 2000US-00510662.
PR 10-MAR-2000; 2000US-00523586.
PR 07-APR-2000; 2000US-00545068.
PR 15-MAY-2000; 2000US-00571025.
PR 06-FEB-2001; 2001US-00778320.
XX
XX (DILL/) DILLON D C.
PA (DAYC/) DAY C H.
PA (JIAN/) JIANG Y.
PA (HOUG/) HOUGHTON R L.
PA (MITC/) MITCHAM J L.
PA (WANG/) WANG T.
PA (MCNE/) MCNEILL P D.
PA (HARL/) HARLOCKER S L.
XX

PI Dillon DC, Day CH, Jjiang Y, Houghton RL, Mitcham JL, Wang T;
PI McNeill PD, Harlocker SL;
XX WPI; 2002-657500/70.
DR N-PSDB; ADU01424.
XX
PT Novel breast cancer polynucleotides and polypeptides encoded by the
PT polynucleotides, useful for detecting the presence of breast cancer in
PT patient, and in pharmaceutical compositions, for treating breast cancer.
XX
PS Claim 2; SEQ ID NO 206; 159pp; English.
XX
CC The invention describes an isolated breast cancer polynucleotide (I)
CC comprising a sequence (S1) selected from the 249 nucleotide sequences
CC fully defined in the specification, complements of S1, a sequence that
CC comprising at least 20 contiguous residues of S1, a sequence that
CC hybridise to S1, under moderately stringent conditions, a sequence having
CC at least 75%, preferably 90% identity to S1, or degenerate variants of
CC S1. Also described are: an isolated polypeptide (II) encoded by (I), or
CC sequences having at least 70%, preferably 90% identity to (I); an
CC expression vector (III); a host cell (IV) transformed or transfected with
CC (III); an isolated antibody (Ab) that specifically binds to (II);
CC detecting (M1) the presence of cancer in a patient; a fusion protein (V)
CC comprising (II); an oligonucleotide (VI) that hybridises to S1;
CC stimulating and/or expanding (M2) T cells specific for a tumour protein;
CC a composition (C) comprising physiologically acceptable carriers and
CC immunostimulants as first component, and a second component selected from
CC (I), (II), Ab, (VI), (VII) and antigen presenting cells that express (II);
CC and inhibiting (M3) the development of a cancer in a patient. (C) is
CC useful for stimulating immune response in a patient, and for treating
CC cancer in a patient. (VI) is useful for determining the presence of
CC cancer in a patient, by obtaining a biological sample from the patient,
CC contacting the biological sample with a monoclonal antibody that bind to
CC O8E, isolating cells that bind to the antibody that binds to O8E,
CC isolating polynucleotides from the isolated cells, and contacting the
CC polynucleotides with (VI), detecting an amount of polynucleotides that
CC hybridise to the oligonucleotide, and comparing the amount of
CC polynucleotides that hybridise to the oligonucleotide to a predetermined
CC cut-off value, and thus determining the presence of cancer in the
CC patient. (I) and (II) are useful in pharmaceutical compositions, e.g.
CC vaccines. (I) is useful in the design and preparation of ribozyme
CC molecules for inhibiting expression of the tumour polypeptides and
CC proteins in tumour cells. (I) is useful as marker to indicate the
CC presence or absence of a cancer such as breast cancer. (C) is useful for
CC inhibiting the development of breast cancer in a patient, and for
CC removing tumour cells from a biological sample. Ab (binding agent for
CC (I)) is useful for detecting the presence of cancer in a patient. This
CC sequence represents a breast cancer associated protein.
XX
SQ Sequence 914 AA;
Query Match 92.9%; Score 3663; DB 5; Length 914;
Best Local Similarity 99.9%; Pred. No. 2.5e-315; Indels 0; Gaps 0;
Matches 696; Conservative 0; Mismatches 1;
QY 14 FTHRSSVSTTSTPGTPTVYLGASKTPASIFGSAASHLLILFTLNTITNLRYEENWPG 73
Db 159 FTHRSSVSTTSTPGTPTVYLGASKTPASIFGSAASHLLILFTLNTITNLRYEENWPG 218
QY 74 SRKFNTTERTVLOGLLPLPKNTSVGLYSGCRLLTLRPEKDGATGVDAICTHRPDTGP 133
Db 219 SRKFNTTERTVLOGLLPLPKNTSVGLYSGCRLLTLRPEKDGATGVDAICTHRPDTGP 278
QY 134 GLDREQLYLELSQTHSITELGPYTLDRDLSLVNGFTHRSSVPTTGTGVVSEBPFLLNFT 193
Db 279 GLDREQLYLELSQTHSITELGPYTLDRDLSLVNGFTHRSSVPTTGTGVVSEBPFLLNFT 338
QY 194 INNLRYMADMGQPSGLKFNITDNVMKHLSPFQSSSLGARYTGCRVIALRSVKNAGETR 253
Db 339 INNLRYMADMGQPSGLKFNITDNVMKHLSPFQSSSLGARYTGCRVIALRSVKNAGETR 398
QY 254 VDLCTYQLPSLPGPIKQVHFELSOOTHGIRLGPYSLDKDSLYLNGVNBEPGPBPPT 313

Db 399 VDLLCTYLQPLSGPLPIKQVHFLSQTHGTRIGLPSYSLDKSLYNGYNEPGDPPT 458
Qy 314 TPKPATTFPLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFSTGVQLHLR 373
Db 459 TPKPATTFPLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFSTGVQLHLR 518
Qy 374 PLFKSSMGPFYLGCLISLRPEKGAATGVDTTCTVHPDPVPGGLDIQQLYNELSOLTH 433
Db 519 PLFKSSMGPFYLGCLISLRPEKGAATGVDTTCTVHPDPVPGGLDIQQLYNELSOLTH 578
Qy 434 GVTQLGPFYVLDRLDSFLNGYAPQNLISIRGEYQINFIHVNWNLNPDPTSEYITLLRDIQ 493
Db 579 GVTQLGPFYVLDRLDSFLNGYAPQNLISIRGEYQINFIHVNWNLNPDPTSEYITLLRDIQ 638
Qy 494 DKVTTLKGSQQLHDTFRFCLVNTLWDSVLVTKALFSSNLDSLVEQVFLDKTLNASFH 553
Db 639 DKVTTLKGSQQLHDTFRFCLVNTLWDSVLVTKALFSSNLDSLVEQVFLDKTLNASFH 698
Qy 554 WLGSYQLVDIHVTMESSVYQPTSSSTQHFYLNFTITNLPSQDKAQPCTTNYQRNKR 613
Db 699 WLGSYQLVDIHVTMESSVYQPTSSSTQHFYLNFTITNLPSQDKAQPCTTNYQRNKR 758
Qy 614 NIEDALNQLFRNSIKSYFSDCQVSTFRSPNRHHTGVDSLNCNFSPLARRVDRVAIYEEF 673
Db 759 NIEDALNQLFRNSIKSYFSDCQVSTFRSPNRHHTGVDSLNCNFSPLARRVDRVAIYEEF 818
Qy 674 LRMTNQTQNFILDRSSVLVDGYSNRPNEPLTGN 710
Db 819 LRMTNQTQNFILDRSSVLVDGYSNRPNEPLTGN 855

RESULT 14

ADZ41689
ID ADZ41689 standard; protein; 914 AA.
XX
AC ADZ41689;
XX
DT 16-JUN-2005 (first entry)
XX
DE Human breast cancer associated protein SEQ ID NO 206.
XX
KW cytostatic; gene therapy; vaccine; diagnosis; cancer; pharmaceutical; cancer;
KW neoplasm; breast tumor; endocrine disease; gynecology and obstetrics.
OS Homo sapiens.
XX
PN W0200262203-A2.
XX
PD 15-AUG-2002.
XX
PF 04-FEB-2002; 2002WO-US003332.
XX
PR 06-FEB-2001; 2001US-00778320.
PR 20-JUL-2001; 2001US-00910689.
PR 30-NOV-2001; 2001US-00010742.
XX
PA (CORI-) CORIXA CORP.
XX
PI Dillion DC, Day CH, Jiang Y, Houghton RL, Mitcham JL, Wang T;
PI McNeill PD, Harlocker SL, Bennington AA, Zehentner B, Fanger GR;
PI Retter MW;
XX
DR WPI; 2002-657500/70.
DR N-PSDB; ADZ41688.
XX
XX Novel breast cancer polynucleotides and polypeptides encoded by the
PT polynucleotides, useful for detecting the presence of breast cancer in
PT patient, and in pharmaceutical compositions, for treating breast cancer.
XX
XX Claim 2; SEQ ID NO 206; 237pp; English.
PS
XX The invention describes an isolated breast cancer polynucleotide (I)
CC comprising a sequence (S1) selected from the 249 nucleotide sequences
CC

CC fully defined in the specification, complements of S1, a sequence
CC comprising at least 20 contiguous residues of S1, a sequence that
CC hybridize to S1, under moderately stringent conditions, a sequence having
CC at least 75%, preferably 90% identity to S1, or degenerate variants of
CC S1. Also described are: an isolated polypeptide (II) comprising a
CC sequence (S2) selected from any one of the 11 sequences mentioned in the
CC specification, sequences encoded by (I), or sequences having at least
CC 70%, preferably 90% identity to (I); an expression vector (III)
CC comprising (I) operably linked to an expression control sequence; a host
CC cell (IV) transformed or transfected with (III); an isolated antibody
CC (Ab) or its antigen-binding fragment, that specifically binds to (II);
CC detecting (M1) the presence of cancer in a patient; a fusion protein (V)
CC comprising (II); an oligonucleotide (VI) that hybridizes to S1;
CC stimulating and/or expanding (M2) T cells specific for a tumor protein;
CC an isolated T cell population (VII), comprising T cells prepared by (M2);
CC a composition (C) comprising physiologically acceptable carriers and
CC immunostimulants as first component, and a second component selected from
CC (I), (II), Ab, (V), (VII) and antigen presenting cells that express (II);
CC a diagnostic kit (VIII) comprising (VI), or Ab and a detection reagent
CC comprising a reporter group; and inhibiting (M3) the development of a
CC cancer in a patient, by incubating CD4+ and/or CD8+ T cells isolated from
CC a patient with (I), (II) or antigen presenting cells that express (II), the
CC so that T cell proliferate, administering the proliferated T cells to the
CC patient, and therefore inhibiting the development of a cancer in the
CC patient. The following are disclosed: monitoring the progression of
CC cancer; fragments of (II); (xenogeneic) variants of (I); polynucleotide
CC compositions comprising antisense oligonucleotide; and kit for use in
CC diagnostic methods. (C) is useful for stimulating immune response in a
CC patient, and for treating cancer in a patient. (VI) is useful for
CC determining the presence of cancer in a patient. (I) and (II) are useful
CC in pharmaceutical compositions, e.g. vaccines. (I) is useful in the
CC design and preparation of ribozyme molecules for inhibiting expression of
CC the tumor polypeptides and proteins in tumor cells. (I) is useful as
CC marker to indicate the presence or absence of a cancer such as breast
CC cancer. (C) is useful for inhibiting the development of breast cancer in
CC a patient, and for removing tumor cells from a biological sample. Ab
CC (binding agent for (I)) is useful for detecting the presence of cancer in
CC a patient. This is the amino acid sequence of a breast cancer associated
CC protein. Note: This sequence has been extracted from the sequence listing
CC of a corrected version of the specification published on the 3rd of March
CC 2005.
XX

Sequence 914 AA;

Query Match 92.9%; Score 3663; DB 5; Length 914;
Best Local Similarity 99.9%; Pred. No. 2.5e-315;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 14 FTHRSSVSTSTPGTPTVILGASKTPASIFGPSAASHLLILFTLFTITNLRYEENMWPG 73
Db 159 FTHRSSVSTSTPGTPTVILGASKTPASIFGPSAASHLLILFTLFTITNLRYEENMWPG 218
Qy 74 SRKFNTTERTVQLGLRPLFKNTSVGLYSGRITLLRPEKDGATGVDAICTHRPDPPTGP 133
Db 219 SRKFNTTERTVQLGLRPLFKNTSVGLYSGRITLLRPEKDGATGVDAICTHRPDPPTGP 278
Qy 134 GLDREQLYELSQLTHSITELGPVYTLDRDSLNYNGFTHRSSVPTTSVGVSEEPFTLNFT 193
Db 279 GLDREQLYELSQLTHSITELGPVYTLDRDSLNYNGFTHRSSVPTTSVGVSEEPFTLNFT 338
Qy 194 INNLRYMADMGQPGSLKFNITDNVMKLLSPLFORSSLGARYTGCRIALRSVNGAETR 253
Db 339 INNLRYMADMGQPGSLKFNITDNVMKLLSPLFORSSLGARYTGCRIALRSVNGAETR 398
Qy 254 VDLLCTYLQPLSGPLPIKQVHFLSQTHGTRIGLPSYSLDKSLYNGYNEPGDPPT 313
Db 399 VDLLCTYLQPLSGPLPIKQVHFLSQTHGTRIGLPSYSLDKSLYNGYNEPGDPPT 458
Qy 314 TPKPATTFPLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFSTGVQLHLR 373
Db 459 TPKPATTFPLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFSTGVQLHLR 518
Qy 374 PLFKSSMGPFYLGCLISLRPEKGAATGVDTTCTVHPDPVPGGLDIQQLYNELSOLTH 433

|||||
519 PLFKSSMGPFYLGQQLISLRPEKGAATGVTCTYHPDPVGPGLDIQOLYWELSQLTH 578
QY 434 GVTQLGPFYVLDRLSLFNGYAPQNLISIRGEYQINFHIVNWNLSNPDPPTSEYITLLRDIQ 493
Db 579 GVTQLGPFYVLDRLSLFNGYAPQNLISIRGEYQINFHIVNWNLSNPDPPTSEYITLLRDIQ 638
QY 494 DKVTTLTKGSQLHDTFRFCLVNTLWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFH 553
Db 639 DKVTTLTKGSQLHDTFRFCLVNTLWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFH 698
QY 554 WLGSTYQLVDIHVTESSVYQPTSSSTQHFYLNFTITNLPSYQDKAOPGTTNYQRNKR 613
Db 699 WLGSTYQLVDIHVTESSVYQPTSSSTQHFYLNFTITNLPSYQDKAOPGTTNYQRNKR 758
QY 614 NIEDALNQLFRNSSIKSYFSDCOVSTFRSPVNRHHTGVDSLNCNFSPLARRVDRVAIYEEF 673
Db 759 NIEDALNQLFRNSSIKSYFSDCOVSTFRSPVNRHHTGVDSLNCNFSPLARRVDRVAIYEEF 818
QY 674 LRMRNGTQLQNTLDRSSVLVDGYSPNRNEPLTGNS 710
Db 819 LRMRNGTQLQNTLDRSSVLVDGYSPNRNEPLTGNS 855

RESULT 15
ADA08631
ID ADA08631 standard; protein; 914 AA.

AC ADA08631,
XX
DT 06-NOV-2003 (first entry)
XX
DE Human O772P partial protein #1.
DE human; gene therapy; ovarian cancer; cancer.
OS Homo sapiens.

XX
XX US2003091580-A1.
XX
XX 15-MAY-2003.
XX
XX 17-JUL-2001; 2001US-00907969.
XX
XX 18-JUN-2001; 2001US-00884441.

XX (MITC/) MITCHAM J L.
XX (KING/) KING G E.
XX (ALGA/) ALGATE P A.
XX (FLIN/) FLING S P.
XX (RETT/) RETTER M W.
XX (FANG/) FANGER G R.
XX (REED/) REED S G.
XX (VEDV/) VEDVICK T S.
XX (CART/) CARTER D.
XX (HILL/) HILL P.
XX (ALBO/) ALBONE E.

XX Mitcham JL, King GE, Algate PA, Fling SP, Retter MW, Fanger GR;
PI Reed SG, Vedvick TS, Carter D, Hill P, Albone E;
XX WPI; 2003-532352/50.
XX
XX New isolated O772P polypeptides and polynucleotides, useful in gene
XX therapy, particularly for treating or diagnosing cancer, e.g. ovarian
XX cancer.

XX Example 13; SEQ ID NO 478; 371pp; English.
XX
XX The invention relates to an isolated O772P polypeptide, which has the
XX structure fully defined in the specification. The composition containing
XX the polypeptides, polynucleotides, fusion proteins, antibodies, T-cells
XX or antigen presenting cells are useful for stimulating an immune response

CC and treating ovarian cancer. Detecting the presence of the
CC polynucleotides and polypeptides is useful for diagnosing cancer. Ovarian
CC carcinoma cDNAs and protein cDNAs were identified using microarray
CC technology. The present sequence represents a human ovarian carcinoma
CC antigen.
XX
SQ Sequence 914 AA;

Query Match 92.9%; Score 3663; DB 7; Length 914;
Best Local Similarity 99.9%; Pred. No. 2.5e-315;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 FTHRSVSTSTPCTPTVYLGASKTPASIFGSPAASHLLILFTLNTITNLRYSNWP 73
Db 159 FTHRSVSTSTPCTPTVYLGASKTPASIFGSPAASHLLILFTLNTITNLRYSNWP 218
QY 74 SRKFNTERVLOQLRPLFNKTSVGLYSGCRLLTLRPEKGEATGVDAICTHRPDP 133
Db 219 SRKFNTERVLOQLRPLFNKTSVGLYSGCRLLTLRPEKGEATGVDAICTHRPDP 278
QY 134 GLDREQLYLELSQLTHSITELGPTLDRDSLXYNGFTHRSSVPTTSTGVVSEFP 193
Db 279 GLDREQLYLELSQLTHSITELGPTLDRDSLXYNGFTHRSSVPTTSTGVVSEFP 338
QY 194 INNLRYMADMGQPSLKFNITDNMKHLLSPLFORSSLGARTGCRVIALRSVNGAETR 253
Db 339 INNLRYMADMGQPSLKFNITDNMKHLLSPLFORSSLGARTGCRVIALRSVNGAETR 398
QY 254 VDLCTYQLPLSGPGLPIKQVFHELSQOQTHGTRGLGYSLDKSLYLVNGVNEGPDP 313
Db 399 VDLCTYQLPLSGPGLPIKQVFHELSQOQTHGTRGLGYSLDKSLYLVNGVNEGPDP 458
QY 314 TPKPATTFLPPLSEATTANGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLOHLLR 373
Db 459 TPKPATTFLPPLSEATTANGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLOHLLR 518
QY 374 PLFQKSSMGPFYLGQQLISLRPEKGAATGVTCTYHPDPVGPGLDIQOLYWELSQLTH 433
Db 519 PLFQKSSMGPFYLGQQLISLRPEKGAATGVTCTYHPDPVGPGLDIQOLYWELSQLTH 578
QY 434 GVTQLGPFYVLDRLSLFNGYAPQNLISIRGEYQINFHIVNWNLSNPDPPTSEYITLLRDIQ 493
Db 579 GVTQLGPFYVLDRLSLFNGYAPQNLISIRGEYQINFHIVNWNLSNPDPPTSEYITLLRDIQ 638
QY 494 DKVTTLTKGSQLHDTFRFCLVNTLWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFH 553
Db 639 DKVTTLTKGSQLHDTFRFCLVNTLWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFH 698
QY 554 WLGSTYQLVDIHVTESSVYQPTSSSTQHFYLNFTITNLPSYQDKAOPGTTNYQRNKR 613
Db 699 WLGSTYQLVDIHVTESSVYQPTSSSTQHFYLNFTITNLPSYQDKAOPGTTNYQRNKR 758
QY 614 NIEDALNQLFRNSSIKSYFSDCOVSTFRSPVNRHHTGVDSLNCNFSPLARRVDRVAIYEEF 673
Db 759 NIEDALNQLFRNSSIKSYFSDCOVSTFRSPVNRHHTGVDSLNCNFSPLARRVDRVAIYEEF 818
QY 674 LRMRNGTQLQNTLDRSSVLVDGYSPNRNEPLTGNS 710
Db 819 LRMRNGTQLQNTLDRSSVLVDGYSPNRNEPLTGNS 855

RESULT 16
ADA08465

ID ADA08465 standard; protein; 914 AA.
XX
AC ADA08465;

XX 06-NOV-2003 (first entry)
XX
XX Human ovarian carcinoma antigen O772P.
XX human; gene therapy; ovarian cancer; cancer.
XX

OS Homo sapiens.
XX US2003091580-A1.
XX PD 15-MAY-2003.
XX PF 17-JUL-2001; 2001US-00907969.
XX PR 18-JUN-2001; 2001US-00884441.
XX (MITC/) MITCHAM J L.
XX (KING/) KING G E.
XX (ALGA/) ALGATE P A.
XX (FLIN/) FLING S P.
XX (RETT/) RETTER M W.
XX (FANG/) FANGER G R.
XX (REED/) REED S G.
XX (VEDV/) VEDVICK T S.
XX (CART/) CARTER D.
XX (HILL/) HILL P.
XX (ALBO/) ALBONE E.
XX Mitcam JL, King GE, Algate PA, Fling SP, Retter MW, Fanger GR;
XX Reed SG, Vedvick TS, Carter D, Hill P, Albone E;
XX WPI; 2003-532352/50.
XX DR N-PSDB; ADA09060.
XX New isolated O772P polypeptides and polynucleotides, useful in gene
XX therapy, particularly for treating or diagnosing cancer, e.g. ovarian
XX cancer.
XX Example 2; SEQ ID NO 312; 371pp; English.
XX The invention relates to an isolated O772P polypeptide, which has the
XX structure fully defined in the specification. The composition containing
XX the polypeptides, polynucleotides, fusion proteins, antibodies, T-cells
XX or antigen presenting cells are useful for stimulating an immune response
XX and treating ovarian cancer. Detecting the presence of the
XX polynucleotides and polypeptides is useful for diagnosing cancer. Ovarian
XX carcinoma cDNAs and protein cDNAs were identified using microarray
XX technology. The present sequence represents a human ovarian carcinoma
XX antigen.
XX SQ Sequence 914 AA;
Query Match 92.9%; Score 3663; DB 7; Length 914;
Best Local Similarity 99.9%; Pred. No. 2.5e-315;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 14 FTHRSSVSTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWPG 73
DB 159 FTHRSSVSTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWPG 218
QY 74 SRKENTTERTVQLRLPLFKNTSGPLYSGCRLTLRLPEKDGATGVDAICTHRPDTGP 133
DB 219 SRKENTTERTVQLRLPLFKNTSGPLYSGCRLTLRLPEKDGATGVDAICTHRPDTGP 278
QY 134 GLDREQLYLELSQLTHSTITELGPTLDRDLSLYNNGFTHRSSVPTTSTGVSEEPFTLNFT 193
DB 279 GLDREQLYLELSQLTHSTITELGPTLDRDLSLYNNGFTHRSSVPTTSTGVSEEPFTLNFT 338
QY 194 INNLRVMDMGQPSGLKFNITDNNVKHLLSPLFORSSIGARYTCRVIALRSVKNGAETR 253
DB 339 INNLRVMDMGQPSGLKFNITDNNVKHLLSPLFORSSIGARYTCRVIALRSVKNGAETR 398
QY 254 VDLICTVYLQPLSGPLPTKQVFHELSQOHTGITRLGPVSLDKSLYNGNEPGRDDEPT 313
DB 399 VDLICTVYLQPLSGPLPTKQVFHELSQOHTGITRLGPVSLDKSLYNGNEPGRDDEPT 458
QY 314 TPKPATTFPLPSEATTAMGYHLKTLTLNFTISNLOYSPDMGKGSATFNSTEGVLOHLR 373
DB 459 TPKPATTFPLPSEATTAMGYHLKTLTLNFTISNLOYSPDMGKGSATFNSTEGVLOHLR 518

374 PLFOKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVGPGLDIQOLYWELSQLTH 433
DB 519 PLFOKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVGPGLDIQOLYWELSQLTH 578
QY 434 GVTQLGFFVLDRLDSLFINGYAPQNLSIRGEYQINFIHVNNLSNPDPSTSEYITLLRDIQ 493
DB 579 GVTQLGFFVLDRLDSLFINGYAPQNLSIRGEYQINFIHVNNLSNPDPSTSEYITLLRDIQ 638
QY 494 DKVTTLTKGSQLHDHTRFCLVTNLTWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASEH 553
DB 639 DKVTTLTKGSQLHDHTRFCLVTNLTWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASEH 698
QY 554 WLGSTYQLVDIHVTMESSVYQPTSSSTQHFYLNFTITNLPYSQDKAOPGTTNYQRNKR 613
DB 699 WLGSTYQLVDIHVTMESSVYQPTSSSTQHFYLNFTITNLPYSQDKAOPGTTNYQRNKR 758
QY 614 NIEDALNQLFRNSSIKSYFSDCOVSTFRSPNNRHHTGVDLSLNFSPPLARRVDRVAIYEEF 673
DB 759 NIEDALNQLFRNSSIKSYFSDCOVSTFRSPNNRHHTGVDLSLNFSPPLARRVDRVAIYEEF 818
QY 674 LMRTRNGTQLQNFTRDSSSVLVDCGYSPNRNEPLTGNS 710
DB 819 LMRTRNGTQLQNFTRDSSSVLVDCGYSPNRNEPLTGNS 855

RESULT 17
ADFO8974
ID ADFO8974 standard; protein; 914 AA.
XX AC ADF08974;
XX DT 12-FEB-2004 (first entry)
XX DB Secreted ovarian carcinoma antigen seqid 478.
XX KW gene therapy; protein therapy; vaccine; antibody inhibition;
XX KW breast cancer; restorative therapy; diagnostic agent; immunoassay;
XX KW secreted ovarian carcinoma antigen.
XX OS Homo sapiens.
XX PN US2003124140-A1.
XX PD 03-JUL-2003.
XX PF 17-JUL-2002; 2002US-00198053.
XX PR 17-DEC-1998; 98US-00215681.
XX PR 17-DEC-1998; 98US-00216003.
XX PR 23-JUN-1999; 99US-00338933.
XX PR 24-SEP-1999; 99US-00404879.
XX PR 17-JUL-2000; 2000US-00617747.
XX PR 10-AUG-2000; 2000US-00636801.
XX PR 20-SEP-2000; 2000US-00667857.
XX PR 04-APR-2001; 2001US-00827271.
XX PR 18-JUN-2001; 2001US-00884441.
XX PR 17-JUL-2001; 2001US-00907969.
XX (CORI-) CORIXA CORP.
XX PA Bangur CS, Retter MW, Fanger GR, Hill P;
XX PI WPI; 2003-897152/82.
XX DR Oncogenic nucleic acids useful for the prevention, diagnosis and
XX PT treatment of breast cancer.
XX PS Example 13; SEQ ID NO 478; 399pp; English.
XX CC The invention describes nucleic acids (I) and the polypeptides (II) they
XX CC encode. The nucleic acids (I) may be used for preventing, diagnosing and
XX CC treating diseases related to their aberrant expression i.e. breast

CC cancers. For example, (I) and (II) may be used to treat disorders
CC associated with decreased expression by rectifying mutations or deletions
CC in a patient's genome that affect the activity of (II) by expressing
CC inactive proteins or to supplement the patients own production of (II).
CC Additionally, (I) may be used to produce (II), by inserting (I) into a
CC host cell and culturing the cell to express the protein (II). (I) And its
CC complementary sequences may also be used as DNA probes in diagnostic
CC assays to detect and quantitate the presence of similar nucleic acids in
CC samples, and therefore which patients may be in need of restorative
CC therapy. The host cell may also be used as antigens in the production of
CC antibodies against (II) and in assays to identify modulators of (II)'s
CC expression and activity. The anti-(II) antibodies, agonists and
CC antagonists may be used to regulate expression and activity and as
CC diagnostic agents for detecting the presence of (II) in samples (e.g. by
CC immunoassay). This sequence represents a secreted ovarian carcinoma
CC antigen.
XX
SQ Sequence 914 AA;

Query Match 92.9%; Score 3663; DB 7; Length 914;
Best Local Similarity 99.9%; Pred. No. 2.5e-315;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 FTHRSSVSTSTPGTPTVYLKASKTPASIFGSAASHLLILFTLNFTITNLRYEENWPG 73
DB 159 FTHRSSVSTSTPGTPTVYLKASKTPASIFGSAASHLLILFTLNFTITNLRYEENWPG 218

QY 74 SRKFNTTERTVQLGLLPFNKTSVGLYSGCRITLLRPEKDGATGVDAICTHRPPTGP 133
DB 219 SRKFNTTERTVQLGLLPFNKTSVGLYSGCRITLLRPEKDGATGVDAICTHRPPTGP 278

QY 134 GLDRQLYLSELSQTHSITELGPTTLDRLSYNGFTHRSSVPTTSTGVVSEPPFTLNFT 193
DB 279 GLDRQLYLSELSQTHSITELGPTTLDRLSYNGFTHRSSVPTTSTGVVSEPPFTLNFT 338

QY 194 INNLRYMADMGQPSLKFNTTNNMKHLLSPILQSSSLGARYTGCVRIALRSYKGAETR 253
DB 339 INNLRYMADMGQPSLKFNTTNNMKHLLSPILQSSSLGARYTGCVRIALRSYKGAETR 398

QY 254 VDLCTYLOPLSGPGLPIKQVHLSQTHGIRLGPYSLDKSLYNGVNEGPDEPPT 313
DB 399 VDLCTYLOPLSGPGLPIKQVHLSQTHGIRLGPYSLDKSLYNGVNEGPDEPPT 458

QY 314 TPKPATTFPLPSEATTAMGYHLKTLTLNFTISNLOYSPDMGKGSATFNSTEGVLQHLR 373
DB 459 TPKPATTFPLPSEATTAMGYHLKTLTLNFTISNLOYSPDMGKGSATFNSTEGVLQHLR 518

QY 374 PLFQKSMGPFYLGCOLISLRPEKGAATGVDTCTTHDPVCPGLDIOQLYWELSLTH 433
DB 519 PLFQKSMGPFYLGCOLISLRPEKGAATGVDTCTTHDPVCPGLDIOQLYWELSLTH 578

QY 434 GVTQLGFYVLDRLSFLNGVAPQNLISIRGEYQINPHIWNWNLNPDPTSEYITLLRDQ 493
DB 579 GVTQLGFYVLDRLSFLNGVAPQNLISIRGEYQINPHIWNWNLNPDPTSEYITLLRDQ 638

QY 494 DKVTTLKGSQSLDHTFRCLVNTLWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFH 553
DB 639 DKVTTLKGSQSLDHTFRCLVNTLWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFH 698

QY 554 WLGSTVQLVDIHVTENESSYQPTSSSTQHFYLNFTITNLPYSQKAPGTTNYQRNR 613
DB 699 WLGSTVQLVDIHVTENESSYQPTSSSTQHFYLNFTITNLPYSQKAPGTTNYQRNR 758

QY 614 NIEDALNQLFRNSIISYFSDCOVSTFRSPNRRHTGVDSLCNFSPLARRVDVAIYERF 673
DB 759 NIEDALNQLFRNSIISYFSDCOVSTFRSPNRRHTGVDSLCNFSPLARRVDVAIYERF 818

QY 674 LRMRNGTQLQNFLLDRSSVLVDGYSFNREPLTGN 710
DB 819 LRMRNGTQLQNFLLDRSSVLVDGYSFNREPLTGN 855

ADF08808
ID ADF08808 standard; protein; 914 AA.
XX
AC ADF08808;
DT 12-FEB-2004 (first entry)
XX
DE Secreted ovarian carcinoma antigen seqid 312.
XX
KW gene therapy; protein therapy; vaccine; antibody inhibition;
KW breast cancer; restorative therapy; diagnostic agent; immunoassay;
KW secreted ovarian carcinoma antigen.
XX
OS Homo sapiens.
XX
PN US2003124140-A1.
XX
PD 03-JUL-2003.
XX
PF 17-JUL-2002; 2002US-00198053.
XX
PR 17-DEC-1998; 98US-00215681.
PR 17-DEC-1998; 98US-00215603.
PR 23-JUN-1999; 99US-00338933.
PR 24-SEP-1999; 99US-00404879.
PR 17-JUL-2000; 2000US-00617747.
PR 10-AUG-2000; 2000US-00636801.
PR 20-SEP-2000; 2000US-00667857.
PR 04-APR-2001; 2001US-00827271.
PR 18-JUN-2001; 2001US-00884441.
PR 17-JUL-2001; 2001US-00907969.
XX
PA (CORI-) CORIXA CORP.
XX
PI Bangor CS, Retter MW, Fanger GR, Hill P;
XX
XX WPI; 2003-897152/82.
DR N-PSDB; ADF08807.
XX
PT Oncogenic nucleic acids useful for the prevention, diagnosis and
XX treatment of breast cancer.
PS Example 2; SEQ ID NO 312; 399pp; English.
XX
CC The invention describes nucleic acids (I) and the polypeptides (II) they
CC encode. The nucleic acids (I) may be used for preventing, diagnosing and
CC treating diseases related to their aberrant expression i.e. breast
CC cancers. For example, (I) and (II) may be used to treat disorders
CC associated with decreased expression by rectifying mutations or deletions
CC in a patient's genome that affect the activity of (II) by expressing
CC inactive proteins or to supplement the patients own production of (II).
CC Additionally, (I) may be used to produce (II), by inserting (I) into a
CC host cell and culturing the cell to express the protein (II). (I) And its
CC complementary sequences may also be used as DNA probes in diagnostic
CC assays to detect and quantitate the presence of similar nucleic acids in
CC samples, and therefore which patients may be in need of restorative
CC therapy. The host cell may also be used as antigens in the production of
CC antibodies against (II) and in assays to identify modulators of (II)'s
CC expression and activity. The anti-(II) antibodies, agonists and
CC antagonists may be used to regulate expression and activity and as
CC diagnostic agents for detecting the presence of (II) in samples (e.g. by
CC immunoassay). This sequence represents a secreted ovarian carcinoma
CC antigen.
XX
SQ Sequence 914 AA;

Query Match 92.9%; Score 3663; DB 7; Length 914;
Best Local Similarity 99.9%; Pred. No. 2.5e-315;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 FTHRSSVSTSTPGTPTVYLKASKTPASIFGSAASHLLILFTLNFTITNLRYEENWPG 73
DB 159 FTHRSSVSTSTPGTPTVYLKASKTPASIFGSAASHLLILFTLNFTITNLRYEENWPG 218

```
QY 74 SRKFNTERVLOGLLRPLFKNTSVGLYSGRLTLRPEKDGATGVDALCTHRPDPGP 133
Db 219 SRKFNTERVLOGLLRPLFKNTSVGLYSGRLTLRPEKDGATGVDALCTHRPDPGP 278
QY 134 GLDREQLYLELSQTHSITELGPTVTLDRDLSLVNGFTHRSSVPTTSTGVVSEEPFTLNFT 193
Db 279 GLDREQLYLELSQTHSITELGPTVTLDRDLSLVNGFTHRSSVPTTSTGVVSEEPFTLNFT 338
QY 194 INNLRYMADMGQPSGLKFNITDNVMKHLSPFORSLGARYTCRVIARLSVKNAGETR 253
Db 339 INNLRYMADMGQPSGLKFNITDNVMKHLSPFORSLGARYTCRVIARLSVKNAGETR 398
QY 254 VDLICTYLOPLSGPLPIKQVFHELSSQTHGIRLGPVSLDKDLSLYLNGYNEGPDEPPT 313
Db 399 VDLICTYLOPLSGPLPIKQVFHELSSQTHGIRLGPVSLDKDLSLYLNGYNEGPDEPPT 458
QY 314 TPKPATTFPLPSEATTAMGYHLKTLTLNFTISNLQSPDMGKGSATFNSTEGVLOHLR 373
Db 459 TPKPATTFPLPSEATTAMGYHLKTLTLNFTISNLQSPDMGKGSATFNSTEGVLOHLR 518
QY 374 PLFOKSSMGPPYLGQQLISLRPEKDGATGVDTTCTYHPDPVGPGLDIQQLYWELSQLTH 433
Db 519 PLFOKSSMGPPYLGQQLISLRPEKDGATGVDTTCTYHPDPVGPGLDIQQLYWELSQLTH 578
QY 434 GVTOLGFVLDRLDLSLFIINGVAPQNLISIRGEVQINFIHVNWNLSPDPTSSSEYITLLRDIQ 493
Db 579 GVTOLGFVLDRLDLSLFIINGVAPQNLISIRGEVQINFIHVNWNLSPDPTSSSEYITLLRDIQ 638
QY 494 DKVTLLYKGSQQLHDTFRFCLVTNLTMDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFH 553
Db 639 DKVTLLYKGSQQLHDTFRFCLVTNLTMDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFH 698
QY 554 WLGSTYQLVDIHVTMESSVYQPTSSSTQHFYLNFTITNLPSQDKAQPCTTNYQRNKR 613
Db 699 WLGSTYQLVDIHVTMESSVYQPTSSSTQHFYLNFTITNLPSQDKAQPCTTNYQRNKR 758
QY 614 NIEDALNQLFRNSIKSYFSDCQVSTFRSPNRRHTGVDLSLNFSPARRVDRVAIYEEF 673
Db 759 NIEDALNQLFRNSIKSYFSDCQVSTFRSPNRRHTGVDLSLNFSPARRVDRVAIYEEF 818
QY 674 LRMTNRGTQLQNFTRDSSVLVDGYSNRPNEPLTGNS 710
Db 819 LRMTNRGTQLQNFTRDSSVLVDGYSNRPNEPLTGNS 855
RESULT 19
ADG46095
ID ADG46095 standard; protein; 914 AA.
XX AC ADG46095;
XX AC
XX DT 26-FEB-2004 (first entry)
XX DE Human ovarian carcinoma polypeptide #1.
XX KW Human; ovarian carcinoma; O8E; ovarian cancer; secreted tumour antigen;
XX KW cytosolic; O772P.
XX OS Homo sapiens.
XX FN US2003165504-A1.
XX PD 04-SEP-2003.
XX PF 04-APR-2001; 2001US-00827271.
XX PR 17-DEC-1998; 98US-00215681.
XX PR 17-DEC-1998; 98US-00216003.
XX PR 23-JUN-1999; 99US-00338933.
XX PR 24-SEP-1999; 99US-00404879.
XX PR 17-JUL-2000; 2000US-00617747.
XX PR 10-AUG-2000; 2000US-00636801.

PR 20-SEP-2000; 2000US-00667857.
XX (RETT/) RETTER M W.
PA (FANG/) FANGER G R.
XX Retter MW, Fanger GR;
XX WPI; 2003-898035/82.
XX N-PSDB; ADG46555.
XX New isolated O8E or O772P polypeptides, useful for diagnosing,
PT preventing, treating and monitoring cancer, e.g. ovarian cancer,
PT stimulating the immune response in patient.
XX Claim 5; SEQ ID NO 312; 290pp; English.
XX The invention relates to human ovarian carcinoma polypeptides, designated
CC O8E or O772P, and the polynucleotides encoding them. The invention also
CC relates to methods for inhibiting the development of cancer, e.g. ovarian
CC cancer in a patient, methods for stimulating and/or expanding T cells and
CC methods for identifying secreted tumour antigens. The polypeptides,
CC compositions, antibodies to the polypeptides and methods are useful for
CC diagnosing, preventing, treating and monitoring cancer, e.g. ovarian
CC cancer. The composition is particularly useful for stimulating an immune
CC response in patient. This sequence represents a human ovarian carcinoma
CC polypeptide of the invention.
XX Sequence 914 AA;
QY Query Match 92.9%; Score 3663; DB 7; Length 914;
Db Best Local Similarity 99.9%; Pred. No. 2.5e-315;
QY Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 14 FTHRSSVSTSTGTPPTVYLGASKTPASIRGPSAASHLLILFTLNFTITNLRYEENWMPG 73
159 FTHRSSVSTSTGTPPTVYLGASKTPASIRGPSAASHLLILFTLNFTITNLRYEENWMPG 218
QY 74 SRKFNTERVLOGLLRPLFKNTSVGLYSGRLTLRPEKDGATGVDALCTHRPDPGP 133
Db 219 SRKFNTERVLOGLLRPLFKNTSVGLYSGRLTLRPEKDGATGVDALCTHRPDPGP 278
QY 134 GLDREQLYLELSQTHSITELGPTVTLDRDLSLVNGFTHRSSVPTTSTGVVSEEPFTLNFT 193
Db 279 GLDREQLYLELSQTHSITELGPTVTLDRDLSLVNGFTHRSSVPTTSTGVVSEEPFTLNFT 338
QY 194 INNLRYMADMGQPSGLKFNITDNVMKHLSPFORSLGARYTCRVIARLSVKNAGETR 253
Db 339 INNLRYMADMGQPSGLKFNITDNVMKHLSPFORSLGARYTCRVIARLSVKNAGETR 398
QY 254 VDLICTYLOPLSGPLPIKQVFHELSSQTHGIRLGPVSLDKDLSLYLNGYNEGPDEPPT 313
Db 399 VDLICTYLOPLSGPLPIKQVFHELSSQTHGIRLGPVSLDKDLSLYLNGYNEGPDEPPT 458
QY 314 TPKPATTFPLPSEATTAMGYHLKTLTLNFTISNLQSPDMGKGSATFNSTEGVLOHLR 373
Db 459 TPKPATTFPLPSEATTAMGYHLKTLTLNFTISNLQSPDMGKGSATFNSTEGVLOHLR 518
QY 374 PLFOKSSMGPPYLGQQLISLRPEKDGATGVDTTCTYHPDPVGPGLDIQQLYWELSQLTH 433
Db 519 PLFOKSSMGPPYLGQQLISLRPEKDGATGVDTTCTYHPDPVGPGLDIQQLYWELSQLTH 578
QY 434 GVTOLGFVLDRLDLSLFIINGVAPQNLISIRGEVQINFIHVNWNLSPDPTSSSEYITLLRDIQ 493
Db 579 GVTOLGFVLDRLDLSLFIINGVAPQNLISIRGEVQINFIHVNWNLSPDPTSSSEYITLLRDIQ 638
QY 494 DKVTLLYKGSQQLHDTFRFCLVTNLTMDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFH 553
Db 639 DKVTLLYKGSQQLHDTFRFCLVTNLTMDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFH 698
QY 554 WLGSTYQLVDIHVTMESSVYQPTSSSTQHFYLNFTITNLPSQDKAQPCTTNYQRNKR 613
Db 699 WLGSTYQLVDIHVTMESSVYQPTSSSTQHFYLNFTITNLPSQDKAQPCTTNYQRNKR 758
```


QY 614 NIEDALNQLFRNSSIKSYFSDCQVSTFRSVPNRHHTGVDSLCNFSPLARRVDRVAIYEEF 673
Db 759 NIEDALNQLFRNSSIKSYFSDCQVSTFRSVPNRHHTGVDSLCNFSPLARRVDRVAIYEEF 818
QY 674 LRMRNGTQLQNFRTDRSSVLVDGYSPNRNEPLTGNS 710
Db 819 LRMRNGTQLQNFRTDRSSVLVDGYFPNRNEPLTGNS 855

RESULT 20

ADN40451
ID ADN40451 standard; protein; 914 AA.
XX AC ADN40451;
XX DT 12-AUG-2004 (first entry)
XX DE Human breast cancer associated polypeptide sequence #4.
XX KW Human; breast cancer; T cell; tumour protein; antigen presenting cell;
KW Immune response; CD4+; CD8+; cytostatic.
XX OS Homo sapiens.
XX US2004101899-A1.
PN 27-MAY-2004.
XX 13-NOV-2003; 2003US-00714389.
XX 30-NOV-1999; 99US-00451651.
PR 22-FEB-2000; 2000US-00510662.
PR 10-MAR-2000; 2000US-00523586.
PR 07-APR-2000; 2000US-00545068.
PR 15-MAY-2000; 2000US-00571025.
PR 06-FEB-2001; 2001US-00778320.
XX (CORI-) CORIXA CORP.
XX Dillon DC, Day CH, Jiang Y, Houghton RL, Mitcham JL, Wang T;
PI McNeill PD;
XX WPI; 2004-399689/37.
DR N-PSDB; ADN40450.

XX New polynucleotides, useful for treating and diagnosing cancer,
PT particularly breast cancer by stimulating immune response in a patient
PT and inhibiting the development of cancer.
XX Claim 2; SEQ ID NO 206; 151pp; English.
XX The present invention relates to polynucleotide and polypeptide sequences
CC associated with breast cancer. Also disclosed are expression vectors
CC comprising the polynucleotide sequences of the invention operably linked
CC to an expression control sequence, host cells comprising the vector,
CC antibodies (or antigen binding fragments of antibodies) specifically
CC binding the polypeptides of the invention, fusion proteins comprising at
CC least one of the polypeptides, stimulating and/or expanding T cells
CC specific for a tumour protein. The polynucleotide sequences, polypeptide
CC sequences, and antigen presenting cells can be administered
CC therapeutically/prophylactically to induce an immune response. They can
CC be included with a physiological carrier/immunostimulant in compositions
CC such as vaccines, particularly to treat or prevent cancers such as breast
CC cancer. They can also be used to inhibit the development of cancer by
CC incubating one or more of them with CD4+ and/or CD8+ T cells isolated
CC from a patient, such that the T cells proliferate, and administering the
CC proliferated T cells to the patient. The polynucleotide sequences are
CC useful for detecting cancer in a patient, producing fusion proteins,
CC producing T cell populations and antigen presenting cells. The present
CC sequence represents a polypeptide sequence of the invention.

Sequence 914 AA;

Query Match 92.9%; Score 3663; DB 8; Length 914;
Best Local Similarity 99.9%; Pred. No. 2.5e-315;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 14 FTHRSSVSTSTPGPTVYLGASKTPASIFGSPSAASHLLILFTLNFTITNLRYEENWMPG 73
Db 159 FTHRSSVSTSTPGPTVYLGASKTPASIFGSPSAASHLLILFTLNFTITNLRYEENWMPG 218
QY 74 SRKFNTTTERVLOGLLRPLFKNTSVGLYSGCRLLTLRPEKDGATGVDAICTHRPDTGP 133
Db 219 SRKFNTTTERVLOGLLRPLFKNTSVGLYSGCRLLTLRPEKDGATGVDAICTHRPDTGP 278
QY 134 GLDREQLYLELSQLTHSITELGPYTLDRSLYNGFTHRSSVPTTSTGVVSEBPTLNFT 193
Db 279 GLDREQLYLELSQLTHSITELGPYTLDRSLYNGFTHRSSVPTTSTGVVSEBPTLNFT 338
QY 194 INNLRYMDMGOPGSLKFNITDNVMKHLSPFORSSLGARYTGCRIALRSVKNGAETR 253
Db 339 INNLRYMDMGOPGSLKFNITDNVMKHLSPFORSSLGARYTGCRIALRSVKNGAETR 398
QY 254 VDLCTYLOPLSGPLPIKQVFHELSQQTHGTRIGPYSIDKDSLYLNGYNBPGPBPPT 313
Db 399 VDLCTYLOPLSGPLPIKQVFHELSQQTHGTRIGPYSIDKDSLYLNGYNBPGPBPPT 458
QY 314 TPKPATTFPLPSEATTAMGYHLKTLTLNFTISNLOYSMDMGKSGATFSTEGVLOHLR 373
Db 459 TPKPATTFPLPSEATTAMGYHLKTLTLNFTISNLOYSMDMGKSGATFSTEGVLOHLR 518
QY 374 PLFOKSSMGPFYLGCOLISLRPEKDGATGVDTTCTYHDPVGPGLDIOOLYWELSQTH 433
Db 519 PLFOKSSMGPFYLGCOLISLRPEKDGATGVDTTCTYHDPVGPGLDIOOLYWELSQTH 578
QY 434 GVTQLGFFYVLDRLDSLFINGYAPQNLSIRGEYQINFIHVMNLSNPDPTSEYITLLRDIQ 493
Db 579 GVTQLGFFYVLDRLDSLFINGYAPQNLSIRGEYQINFIHVMNLSNPDPTSEYITLLRDIQ 638
QY 494 DKVTLYKGSQSLHDTFRFCLVNLNMDSVLTVTKALFSSNLDPSLVEQVFLDKTLNASEPH 553
Db 639 DKVTLYKGSQSLHDTFRFCLVNLNMDSVLTVTKALFSSNLDPSLVEQVFLDKTLNASEPH 698
QY 554 WLGSTYQLVDIHVTMESSVYQPTSSSTQHFVLAFTITNLPSQDKAQPGTTNYORNR 613
Db 699 WLGSTYQLVDIHVTMESSVYQPTSSSTQHFVLAFTITNLPSQDKAQPGTTNYORNR 758
QY 614 NIEDALNQLFRNSSIKSYFSDCQVSTFRSVPNRHHTGVDSLCNFSPLARRVDRVAIYEEF 673
Db 759 NIEDALNQLFRNSSIKSYFSDCQVSTFRSVPNRHHTGVDSLCNFSPLARRVDRVAIYEEF 818
QY 674 LRMRNGTQLQNFRTDRSSVLVDGYSPNRNEPLTGNS 710
Db 819 LRMRNGTQLQNFRTDRSSVLVDGYFPNRNEPLTGNS 855

Search completed: March 20, 2006, 07:35:37
Job time : 277.726 secs

THIS PAGE BLANK (uspto)

GenCore version 5.1.7

Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 20, 2006, 07:28:38 ; Search time 140.158 Seconds
(without alignments)
3765.293 Million cell updates/sec

Title: US-10-687-035-1

Perfect score: 3945

Sequence: 1 AQAARRARTKLFTHRSSV.....QKLISEDLMNMTGHHHHH 748

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Uniprot 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	3655	92.9	6995	2	Q96RK2_HUMAN
2	3649	92.5	22152	2	Q8WX17_HUMAN
3	3642	92.3	1148	2	Q9H7S7_HUMAN
4	1562.5	39.6	867	2	Q6ZQW5_HUMAN
5	736.5	18.7	258	2	Q9DLH1_MOUSE
6	144.5	3.7	1408	2	Q27557_METH
7	143.5	3.6	656	2	Q7RJF3_GIALA
8	141.5	3.6	5010	2	Q4MT18_BACCE
9	138	3.5	3443	2	Q8JZM8_MOUSE
10	136	3.4	605	2	Q9AK06_ARATH
11	135.5	3.4	1117	1	YN96_YEAST
12	134.5	3.4	1526	2	Q6BL88_DEBHA
13	132.5	3.4	797	2	Q54E23_DICDI
14	131	3.3	1230	2	Q54E54_DICDI
15	131	3.3	1447	2	Q54JR7_DICDI
16	128	3.2	879	2	Q4J6T1_SULAC
17	128	3.2	5017	2	Q81F10_BACCR
18	127	3.2	1166	2	Q4UDD4_THERAN
19	127	3.2	1364	2	Q86AL8_DICDI
20	126.5	3.2	885	2	Q54V40_DICDI
21	126.5	3.2	2340	2	Q8U227_9POTY
22	126	3.2	1056	2	Q4VWF3_9HERP
23	126	3.2	1818	2	Q54HY5_DICDI
24	125.5	3.2	1011	2	Q5T0W9_HUMAN
25	125.5	3.2	5017	2	Q81SNO_BACAN
26	125	3.2	1084	2	Q8EUS5_MYCPE
27	125	3.2	5572	2	Q7QSA1_GIALA
28	125	3.2	10791	2	Q7U7M8_SYNPX
29	124.5	3.2	1012	2	Q6FQ05_CANGA
30	124.5	3.2	2121	2	Q733G8_BACCI
31	124.5	3.2	2535	2	Q755B8_ASHBYA

ALIGNMENTS

32	124.5	3.2	5017	2	Q63DF3_BACCZ
33	124	3.1	856	2	Q6FXG3_CANGA
34	124	3.1	1442	2	Q96YH5_SULGO
35	123.5	3.1	1837	2	Q9N5F6_CABEL
36	123.5	3.1	2477	1	FINC_RAT
37	123.5	3.1	2520	2	Q4NMN6_BACCE
38	123	3.1	1085	2	Q54B86_DICDI
39	123	3.1	2959	2	Q5UBY0_MIMIV
40	123	3.1	3441	2	Q89PB9_BRAJA
41	122.5	3.1	393	2	Q59Q37_CANAL
42	122.5	3.1	767	2	Q5W2S2_SULIS
43	122.5	3.1	1206	2	Q5CHP8_CRYHO
44	122.5	3.1	1260	2	Q4ULL1_THERAN
45	122.5	3.1	1390	2	Q8PXA4_METMA
46	122.5	3.1	2520	2	Q6HFE0_BACHK
47	122	3.1	1608	2	Q8PVI0_METMA
48	122	3.1	2319	2	Q5CTK9_CRYPV
49	122	3.1	2520	2	Q637G8_BACCZ
50	122	3.1	8591	2	Q81B94_PLAF7
51	121.5	3.1	1377	2	Q5SVH8_MOUSE
52	121.5	3.1	1475	1	NUI53_HUMAN
53	121.5	3.1	2471	2	Q9YTK3_9HERP
54	121.5	3.1	5005	2	Q9PPZ5_UREPA
55	121	3.1	1131	1	ADG3_SCHPO
56	121	3.1	1632	2	Q8T141_METAC
57	120.5	3.1	936	2	Q66853_ADEGX
58	120.5	3.1	1322	2	Q4UBT5_THERAN
59	120.5	3.1	1377	1	CBPD_MOUSE
60	120.5	3.1	1380	2	Q556L7_DICDI
61	120.5	3.1	1921	2	Q4M222_THERA
62	120.5	3.1	2833	2	Q9VPI3_DROME
63	120.5	3.1	3080	2	Q5EGP2_HUMAN
64	120.5	3.1	5017	2	Q6HKW5_BACHK
65	120	3.0	651	2	Q6CNL5_KLULA
66	120	3.0	1093	2	Q8SV69_MYCPE
67	120	3.0	1397	1	CID_DROME
68	120	3.0	1447	2	Q5CFG8_CRYHO
69	120	3.0	1449	2	Q9U112_DROME
70	120	3.0	1836	2	Q54KW5_DICDI
71	120	3.0	2409	2	Q960G6_DROME
72	119.5	3.0	631	2	Q99K60_MOUSE
73	119.5	3.0	846	2	Q54HL8_DICDI
74	119.5	3.0	1111	2	Q5AMQ6_CANAL
75	119.5	3.0	1225	2	Q5A849_CANAL
76	119.5	3.0	2306	2	Q4SEE4_TETNG
77	119.5	3.0	11696	2	Q5CV09_CRYPV
78	119	3.0	957	2	Q9UKN0_HUMAN
79	119	3.0	2206	2	Q99FJ4_9PICO
80	119	3.0	2392	1	YCF2_ANTFO
81	118.5	3.0	738	2	Q41980_GIBZE
82	118.5	3.0	967	2	Q4J9K1_SULAC
83	118.5	3.0	1463	2	Q70320_CAVPO
84	118.5	3.0	1941	2	Q54JEL_DICDI
85	118.5	3.0	2193	2	Q6WZM7_HUMAN
86	118.5	3.0	2267	2	Q68DP9_HUMAN
87	118.5	3.0	2283	2	Q8VQ99_STAAN
88	118.5	3.0	2477	1	FINC_MOUSE
89	118.5	3.0	3229	2	Q63UE4_BURPS
90	118.5	3.0	9439	2	Q8CF76_STAEP
91	118.5	3.0	10203	2	Q5HPA2_STAEP
92	118	3.0	699	2	Q5KFX2_CRYNE
93	118	3.0	1804	2	Q66IN2_XENLA
94	118	3.0	5010	2	Q81CV2_BACCR
95	117.5	3.0	668	2	Q7QWQ2_GIALA
96	117.5	3.0	704	2	Q6COT3_KLULA
97	117.5	3.0	729	2	Q8DKG0_SYNEL
98	117.5	3.0	870	2	Q4N9G2_THERA
99	117.5	3.0	1045	2	Q76037_HUMAN
100	117.5	3.0	1136	2	Q5LGX7_BACFN

Q63df3 bacillus ce
Q6fxg3 candida gla
Q96yh5 sulfolobus
Q9n5f6 caenorhabdi
P04937 rattus norv
Q4nmn6 bacillus ce
Q54b86 dictyosteli
Q5ubp0 mimivirus
Q89pb9 bradyrhizob
Q59q37 candida alb
Q5w2s2 sulfolobus
Q5chp8 cryptospori
Q4ull1 theileria a
Q8pxa4 methanosarc
Q6hfe0 bacillus th
Q8pvi0 methanosarc
Q5ctk9 cryptospori
Q637g8 bacillus ce
Q5svh8 mus musculu
P49790 homo sapien
Q9ytk3 ateline her
Q9ppz5 ureaplasma
Q74851 schizosacch
Q8t141 methanosarc
Q66853 avian adeno
Q4ubt5 theileria a
Q89001 mus musculu
Q556l7 dictyosteli
Q4m222 theileria p
Q9vpi3 drosophila
Q5egp2 homo sapien
Q6hkw5 bacillus th
Q6cnl5 kluyveromyc
Q8sv69 mycoplasma
P19338 drosophila
Q5cfgh cryptospori
Q9u112 drosophila
Q54kw5 dictyosteli
Q960g6 drosophila
Q99k60 mus musculu
Q54hl8 dictyosteli
Q5amq6 candida alb
Q5a849 candida alb
Q4see4 tetraodon n
Q5cv09 cryptospori
Q9ukn0 homo sapien
Q99fj4 porcine tes
Q859w7 anthoceros
Q41980 gibberella
Q4j9k1 sulfolobus
Q70320 cavia porce
Q54jel dictyosteli
Q54jel dictyosteli
Q6wzm7 homo sapien
Q68dp9 homo sapien
Q8vq99 staphylococ
P11376 mus musculu
Q63ue4 burkholderi
Q8cf76 staphylococ
Q5hpa2 staphylococ
Q5kfx2 cryptococcu
Q66in2 xenopus lae
Q81cv2 bacillus ce
Q7qww2 giardia lam
Q6cot3 kluyveromyc
Q8dkg0 synecococc
Q4n9g2 theileria p
Q76037 homo sapien
Q5lgx7 bacteroides

```
RESULT 1
Q96RK2_HUMAN
ID Q96RK2_HUMAN PRELIMINARY; PRT; 6995 AA.
AC Q96RK2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mucin 16 (Fragment).
GN Name=MUC16;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21347965; PubMed=11369781; DOI=10.1074/jbc.M103554200;
RA Yin B.W., Lloyd K.O.;
RT "Molecular cloning of the cal25 ovarian cancer antigen. identification
as a new mucin, muc16.";
RL J. Biol. Chem. 276:27371-27375(2001).
[2]
RN NUCLEOTIDE SEQUENCE.
RA Lloyd K.O., Yin B.W.T.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF361486; AAK74120.3; -; mRNA.
DR HSP; Q9D1H1; IIVZ.
DR SMR; Q96RK2; 6803-6922.
DR Ensembl; ENSG00000181143; Homo sapiens.
DR InterPro; IPR000194; ATPase_a/bcentre.
DR InterPro; IPR000082; SEA.
DR Pfam; PF01390; SEA; 20.
DR SMART; SM00200; SEA; 10.
DR PROSITE; PS00152; ATPASE_ALPHA_BETA; UNKNOWN_1.
DR PROSITE; PS50024; SEA; 6.
FT NON TER 1
SQ SEQUENCE 6995 AA; 744958 MW; 80C797DDBBF33A2B CRC64;

Query Match 92.9%; Score 3665; DB 2; Length 6995;
Best Local Similarity 99.9%; Pred. No. 2.7e-237;
Matches 696; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 14 FTHRSSVSTSTPGTPTVYLKASCTPASIFGPSAASHLLILFTLNFTITNLYEENWMPG 73
Db 6240 FTHRSSVSTSTPGTPTVYLKASCTPASIFGPSAASHLLILFTLNFTITNLYEENWMPG 6299
Qy 74 SRKFTTERTVQLGLRLPLFKNTSVGPLYSGCRLTLRPEKDGATGVDAICTHRPDPTGP 133
Db 6300 SRKFTTERTVQLGLRLPLFKNTSVGPLYSGCRLTLRPEKDGATGVDAICTHRPDPTGP 6359
Qy 134 GLDREQLYLELSQTHSITELGPVTLDRDLSLVNGFTHRSSVPTTSTGVWSEEPFTLNFT 193
Db 6360 GLDREQLYLELSQTHSITELGPVTLDRDLSLVNGFTHRSSVPTTSTGVWSEEPFTLNFT 6419
Qy 194 INNLYRMADMGQPSGLKFNITDNTWKHLLSLPLFORSSIGARYTCRVIALRSVKGAEFR 253
Db 6420 INNLYRMADMGQPSGLKFNITDNTWKHLLSLPLFORSSIGARYTCRVIALRSVKGAEFR 6479
Qy 254 VDLICTVQLPUSGGLPLTKQVFHELSSQTHGITHLGPVSLDKSLYLVNGYNEPDPDPPT 313
Db 6480 VDLICTVQLPUSGGLPLTKQVFHELSSQTHGITHLGPVSLDKSLYLVNGYNEPDPDPPT 6539
Qy 314 TPKEATTFPLPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVQLHLR 373
Db 6540 TPKEATTFPLPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVQLHLR 6599
Qy 374 PLFOKSSMGPIYLGQILSLRPEKDGATGVDTCTTHPDPVGPGLDIOQLYWLSQLTH 433
Db 6600 PLFOKSSMGPIYLGQILSLRPEKDGATGVDTCTTHPDPVGPGLDIOQLYWLSQLTH 6659
Qy 434 GVTQLGFVLDRLDSLFINGYAPQNLIRGEYQINPHIVNMNLSNPDPPTSEYITLLRDIQ 493
```

```
Db 6660 GVTQLGFVLDRLDSLFINGYAPQNLIRGEYQINPHIVNMNLSNPDPPTSEYITLLRDIQ 6719
Qy 494 DKVTTLYKGSQSLHDTFPCIVTNLTWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASPH 553
Db 6720 DKVTTLYKGSQSLHDTFPCIVTNLTWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASPH 6779
Qy 554 WLGSTYQLVDIHVTENESSYQPTSSSTQHFYLNFTITNLYPSQDKAOPGTTNYQRNKR 613
Db 6780 WLGSTYQLVDIHVTENESSYQPTSSSTQHFYLNFTITNLYPSQDKAOPGTTNYQRNKR 6839
Qy 614 NIEDALNQLFRNSSIKSYSDCOVSTFRSPVNRHHTGVDSLCNFSPLARVDRVAIYEEF 673
Db 6840 NIEDALNQLFRNSSIKSYSDCOVSTFRSPVNRHHTGVDSLCNFSPLARVDRVAIYEEF 6899
Qy 674 LRMRNGTQLQNFETLDRSSVLVDGYSPNRNEPLTGNS 710
Db 6900 LRMRNGTQLQNFETLDRSSVLVDGYSPNRNEPLTGNS 6936

RESULT 2
Q8WXI7_HUMAN
ID Q8WXI7_HUMAN PRELIMINARY; PRT; 22152 AA.
AC Q8WXI7;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Ovarian cancer related tumor marker CAL25.
GN Name=MUC16;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21646939; PubMed=11786729; DOI=10.1159/000050638;
RA O'Brien T.J., Beard J.B., Underwood L.J., Dennis R.A., Santin A.D.,
RA York L.;
RT "The CA 125 gene: an extracellular superstructure dominated by repeat
sequences.";
RL Tumour Biol. 22:348-366(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA O'Brien T.J., Underwood L.J., Beard J.B.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF414442; AAL65133.2; -; mRNA.
DR SMR; Q8WXI7; 21960-22079.
DR Ensembl; ENSG00000181143; Homo sapiens.
DR HGNC; HGNC:15582; MUC16.
DR InterPro; IPR000194; ATPase_a/bcentre.
DR InterPro; IPR000082; SEA.
DR Pfam; PF01390; SEA; 51.
DR SMART; SM00200; SEA; 23.
DR PROSITE; PS00152; ATPASE_ALPHA_BETA; UNKNOWN_1.
DR PROSITE; PS50024; SEA; 11.
SQ SEQUENCE 22152 AA; 2355668 MW; B3E7BDF19997A440 CRC64;

Query Match 92.5%; Score 3649; DB 2; Length 22152;
Best Local Similarity 99.7%; Pred. No. 1.9e-235;
Matches 695; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 14 FTHRSSVSTSTPGTPTVYLKASCTPASIFGPSAASHLLILFTLNFTITNLYEENWMPG 73
Db 21397 FTHRSSVSTSTPGTPTVYLKASCTPASIFGPSAASHLLILFTLNFTITNLYEENWMPG 21456
Qy 74 SRKFTTERTVQLGLRLPLFKNTSVGPLYSGCRLTLRPEKDGATGVDAICTHRPDPTGP 133
Db 21457 SRKFTTERTVQLGLRLPLFKNTSVGPLYSGCRLTLRPEKDGATGVDAICTHRPDPTGP 21516
Qy 134 GLDREQLYLELSQTHSITELGPVTLDRDLSLVNGFTHRSSVPTTSTGVWSEEPFTLNFT 193
Db 21517 GLDREQLYLELSQTHSITELGPVTLDRDLSLVNGFTHRSSVPTTSTGVWSEEPFTLNFT 21576
```

194 INNRYMADMGQPSGLKFNITDNNMKHLLSPLFORSSIGARYTGCRCVIALRSVKNAGETR 253
21577 INNRYMADMGQPSGLKFNITDNNMKHLLSPLFORSSIGARYTGCRCVIALRSVKNAGETR 21636
254 VDLCTYQLPSGLPIKQVHLSOOTHGIFLPGYSIDKSLYNGNEGPDPPT 313
21637 VDLCTYQLPSGLPIKQVHLSOOTHGIFLPGYSIDKSLYNGNEGPDPPT 21696
314 TPKPATFLPPLSEATTAMGYHLKTLTNFTISNLOYSQPMGKGSATFNSSTEGVLOHLR 373
21697 TPKPATFLPPLSEATTAMGYHLKTLTNFTISNLOYSQPMGKGSATFNSSTEGVLOHLR 21756
374 PLFQKSSMGPFYLGQCLISLRPEKGAATGVTCTTHPDPVPGGLDIOQLYWELSLTH 433
21757 PLFQKSSMGPFYLGQCLISLRPEKGAATGVTCTTHPDPVPGGLDIOQLYWELSLTH 21816
434 GVTQLGYVLDRLDSLFNGVAPQNLSTIRGEYQINFHVNKLSNPDPTSEYITLLRDIO 493
21817 GVTQLGYVLDRLDSLFNGVAPQNLSTIRGEYQINFHVNKLSNPDPTSEYITLLRDIO 21876
494 DKVTTLKGSQSLDHTFRCLVTLNLTWDSVLVTKALFSSNLDPSLVEQVFLDKTLNASFH 553
21877 DKVTTLKGSQSLDHTFRCLVTLNLTWDSVLVTKALFSSNLDPSLVEQVFLDKTLNASFH 21936
554 WLSTYQLVDIHVTMESSYVQPTSSSTQHFYLNFTITNLPYSQDKAQPGTTNYQRNR 613
21937 WLSTYQLVDIHVTMESSYVQPTSSSTQHFYLNFTITNLPYSQDKAQPGTTNYQRNR 21996
614 NIEDALNQLFRNSSIKSYFSDCQVSTFRSPNRRHTGVDSLNCNFSPLARRVDRVAIYEEF 673
21997 NIEDALNQLFRNSSIKSYFSDCQVSTFRSPNRRHTGVDSLNCNFSPLARRVDRVAIYEEF 22056
674 LRMTNGTQLOQNTLDRSSVLVDGYSNRRNEPLTGN 710
22057 LRMTNGTQLOQNTLDRSSVLVDGYSNRRNEPLTGN 22093

RESULT 3
Q9H7S7 HUMAN
ID Q9H7S7 HUMAN PRELIMINARY; PRT; 1148 AA.
AC Q9H7S7
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein FLJ14303.
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Placenta.
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Iehi S.,
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
RA Omura Y., Abe K., Kamihara K., Katsuma N., Sato K., Tanikawa M.,
RA Yamazaki M., Ninomiya K., Iehibashi T., Yamashita H., Murakawa K.,
RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y.,
RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yoshida M., Hottu T.,
RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
RA Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,
RA Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,

Fujimori Y., Komiya M., Tashiro H., Tanigami A., Fujiwara T.,
Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamaguchi R.,
Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
cDNAs";
RL Nat. Genet. 36:40-45(2004).
DR EMBL; AK024365; BAB14899.1; -; mRNA.
DR HSSP; Q9D1H1; 11VZ.
DR SNR; Q9H7S7; 956-1075.
DR InterPro; IPR000082; SEA.
DR Pfam; PF01390; SEA: 7.
DR PROSITE; P55004; SEA: 3.
SQ SEQUENCE 1148 AA; 127957 MW; 386180D5EFD8ABC CRC64;
Query Match 92.3%; Score 3642; DB 2; Length 1148;
Best Local Similarity 99.6%; Pred. No. 6.4e-237;
Matches 694; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 14 FTHRSSVSTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWPG 73
DB 393 FTHRSSVSTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWPG 452
QY 74 SRKFNTERVLOGLLPLPKNTSVGLYSGRLTLRPEKDGATGDAICTHRPDPPTGP 133
DB 453 SRKFNTERVLOGLLPLPKNTSVGLYSGRLTLRPEKDGATGDAICTHRPDPPTGP 512
QY 134 GLDREQLYLELSOLTHSITELGPTLDRDSLTVNGFTHRSSVPTTGTGVVSEBPFITNFT 193
DB 513 GLDREQLYLELSOLTHSITELGPTLDRDSLTVNGFTHRSSVPTTGTGVVSEBPFITNFT 572
QY 194 INNRYMADMGQPSGLKFNITDNNMKHLLSPLFORSSIGARYTGCRCVIALRSVKNAGETR 253
DB 573 INNRYMADMGQPSGLKFNITDNNMKHLLSPLFORSSIGARYTGCRCVIALRSVKNAGETR 632
QY 254 VDLCTYQLPSGLPIKQVHLSOOTHGIFLPGYSIDKSLYNGNEGPDPPT 313
DB 633 VDLCTYQLPSGLPIKQVHLSOOTHGIFLPGYSIDKSLYNGNEGPDPPT 692
QY 314 TPKPATFLPPLSEATTAMGYHLKTLTNFTISNLOYSQPMGKGSATFNSSTEGVLOHLR 373
DB 693 TPKPATFLPPLSEATTAMGYHLKTLTNFTISNLOYSQPMGKGSATFNSSTEGVLOHLR 752
QY 374 PLFQKSSMGPFYLGQCLISLRPEKGAATGVTCTTHPDPVPGGLDIOQLYWELSLTH 433
DB 753 PLFQKSSMGPFYLGQCLISLRPEKGAATGVTCTTHPDPVPGGLDIOQLYWELSLTH 812
QY 434 GVTQLGYVLDRLDSLFNGVAPQNLSTIRGEYQINFHVNKLSNPDPTSEYITLLRDIO 493
DB 813 GVTQLGYVLDRLDSLFNGVAPQNLSTIRGEYQINFHVNKLSNPDPTSEYITLLRDIO 872
QY 494 DKVTTLKGSQSLDHTFRCLVTLNLTWDSVLVTKALFSSNLDPSLVEQVFLDKTLNASFH 553
DB 873 DKVTTLKGSQSLDHTFRCLVTLNLTWDSVLVTKALFSSNLDPSLVEQVFLDKTLNASFH 932
QY 554 WLSTYQLVDIHVTMESSYVQPTSSSTQHFYLNFTITNLPYSQDKAQPGTTNYQRNR 613
DB 933 WLSTYQLVDIHVTMESSYVQPTSSSTQHFYLNFTITNLPYSQDKAQPGTTNYQRNR 992
QY 614 NIEDALNQLFRNSSIKSYFSDCQVSTFRSPNRRHTGVDSLNCNFSPLARRVDRVAIYEEF 673
DB 993 NIEDALNQLFRNSSIKSYFSDCQVSTFRSPNRRHTGVDSLNCNFSPLARRVDRVAIYEEF 1052
QY 674 LRMTNGTQLOQNTLDRSSVLVDGYSNRRNEPLTGN 710
DB 1053 LRMTNGTQLOQNTLDRSSVLVDGYSNRRNEPLTGN 1089

4

[4]
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Whole body;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Shobata K., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Carninci P., Shihata Y., Muramatsu M., Hayashizaki Y.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 [5]
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Whole body;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shobata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsumura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 [6]
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Whole body;
 RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
 RA Akakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
 RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
 RA Inotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
 RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
 RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
 RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
 RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
 RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi P., Tanaka T.,
 RA Teijima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
 RA Muramatsu M., Hayashizaki Y.,
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK035777; BAB22869.1; -; mRNA.
 DR PDB; 1LV2; NMR; A=67-185.
 DR Ensembl; ENSMUSG0000032134; Mus musculus.
 DR MGI; MGI:1920982; 1110008114Rik.
 DR InterPro; IPR000082; SEA.
 DR Pfam; PF01390; SEA; 1.
 DR PROSITE; PS50024; SEA; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 258 AA; 29426 MW; B64D9B63394D84E7 CRC64;
 Query Match 18.7%; Score 736.5; DB 2; Length 258;
 Best Local Similarity 73.4%; Pred. No. 1.5e-41;
 Matches 146; Conservative 23; Mismatches 25; Indels 5; Gaps 2;
 QY 517 LTWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFWLSTQVLDIHVTMESSVYQ- 575
 DB 1 MTSGSTVTVLEALFSSHLDPNFKVQFNKTLNASFWLSTQVLDIHVTMESSVYQ- 60
 QY 576 ---PTSSSSOHFLNFTITNLPSYQDAQPGTTNYORNRNIEDALNQLFRNSSIKSYF 632
 DB 61 AEPTSSSSOHFLNFTITNLPSYQDAQPGTTNYORNRNIEDALNQLFRNSSIKSYF 120
 QY 633 SDQGVSTFRSVP-NRHTGVDSLNCFSPLARRVDRVAIEEFLRMTRNGTQLQNTLDRS 691
 DB 121 SDQVLAFRSVNNHTGVDSLNCFSPLARRVDRVAIEEFLRMTRNGTQLQNTLDRK 180
 QY 692 SVLDVGSVPNEPLTGN 710
 DB 181 SVFDVGSQNRDDDMKNS 199
 RESULT 6
 O27557 METHH
 ID O27557 METHH PRELIMINARY; PRT; 1408 AA.
 AC O27557;
 DT 01-JAN-1998 (TREMELrel. 05, Created)
 DT 01-JAN-1998 (TREMELrel. 05, Last sequence update)
 DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
 DE Cell surface glycoprotein (S-layer protein) related protein.
 GN OrderedLocusNames=MT1513;
 OS Methanobacterium thermoautotrophicum.
 OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
 OC Methanobacteriaceae; Methanothermobacter.
 OX NCBI_TaxID=187420;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Delta H;
 RX MEDLINE=98037514; PubMed=9371463;
 RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
 RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
 RA Harrison D., Hoang L., Keagle P., Lum W., Pothier B., Qiu D.,
 RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
 RA Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
 RA McDougall S., Shimer G., Goyal A., Pietrowski S., Church G.M.,
 RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
 RT "Complete genome sequence of Methanobacterium thermoautotrophicum
 RT deltaH: functional analysis and comparative genomics.";
 RL J. Bacteriol. 179:7135-7155(1997).
 DR EMBL; AS000911; BAB85988.1; -; Genomic_DNA.
 DR PIR; H69068; H69068.
 DR InterPro; IPR010620; SBBP.
 DR Pfam; PF06739; SBBP; 7.
 KW Complete proteome.
 SQ SEQUENCE 1408 AA; 152736 MW; 294EC742ABB29F2 CRC64;
 Query Match 3.7%; Score 144.5; DB 2; Length 1408;
 Best Local Similarity 20.1%; Pred. No. 1.9;
 Matches 157; Conservative 99; Mismatches 258; Indels 269; Gaps 40;
 QY 58 NPTITNLRYEENMPCGRKFNFTT---ERVLQGLRLPLEKNTSVGLYSGCRLTLRPEKD 114
 DB 444 NPTIT---PDACKNLTGLSDGFLTRTPFIINISVTPL----- 480
 QY 115 GEATGVDAICTHRPDTGTGDLREQYLLEL-SOLTHSITELGFTYTLDRSLYVNGFTHRS 173
 DB 481 -----NCTGP-----LTVLRGNITNCGDSTGWYRLD---LYINGV--RT 515
 QY 174 SVPTTGTGVSEEPFTLNFTI-----NNLRMADMGQ 205
 DB 516 AGKWEVGSLETPPEFTEFLNRNRAVSQVNNFPATVRVFLGLIIPENLRVTPSGGQ 575
 QY 206 PGSLEKNTDVMKHLSPFQRSSIGARYTCGRVIALRSVKNGAETRV----- 254
 DB 576 E-PLKVNVTADLVNYGDLPSYTAEL---YIDGVLLDSRNVTVNASRRTVSFNRTLAAG 631
 QY 255 --DLLCTYLQP-----LSGPGPLIKQVHFELSQOHTG-----ITRL--GPYSLDK 295
 DB 632 LYEITINDLEPELVVYMEGKFIEN--FLTTPSGAALPLTVTVSAMITNDSNPSRYTA 689
 QY 296 DSIYING-----YNEPGDEPPTPKPATTPPLPSEATTANGYH---LKTLT-LNF 343
 DB 690 -TIYNGVDPHTKVLNIPGES---TVPFSTISLLPDRGLYTIISLNNVSGTVRVLSEANF 745
 QY 344 TISNLQYSDMGKGSATFNSTEGVQLHLLRPLQKSSMGPFYLCQLISLRPEKGAATG 403
 DB 746 TISNVTSPVEGKSLNVTVAIV-----RNGDLAG 777
 QY 404 VDTTCTYHPDPVPGGLDIQOLYWELSQHTGVTLQGLFYVLDRLDRSLFINGYAPQNLIRGE 463
 DB 778 -DFAVTLYLDDVA-----WETRTVS-----VPGKSSVLVS--FKELAPPG 816
 QY 464 YQINFHI---VNNLNSNDPPTSSEYITLLRDIDQKVTTLTKGSLQHDTPFCL-VTN--- 516
 DB 817 YRLRLNSGTDVTRVLEPDPITGF-----NVTPTGPAFL--SVRASLNVNTPHD 865
 QY 517 -----LTMDSVLTVTKALFSSNLDPSLVEQVFLDKTLNASFWLHG----- 556
 DB 866 LVIGFTARLMVDGVVQENIV---SLSPGSETREIAMGTLTPGNHTVGINEFSKIVRLR 922


```
Db 2094 DTGHSTVITTHGSLATTQVSLTPSSQNMSTVSMPTSSSQELTSLPQHQHTG--SMETSS 2151
Qy 659 PLARRVDRAVYEEFLMRNTRNGTOLQNFITLDRSS 692
Db 2152 QPQNITPTVTTTSLTSFSRSGSTELQTMWGTS 2185

RESULT 10
Q94K06_ARATH
ID Q94K06_ARATH PRELIMINARY; PRT; 605 AA.
AC Q94K06;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE TRNA adenylyltransferase-like protein.
GN Name=r22J18.17; Synonyms=At1G22660;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OC NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lam B., Southwick A., Karlin-Neumann G., Nguyen M., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.;
RA Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Nguyen M., Karlin-Neumann G., Southwick A., Tripp M., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.;
RA Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF370489; AAK43866.1; -; mRNA.
DR EMBL; BT000361; AAN15680.1; -; mRNA.
DR GO; GO:0005739; C-mitochondrion; IDA.
DR InterPro; IPR012222; PAP_CCA.
DR InterPro; IPR012277; Poly(A).
DR InterPro; IPR002646; PolyA_pol_reg.
DR PANTHER; PTHR13734; PolyA_pol.1.
DR Pfam; PF01743; PolyA_pol.1.
DR PIRSF; PIRSF000814; PolyA_pol.1.
DR Nucleotide; Nucleotide; RNA-binding; Transferase.
SQ SEQUENCE 605 AA; 68953 MW; 2DB2778EA9368A18 CRC64;

Query Match 3.4%; Score 136; DB 2; Length 605;
Best Local Similarity 20.6%; Pred. No. 2;
Matches 99; Conservative 67; Mismatches 185; Indels 130; Gaps 20;

Qy 113 KGEATGDAICTHRPPTGPGDRLDQYLSLTHSITELGPTLDRSLYNGGTHR 172
Db 152 RDEEVQVQ-DTVIERNPD-----QSKHLETAKL-----RIYDQWIDFVNLRSSEYTEN 197
Qy 173 SSVPTSTGVSEPPFTLNFTNNLRNLYMADMGQPSL-KFNITDNVKKHLSPFLFRSS- 230
Db 198 SRITPMFGTAKDAFRDLTINSFLFYNGSAGEDLTERGIDDLKSGKIVTLPKATPF 257
Qy 231 -----LGARYTGCRVIALRSVKNGAETRVLLCTYLOPLSGPLPIKQVFHEL 278
Db 258 LDDPLRLVLRVFRGAFGFTLDEELKEAASSEVRVAL-----GEKISRERIGNEI 308
Qy 279 SQQTHG-----ITFLGYSLDKSLYNGVNEFGPDPEP-----PTTPKP 317
Db 309 DLMTSGNGPVSATYLSDLKLFVSVFALPSSAEPSPENCGSLSQSVLEAMWSLLKTPRP 368
Qy 318 -----ATTFLP-----PLSEATTANGVHLK 337
```

```
Db 369 GKFSGEORRLALYAAMFLPRKTVYKDTKGKSIPIVVNHIKFKSMKRKTSDAETVMNIHOT 428
Qy 338 TLTLNFTISNLQYSPDMGKGSATFNSTEGVLOH-----LLRPLFKSSMGPFYLGCCQLIS 392
Db 429 TERFRSLIPSLEVKDVELDELWTW--AADILEHWKSIITLNDPVPATSKIRVLGTG----FL 483
Qy 393 LRPEKD----GAATGVDITCTYHPDPVPGCLDTCQLYWELSQL--THGVTLQGLFVVLDRD 446
Db 484 LRDIKDFWRVSLTSLTSLSATV--DGSNDHODIGQLDFQLERKRETYLTVEATITHELGLD 541
Qy 447 SLF-----INGYAPQNLIS-IRG-----EYQINPHVNNMNSNPDPTSSSYITLLRIQD 494
Db 542 KIWDAKPLVNGREIMQIAELKGGSLRIREWQOK--LLTWLAYPNGTAEBCKEKWRMDIKA 599
Qy 495 K 495
Db 600 K 600

RESULT 11
YN96_YEAST
ID YN96_YEAST STANDARD; PRT; 1117 AA.
AC P53753;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-MAY-2005 (Rel. 47, Last annotation update)
DE Hypothetical 121.1 kDa protein in BIO3-HXT17 intergenic region precursor.
DE OrderedLocusNames=YNR067C; ORFNames=N3547;
GN Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OC NCBI_TaxID=4932;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=97313269; PubMed=9169873;
RA Hegenann J.H., Obermaier B., Urrestarazu L.A., Aert R., Albermann K.,
RA Altmann R., Andre B., Baladron V., Ballesta J.P.G., Becam A.-M.,
RA Beinbauer J.D., Boskovic J., Buitrago M.J., Bussereau F., Coster F.,
RA Crouzet M., D'Angelo M., Dal Pero F., De Antoni A., del Rey F.,
RA Dolignon F., Domdey H., Dubois E., Fiedler T.A., Fleig U., Floeth M.,
RA Fritz C., Gaillardin C., Garcia-Cantalejo J.M., Glansdorff N.,
RA Goffeau A., Guellderer U., Herbert C.J., Heumann K., Heuss-Neitzel D.,
RA Hilbert H., Himi K., Iraqui Houssaini I., Jacquet M., Jimenez A.,
RA Jonnaux J.-L., Karpfinger-Hartl L., Lanfranchi G., Lepingle A.,
RA Levesque H., Lyck R., Matfahi M., Mallet L., Maurer C.T.C.,
RA Messenguy R.K., Pandolfo D., Pierard A., Nasr F., Nicaud J.-M.,
RA Niedenthal R.K., Pierard A., Pierard A., Piravandi B., Planta R.J.,
RA Pohl T.M., Purnelle B., Rebischung C., Remacha M.A., Revuelta J.L.,
RA Rinke M., Saiz J.E., Sartorello F., Scherens B., Sen-Gupta M.,
RA Soler-Mira A., Urbanus J.H.M., Valle G., Van Dyck L., Verhasselt P.,
RA Vierendeels F., Vissers S., Voet M., Volckaert G., Wach A.,
RA Wambutt R., Wedler H., Zollner A., Hani J.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XIV and its evolutionary implications.";
RL Nature 387:93-98(1997).
CC -!- SIMILARITY: Belongs to the glycosyl hydrolase 81 family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
CC EMBL; Z71682; CAA96349.1; -; Genomic_DNA.
DR PIR; S63399; S63399.
DR GenOnline; 143412.
DR Ensembl; YNR067C; Saccharomyces cerevisiae.
DR SGD; S000005350; D8E4.
DR GO; GO:0030428; C:cell septum; IDA.
DR GO; GO:0009277; C:cell wall (sensu Fungi); IDA.
DR GO; GO:0007109; P:cytokinesis, completion of separation; IEF.
```


Db 357 SYDKIADALQFNYSNDRSSLSQNSKFV---PLMLNLKGMKPNYVTKPTVTFMENN--YL 411
Qy 201 ADMGQPSGL-KFNITDNVMKHLSPFQ----- 227
Db 412 ----QQGSLIILNIFLMSKFKQPLSKAKACELIVALSERVNDCKLDRCLPYLCNLLD 467
Qy 228 ----RSSLGARYTG---CRVIALRSVKGAEATRVLDLLCTVLOPLSGPL 269
Db 468 EYDSSSINTQPNFQNLSENFTSSSEVACIALTSI-----TYLMSCSYINPIN--- 518
Qy 270 PIQGVFHELQOOTHGIRLGPYSLDKSLYNGYNEPFGDPPTTPKPAATFPLPSEAT 329
Db 519 -VLMFSEVLLPKHALISIPKNDKLIKIT-----LAACLPYLANVS 561
Qy 330 TAMGYHUKTL-----TINFTISNLQYSPDMGKGSATFNS-----TEGVLOHLL 372
Db 562 KKFWMGSKTFKNDVLDKLNRLSKPLDDKENVSDSYNSFSIRKEQLDSDFENLASKLL 621
Qy 373 ---RPLFKQSSMGPFYLGCOLISLRPEKGAATGVDTT-----CTYHPDP----- 414
Db 622 TDVNPWKISLVNNIMPLCQFF-----GVDKTNDIILPHLITYLNDSEYELRLA 670
Qy 415 -----VGPGLDIQQLYWELSQLTHGVTOLG-----FYVLDKSLIFNGYA 454
Db 671 FLSSILGIGPVGV--LSFEQYILPLLIQTLGDLQEQFVILKVLRFYFCFVRDL-INPKS 727
Qy 455 PQN-LSIRGEVQINFHVNNLSNPDTSSTSYITLLRD--IQDKVTLYK--GSQLHDTF 509
Db 728 EFNALSIYKELL-----TSSIKLLLPNEWIRQSVICLILALISDNLDDAD 772
Qy 510 RFCLVTLNLTWDSVLVTVKALPSSNLDPSLVEQV-----FLDKTNAASFHGLGSTY 559
Db 773 KYCLYPIVGVFLVDVNTNNTLYFSITKPLSKQIYNLAIWSSNASKSLFWQKSP 832
Qy 560 QLVD-----IHTVEMESSVQPTSSSSTQHFYLNFTITNLPSYQDKAQPGTTNYQR 610
Db 833 SVFNDLKAAPTILPYSTNMKGSVIYKSKNG---FSLNNTNSNIPLSPEKQ-----WVL 884
Qy 611 NKRNIEDALNQLFRNSIKSYFSDCQVSTFRSVNRHHTGVDSL-----CNFSPLARVD 665
Db 885 KLSVGLNDRDLWKIFILRDYIYHSSKS-----NTSPTAKDDFELPKDINITP--RNVF 936
Qy 666 RVAYIEFLMTRNGTQONFTLDRSSVLDVGYSPNRPETGNSADIQHSGRSSLEGP 725
Db 937 FEVCYKSEPPSSGSKTATNF-----ESV-----HTLSNKKDBDSTRLGNSLILP 982
Qy 726 RFEQKLIS-----EEDLNMTGHHHHH 747
Db 983 NFGVKVSLQTVQANVFGELDTSHDSSFNASSSHHHH 1020

RESULT 13

ID Q54E23 DICDI PRELIMINARY; PRT; 797 AA.
AC Q54E23
DT 13-SEP-2005 (TreeBLrel. 31, Created)
DT 13-SEP-2005 (TreeBLrel. 31, Last sequence update)
DE Hypothetical protein AAC1.
GN Name=AAC1; ORFNames=DD80201568;
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RC NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.A.,
RA Suganb R., Beriman M., Song J., Olsen R., Szafranski K., Xu Q.,
RA Tungal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
RA Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.,

RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,
RA Wardner H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
RA Harroper A., Felder M., Thangavelu M., Johnson D., Knights A.,
RA Loubeleg H., Mungall K., Oliver K., Price C., Quail M.A.,
RA Urushihara H., Hernandez J., Rabinowitz E., Steffen D., Sanders M.,
RA Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
RA Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
RA Shaulsky G., Schleicher M., Weinstock G., Rosenthal A., Cox E.C.,
RA Chisholm R.L., Gibbs R., Loomis W.F., Platzner M., Kay R.R.,
RA Williams J., Dear P.H., Neigel A.A., Barrell B., Kuspa A.,
RT "The genome of the social amoeba Dictyostelium discoideum";
RL Nature 0:0-0(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC ENBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AAFI01000264; EAL61460.1; -; Genomic_DNA.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR007091; LRR_RNinh.
DR InterPro; IPR003590; LRR_RNinh_sub.
DR Pfam; PF00560; LRR_1; 2.
DR PRINTS; PR00019; LEURICHRPT.
DR SMART; SM00368; LRR RI; 7.
KW Hypothetical protein; Leucine-rich repeat; Repeat.
SQ SEQUENCE 797 AA; 89497 MW; OCCB0676C5C581PF CRC64;

Query Match 3.4%; Score 132.5; DB 2; Length 797;

Best Local Similarity 19.2%; Pred. No. 5.2;
Matches 173; Conservative 118; Mismatches 311; Indels 299; Gaps 42;

Qy 6 RRARRTKLFTHRSVSTSTPGTPTVVLGASKTPASIFGPSAASHLLILFLTNFTINLR 65
Db 3 RTSNRNEATAKLSSTSTITTTTNNKYNNANAES-----SKSTISNLI 48
Qy 66 YEENMPGSRKFNTERVQLGLRLPKNTSVGLYSGCKRLTLRPKEGEA-----TGV 120
Db 49 PKYSLFNEPNNDT-----NSSTRP--NKQOKLLKSNESTTSTTTTTP 92
Qy 121 DAICTHRPDPGCLDR---EQLYLELSQLTHSITELGPTVLDLDRSLVNGFTHRSSVPT 177
Db 93 TTTTITTTTNNLSKYNNYIEKQEKQNL---PTTETTTITPTLTITTTTTT 148
Qy 178 TSGVWSEE-----PFTL-----NFTINN 196
Db 149 TTTTITTKQIONTTSTINFLPLIIQKEIIFLLVELGSFLNARKVKYKVCNGCVEN 208
Qy 197 LR-YMADMGQPSGLKFNITDNVMKHLSPFQSSLGARYTGCRVIALRSVNGAETRD 255
Db 209 LNTYFTDIHLSASVK-HVSEVFKVSLNSDYFHLQSV-----SPINGAKNSIS 254
Qy 256 LLCTYLOPLSGP-----GLPIKQVPHELSQQTHGITRLGYPYSLDKDS 297
Db 255 YSEFYFNNVILPFIENVVRYNQTIENTFTIGFPIITRNKSSQOL-----LPSYKLVHST 309
Qy 298 LYLNGYNPGPDDEPTTPKP-----ATFPLPSEATTAMGYHUKT----- 338
Db 310 SVSSPP 369
Qy 339 -LTINFTISNLQYSPDMGKGSAT-----FNSTEGVLOHLLRPLPFOKSGMPYLGCOLIS- 392
Db 370 YLTNNFKLKKINLK-NIGLDRDKFDFSSLSNVNNTLETIIICDNIIGD--EGMQLLSV 426
Qy 393 -----LRPEKGAATGVDTTCTVHPDPVGPGLDIQQLYWELSQLTHGVTOLGP 440
Db 427 ILIKNLLKLVKRLQLKN-----QFTNQSAYLNKV-----LSCEQLQLETNLSSN- 473
Qy 441 YVLDKSLIF--NGYAPQNLISIRGEVQINFHVNNLSNPDTSSTSYITLLRDIDQKVTT 498
Db 474 -RIDEQGLIMWKDGFGRNLSLK-----EPIFSKRLGNTDSV-----DFGKSI 517
Qy 499 LYKGSQHLDT-----FRCLVTNLTWDSVLVTVKALPSSNLDPSLVEQVFLDKTL 548
Db 518 L-----DLHDSMVGSKQSIKGLSQYLKFNESITSLNLSFNHIGSNEAIKSLSKSPAVNQT 573


```
Db 488 DSTISSTNYLSVLAQSSSTINCQNQISSTVLTNSQLSSGSGVANITGTNYLS 547
Qy 598 QD-----KAQPTTYQNRKNIB-----DALNQLFRNSSIKSVFSD 634
Db 548 GSSITGVTQNRMSWLSLNTQISSNVNMGVSTLSAGSTINSQNGSTI--YLSN 605
Qy 635 CQV-----STFRSVPNRHHTGV-----DSLGNFSPRLARRVDRVAIYEELFRMTRNG 680
Db 606 SQINGGVNVSSTKLYVTGSTIGVTVSGGSGFISLSSTSSSTVSISDSTLNATGST 665
Qy 681 TQONFLDRSSVLVDGYS--PFRNEPLTNSADIQHS 716
Db 666 ITSTQNIQSTLYISGTTVSNSKOTLTNTNAYISNS 703

RESULT 17
Q81FJ0_BACCR PRELIMINARY; PRT; 5017 AA.
AC Q81FJ0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cell surface protein.
GN OrderedLocuNames=BC1592;
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=226900;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
RA Kaparal V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,
RA Chu L., Mazur M., Coltesan E., Larsen N., D'Souza M., Walunas T.,
RA Grechkin Y., Pusch G., Hasekorn R., fonstein M., Ehrlich S.D.,
RA Overbeek R., Kyrpides N.C.;
RT "Genome sequence of Bacillus cereus and comparative analysis with
RT Bacillus anthracis.";
RL Nature 423:87-91(2003).
DR EMBL; AB017003; NAP08571.1; -; Genomic_DNA.
DR GO; GO:0005727; C:extrachromosomal circular DNA; IEA.
DR InterPro; IPR001434; DUF11.
DR Pfam; PF01345; DUF11; 28.
DR TIGRFAMs; TIGR01451; B_ant_repeat; 35.
KW Complete proteome.
SQ SEQUENCE 5017 AA; 523460 MW; 599E8A8DA930224F CRC64;

Query Match 3.2%; Score 128; DB 2; Length 5017;
Best Local Similarity 18.6%; Pred. No. 1.7e+02;
Matches 152; Conservative 127; Mismatches 327; Indels 212; Gaps 39;

Qy 17 RSVSVTSPTGTTVVLGASKTPASIFGSAASHLLILFTL-----NFTITNLYEENM 70
Db 3658 QAQLATKTSTNPTVDIGGT-----ILYISEVKNGVDAININFTDSI 3701
Qy 71 WPSRKFNTTERTVQLGLRLPLF---KNTSVGLPSYSGRLTLL-----RPEKDEATG-V 120
Db 3702 -PAGTTFVPSDVINGVLQGVNPNENGIPGTPIPANSKTLIFQVQTNPPNETIVNQS 3760

Qy 121 DAICTHRPDPTGFLDR-----EQYLELSQL-----THSITELG 155
Db 3761 SATYQVVISIPTAPVNRANSNIVTTSLNQANIISVKSDVNFVSIGQMITYNTLNQIG 3820

Qy 156 PYTLD-----RDSLYNGFTHRSVP---TTSYGVSVSEPTFLNPTI--N 195
Db 3821 TVPANNIVFDINIPEDTIFEDSLAINNVIPQGNPNENGVLGTIQPNETVTSFQVQLT 3880

Qy 196 NLRYMADMGQPSLKFNITDNVKKLL---SPLFQRSSL--GARYTCGRVIALRSVK--NG 249
Db 3881 NI-----PEGNTVINISTSYEQIDPSPIQRSSLSNAVNTVETRVANSALISANR 3933

Qy 250 AETRVLLCTYLQPLSGP-LPIKQVFHELSQQTHGTRILGPYSLDKDSLNLNGYNPEGP 308
```

```
Db 3934 SITRIGQIITYVAVTNAGTIPITNTL--LLDAIASGTTTVPNSILVDGV-----PRP 3984
Qy 309 DRPPTTPKPAATFPLPLSEATTAMGYHLKTLTL-----NFTISNLQYSPDMGKG--SA 359
Db 3985 NENPITGINLDILP---NNTIIVTFQSVSVIPPQNINNTIAVIHYERPDPSTPISE 4041
Qy 360 TPNSTEGVLQHLRLPLFQKSMGPPFYLGCQLISLRPEKDGAAATGVDTTCTTHPDPVPGGL 419
Db 4042 TTSNATNIQ-----FIDAILIATKSANTVLAT-IDETIETTVFIQNWGS 4085
Qy 420 DIQQLWELSQLTHGVTQGVYVLDLDRDSLFIN-----GYAPONLSIRGEVQINF 468
Db 4086 ATNNSIFFTDTADGT-----VFIPGSVIVNNTVLPADPNIGFSIPNVAAGOMATITP 4139
Qy 469 HIVNWNLS--NPDPYTSSEYI-----TLLRDIQDKVTTLTKGSQLHD-----TFRFCIVTN 516
Db 4140 QVSVTNLPTVNTPTANIVDFINPDPFAPQKSTTSNTTFVQINDADIVLSLKTVDLTS 4199
Qy 517 LTMDSVLTVTKALFSS-NLDPSSLVEQVPLDKTLNASFHWLGSY-----QL-----VDIH 565
Db 4200 VTIGDILTVTTTLTNTGNTATAV--VPTDNIPDGTTFIDGSLVNNIPQLNANPSVGIL 4257
Qy 566 VTEMSSVYQPTSSSTQHFYLNFTITNLPYSQDKAQPCTTNYQNRKNIEDALNQLFRN 625
Db 4258 VGTIAPNISIPVTFS-----VTYVALPASGHVQNSTSRY---TINVEQIST--SN 4304
Qy 626 SSIKSYFSDCOVSTFRSVPNRHHTGVDSLCNFSPLARRVDRVAIYEELFRMTRNGT--QLQ 684
Db 4305 IPTFEVISANVIAT-KTTFIQY-----ADLQTIIPYTSITNNGNIQVE 4347
Qy 685 NF-----TLDRSSVLVDGYSFNRNEPLTNGSAD 712
Db 4348 NIIATDIIIPVNTSFIENSIVNGNRPNDNPLNGIQID 4385

RESULT 18
Q4UDD4_THEAN PRELIMINARY; PRT; 1166 AA.
AC Q4UDD4;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=TA14175;
OS Theileria annulata.
OC Eukaryota; Alveolata; Apicomplexa; Pioplasmda; Theileridae;
OC Theileria.
OX NCBI_TaxID=5874;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Ankara isolate clone C9;
RA Pain A., Renauld H., Murphy L., Harris D.A., Quail M.A., Berriman M.,
RA Hall N., Barrell B.G.;
RT "The chromosome 2 sequence of Theileria annulata.";
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR940348; CAI74905.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 1166 AA; 135275 MW; 2023F80318A19581 CRC64;

Query Match 3.2%; Score 127; DB 2; Length 1166;
Best Local Similarity 20.6%; Pred. No. 22;
Matches 175; Conservative 120; Mismatches 297; Indels 258; Gaps 50;

Qy 16 HRSSVSTSTPTGTTVVLGASKTPASIFGSAASHLLILFTLNFTITNL-----RYEEN 69
Db 47 NNSRLNSNVTPTTNNKGGGT-----DFFDDP-----VTFVREFSSETLWVPEFSFEKN 96
Qy 70 MWPSRKFNTTERTVQLGLRLPLFQKNTSVGLPSYSGRLTLLRPEKDEATGVDALCTHRPD 129
Db 97 VYK-SRYLNTQE--CFALLNAHYKMLMNN--YAPRVQTLVQTOSMITEFT-----KPK 143
Qy 130 PTGPGDLRQLYLEL--SOLT-HSITELGYTLDR-----DSLYVNGFTHRSSVPTTSTGV 182
```

```
Db 144 ETG-----QYYQYTSVTFEALNEMSLFTKDHMSLSILVVLGNHNLNLEGLRT-- 195
Qy 183 VSEPFLLNTINNRYMADMGQPSLKFNITDNVMKHLSPF--QRSLGARYGCRV 240
Db 196 -----YVLN--VMRLLYRAVTGSK-----SNQVEKSRFLFTLTKNYNG-----RA 235
Qy 241 IALRSVKGAEATRVLLCTVLOPL--SGRGLPIKQVF-----HELSSQOHTGIT 286
Db 236 VLYML-----LLCTLEKLLWFSEPOLYDDFVSFAFICSFVESATSKTHQKD 286
Qy 287 RLGPYSLDKSLYLNGYNEPGDEPPTTPKPAATFPLPPLSEATTAMGYHLKTLTLNFTIS 346
Db 287 LTNNYQKGSVL-----TDKPGTSRK--NDLIPAMASNTDMLVRHLSVVCV---LL 333
Qy 347 NLQVSPMGKGSATFNTEGVLOHLLRPLFKQSMGPFYLGCLISLRPEKGAATGVD 406
Db 334 KLVTP---QNKSLLESVFLRNALRSIPNRKNLLLTWSIMIVLDPQEIANT----- 386
Qy 407 TCTVHPDPVGPGLDI--QOLYWELSQLTHGVTLGFGFYVLDRLSLF-----INGYAPQNLIR 461
Db 387 -----FKIPRSLFIEVGEI--NDMTQLVHLVLCIDNCFRDLKFSNFVESINVS 433
Qy 462 GEYQI--NF--HI--VNMWLSNP----- 478
Db 434 TFVQLFLFNWFKWHDALNEDLANEILLANSVLDSYPNLYSVFPAKYISOFTNSSESNTY 493
Qy 479 ---DPTSEYITLARDIQK---VTT-----LYKGSQHLDTFRCLVNTLMTDSVLV 524
Db 494 NALNPQHNQYNYNREOEKKNQMTQEIKLSHRIQKSMELFNIAFGKSRQLQMAAVL 553
Qy 525 TVKALFNSLDPSL-----VEQVFLDKTLNASFWHLGTYQLVDIHVTEMESVYQPT 577
Db 554 ASKLMSSDVTTLPRLINKLYKSNMELD--LLNLS---LNNQYTVND---TDYE---YNTQ 603
Qy 578 SSSSTQH--FYLNFTITNLYPSQDKAQPCTTNYQNRKNRTEDALNQLFRNSSIKSYFSDC 635
Db 604 YNNHTDYDTFYKONKLEPNQDKFVQDLTRL-----TLMSAFINHCWKELISTL 654
Qy 636 QVST-----FRSVPNRHTG---VDSICNFSPLARRVDRVAIYEEFLRMTRNGTQLQNT 687
Db 655 MSKTGPKLFEXQKNRPHNGFVDS--GKLNAVEGYDRKDVYKNYNRM-----E 703
Qy 688 LDRSSVLVDGSPNREPLTNSADIQ-----HSGGRSSLE-----GPREFQK 730
Db 704 IDR-----VDGV--DRESKIDG---DVQRVLVSRLSYLGSNATIDSLYSILFSGP--PPAK 753
Qy 731 LISEEDLNMH 740
Db 754 VLSYEALRAH 763
```

RESULT 19

```
Q86AL8_DICDI
ID Q86AL8_DICDI PRELIMINARY; PRT; 1364 AA.
AC Q86AL8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Similar to Dictyostelium discoideum (Slime mold). Hypothetical 127.0
DE kDa protein.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RX MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847;
RA Gloeckner G., Eichinger L., Szafranski K., Pachebat J.A.,
RA Bankier A.T., Dear P.H., Lehmann R., Baumgart C., Parra G.,
RA Abril J.F., Guigo R., Kumpf K., Tunggal B., Cox E., Quail M.A.,
RA Platzer M., Rosenthal A., Noegel A.A.;
RT "Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";
```

```
RL Nature 418:79-85 (2002).
RN (2)
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RA Baumgart C.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC116984; AAO51349.1; -; Genomic_DNA.
DR InterPro; IPR006209; EGF like.
DR PROSITE; PS00022; EGF_1; UNKNOWN 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN 1.
KW Hypothetical protein.
SQ SEQUENCE 1364 AA; 153737 MW; 3A194428A8D7DD8F CRC64;
```

Query Match 3.2%; Score 127; DB 2; Length 1364;

Best Local Similarity 21.1%; Pred. No. 28;

Matches 114; Conservative 65; Mismatches 190; Indels 172; Gaps 25;

```
Qy 181 GVSEBPFLLNTINNRYMADMGQPSLKFNITDNVMKHLSPFORSLSGA 233
Db 107 GVQVFSRFSLNHSINN-----SISLNFICQAIQIDYKLDYKLMVNRFRKST--S 153
```

```
Qy 234 RYTGCRVIALRSVKGAEATRVLLCTVLOPLSGPLPIKQVHLSQOHTGI---TFLGP 290
Db 154 NYGG-----YLOFTS--EYPLGQL--EYSNTSGVLSTIENT 187
```

```
Qy 291 YSLDKDSLILNGYNEPGDEPPTTPKPAATFPLPPLSEATTAMGVHLKTLTLNFTISNLQY 350
Db 188 ANLAGGSLMTN-----FRNLVSVMFVGIYNNISYIEV----- 221
```

```
Qy 351 SPDMGKGSATFNTEGVLOHLLRPLFKQSMGPFYLGCLISLRPEKGAATGVDTTCT 409
Db 222 -PSLYYTNIDVNSNSIVTMYPNQVQYNEFG--FGCPPLFTITNR-----TTDE 269
```

```
Qy 410 YHDPDPVGPGLDIQOLYWELSQLTHGVTLGFGFYVLDRLSLFINGYAPQNLIRGEYQINFH 469
Db 270 YQP-----YFYV-----SLINGLGTGNIQIYPLYEINQM 298
```

```
Qy 470 IVNMWLSNPDPSTSEYITLARDIQDKVTTYLKGSLQHLDTFRCLVNTLMTD-----SV 522
Db 299 ATYIGHPDGAATVS--YTFLSQSDNLSLTIYK-----VENLTVTKLKQSFSST 345
```

```
Qy 523 LVTVKALFNSLDPSLVEQVFLDKTLNASFWHLGTYQLVDIHVTEMESVYQPTSSSST 582
Db 346 VVIATYLHGN-----ETLYNSSMTYISFN--SGILKQVDFPPT-----VYRFQSSSS- 391
```

```
Qy 583 QHLYLNTITNLYPSQDKAQPCTTNYQNRKNRTEDALNQLFRNSSIKSYFSDCQVSTFRS 642
Db 392 -----VILNWPFGFSGQNFNFKSSH-----LQNLFSINSISSFTTDKNISTVTQ 438
```

```
Qy 643 VPMRHTGVDSLCLNFSPLARRVDRVAIYEEFLRMTRNGTQLQNF-----TLDR--SSVLVDG 697
Db 439 SDIKTLGFSNLIIRYESIVEEDNEVVVFETVDFEKK--YGLGNFYFDSLNRMKSYLVNN 497
```

698 Y 698

498 Y 498

RESULT 20

Q54V40_DICDI

ID Q54V40_DICDI PRELIMINARY; PRT; 885 AA.

AC Q54V40;

DT 13-SEP-2005 (TrEMBLrel. 31, Created)

DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)

DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)

DE Hypothetical protein.

GN ORFNames=DD80206085;

OS Dictyostelium discoideum (Slime mold).

OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.

OX NCBI_TaxID=44689;

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=AX4;

THIS PAGE BLANK (USPTO)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 20, 2006, 07:30:27 ; Search time 39.8343 Seconds
(without alignments)
1552.466 Million cell updates/sec

Title: US-10-687-035-1

Perfect score: 3945

Sequence: 1 AAQPARRRARTKLFTHRSSV.....QKLISEEDLNMTGHHHHH 748

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents AA:*

1: /cgn2_6/prodata/1/iaa/5 COMB.pep.*

2: /cgn2_6/prodata/1/iaa/6 COMB.pep.*

3: /cgn2_6/prodata/1/iaa/H COMB.pep.*

4: /cgn2_6/prodata/1/iaa/PTUS COMB.pep.*

5: /cgn2_6/prodata/1/iaa/RE COMB.pep.*

6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3663	92.9	833	2	US-09-404-879A-389
2	3663	92.9	833	2	US-09-667-857-389
3	3663	92.9	833	2	US-10-198-053-389
4	3663	92.9	833	2	US-09-827-271-389
5	3663	92.9	914	2	US-09-404-879A-312
6	3663	92.9	914	2	US-09-338-933-312
7	3663	92.9	914	2	US-09-667-857-312
8	3663	92.9	914	2	US-10-198-053-312
9	3663	92.9	914	2	US-10-198-053-478
10	3663	92.9	914	2	US-09-827-271-312
11	3651	92.3	3451	2	US-10-198-053-595
12	3642	92.3	1148	2	US-10-198-053-458
13	3642	92.3	1148	2	US-10-198-053-479
14	3642	92.3	1148	2	US-09-827-271-458
15	3642	92.3	1156	2	US-10-198-053-458
16	3642	92.3	1156	2	US-09-827-271-459
17	3189	80.8	772	2	US-09-404-879A-388
18	3189	80.8	772	2	US-09-667-857-388
19	3189	80.8	772	2	US-10-198-053-388
20	3189	80.8	772	2	US-09-827-271-388
21	1996	50.6	438	2	US-10-198-053-483
22	1990	50.4	438	2	US-09-404-879A-390
23	1990	50.4	438	2	US-09-667-857-390
24	1990	50.4	438	2	US-10-198-053-390
25	1990	50.4	438	2	US-09-827-271-390
26	1436	36.4	304	2	US-10-198-053-486
27	1345	34.1	318	2	US-10-198-053-594

28	903	22.9	178	2	US-10-198-053-489	Sequence 489, App
29	903	22.9	233	2	US-10-198-053-488	Sequence 488, App
30	842.5	21.4	294	2	US-10-198-053-487	Sequence 487, App
31	814	20.6	313	2	US-10-198-053-461	Sequence 461, App
32	814	20.6	313	2	US-09-827-271-461	Sequence 461, App
33	809	20.5	155	2	US-10-198-053-591	Sequence 591, App
34	800	20.3	150	2	US-10-198-053-593	Sequence 593, App
35	697	17.7	134	2	US-10-198-053-592	Sequence 592, App
36	675.5	17.1	210	2	US-10-198-053-481	Sequence 481, App
37	662	16.8	230	2	US-10-198-053-480	Sequence 480, App
38	659.5	16.7	156	2	US-10-198-053-589	Sequence 589, App
39	651.5	16.5	156	2	US-10-198-053-596	Sequence 596, App
40	637.5	16.2	156	2	US-10-198-053-590	Sequence 590, App
41	611.5	15.5	268	2	US-10-198-053-485	Sequence 485, App
42	607.5	15.4	156	2	US-10-198-053-584	Sequence 584, App
43	600.5	15.2	156	2	US-10-198-053-587	Sequence 587, App
44	599.5	15.2	156	2	US-10-198-053-583	Sequence 583, App
45	598.5	15.2	156	2	US-10-198-053-586	Sequence 586, App
46	595.5	15.1	156	2	US-10-198-053-588	Sequence 588, App
47	592.5	15.0	156	2	US-10-198-053-580	Sequence 580, App
48	589.5	14.9	156	2	US-10-198-053-577	Sequence 577, App
49	585.5	14.8	156	2	US-10-198-053-574	Sequence 574, App
50	585.5	14.8	156	2	US-10-198-053-585	Sequence 585, App
51	583.5	14.8	156	2	US-10-198-053-582	Sequence 582, App
52	577.5	14.6	156	2	US-10-198-053-581	Sequence 581, App
53	572	14.5	155	2	US-10-198-053-578	Sequence 578, App
54	569	14.4	155	2	US-10-198-053-579	Sequence 579, App
55	568.5	14.4	158	2	US-10-198-053-575	Sequence 575, App
56	564	14.3	216	2	US-10-198-053-484	Sequence 484, App
57	485.5	12.3	122	2	US-10-198-053-576	Sequence 576, App
58	307	7.8	130	2	US-10-198-053-573	Sequence 573, App
59	161.5	4.1	635	2	US-09-545-814-32	Sequence 32, Appl
60	156	4.0	28	2	US-10-198-053-597	Sequence 597, Appl
61	146.5	3.7	466	2	US-09-604-107A-8	Sequence 8, Appl
62	144.5	3.7	50	2	US-09-360-237-53	Sequence 53, Appl
63	140	3.5	28	2	US-10-198-053-598	Sequence 598, App
64	138	3.5	666	2	US-09-213-888-27	Sequence 27, Appl
65	138	3.5	666	2	US-09-328-877D-27	Sequence 27, Appl
66	121.5	3.1	1475	2	US-09-538-092-1160	Sequence 1160, Ap
67	118.5	3.0	10182	2	US-09-134-001C-3159	Sequence 3159, Ap
68	118	3.0	28	2	US-10-198-053-599	Sequence 599, App
69	117.5	3.0	637	2	US-09-489-039A-9243	Sequence 9243, Ap
70	117.5	3.0	2446	1	US-08-551-356-2	Sequence 2, Appl
71	117.5	3.0	2446	1	PCT-US93-12687-2	Sequence 2, Appl
72	117	3.0	21	2	US-09-071-710-41	Sequence 41, Appl
73	117	3.0	21	2	US-08-912-276-25	Sequence 25, Appl
74	117	3.0	21	2	US-09-153-804-17	Sequence 17, Appl
75	117	3.0	21	2	US-08-944-483-76	Sequence 76, Appl
76	117	3.0	21	2	US-09-525-397-41	Sequence 41, Appl
77	117	3.0	21	2	US-09-566-876-16	Sequence 16, Appl
78	117	3.0	21	2	US-09-049-698-51	Sequence 51, Appl
79	117	3.0	21	2	US-09-065-383-33	Sequence 33, Appl
80	117	3.0	21	2	US-09-276-600-11	Sequence 11, Appl
81	117	3.0	21	2	US-09-193-884-29	Sequence 29, Appl
82	117	3.0	21	2	US-09-050-516-49	Sequence 49, Appl
83	117	3.0	21	2	US-10-278-547-49	Sequence 49, Appl
84	117	3.0	21	2	US-09-431-384B-31	Sequence 31, Appl
85	117	3.0	21	2	US-09-052-855A-30	Sequence 30, Appl
86	117	3.0	21	2	US-09-080-140-31	Sequence 31, Appl
87	117	3.0	21	2	US-09-092-297A-22	Sequence 22, Appl
88	116.5	3.0	910	2	US-09-270-767-42083	Sequence 42083, A
89	115.5	2.9	1377	2	US-09-949-016-6058	Sequence 6058, Ap
90	115.5	2.9	838	2	US-09-315-794-52	Sequence 52, Appl
91	112.5	2.9	838	2	US-09-389-341-52	Sequence 52, Appl
92	112.5	2.9	838	2	US-09-564-805-229	Sequence 229, App
93	112.5	2.9	862	2	US-09-328-352-4421	Sequence 4421, Ap
94	112	2.8	2327	6	5455158-1	Patent No. 5455158
95	111	2.8	1241	2	US-08-714-741-34	Sequence 34, Appl
96	111	2.8	2355	2	US-10-360-101-235	Sequence 235, App
97	111	2.8	2386	1	US-09-016-366A-12	Sequence 12, Appl
98	111	2.8	2386	2	US-09-961-403-1	Sequence 1, Appl
99	110.5	2.8	969	2	US-09-198-452A-501	Sequence 501, App
100	110.5	2.8	1155	2	US-09-949-016-9550	Sequence 9550, App

ALIGNMENTS

RESULT 1

US-09-404-879A-389
; Sequence 389, Application US/09404879A
; Patent No. 6468546
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C2
; CURRENT APPLICATION NUMBER: US/09/404, 879A
; CURRENT FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 393
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 389
; LENGTH: 833
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-404-879A-389

Query Match 92.9%; Score 3663; DB 2; Length 833;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 FTHRSSVSTTSTPGTPTVYLKASKTPASIFGPSAASHLLILFTLFTITNLYEENWPG 73
DB 78 FTHRSSVSTTSTPGTPTVYLKASKTPASIFGPSAASHLLILFTLFTITNLYEENWPG 137

QY 74 SRKFNTERVQLGLRLPLFKNTSVGLYSGRLTLRPEKDGATGVDACITHRPDTGP 133
DB 138 SRKFNTERVQLGLRLPLFKNTSVGLYSGRLTLRPEKDGATGVDACITHRPDTGP 197

QY 134 GLDREQLYLELSQTHSITELGPTTLDRDSLYNGFTHRSSVPTTSGVSEEPFTLNFT 193
DB 198 GLDREQLYLELSQTHSITELGPTTLDRDSLYNGFTHRSSVPTTSGVSEEPFTLNFT 257

QY 194 INNLYRMADMGQPSGLKFNITDNNMKHLLSPLFORSSIGARYTCRVIALRSVNGAETR 253
DB 258 INNLYRMADMGQPSGLKFNITDNNMKHLLSPLFORSSIGARYTCRVIALRSVNGAETR 317

QY 254 VDLCTYLQPLSGPLPIKQVFHLSQTHGITRLGYSYLDKSLYLYNGNEPDPDEPPT 313
DB 318 VDLCTYLQPLSGPLPIKQVFHLSQTHGITRLGYSYLDKSLYLYNGNEPDPDEPPT 377

QY 314 TPKPATTFLPPLSEATTAMGYHLKTLTINFTISNLQYSPDMGKSATFNSSTEGVLQHLR 373
DB 378 TPKPATTFLPPLSEATTAMGYHLKTLTINFTISNLQYSPDMGKSATFNSSTEGVLQHLR 437

QY 374 PLFOKSSMGPPYLGCOLISLRPEKDGATGVDTTCTVHPDPVPGGLDIQQLYWLSQLTH 433
DB 438 PLFOKSSMGPPYLGCOLISLRPEKDGATGVDTTCTVHPDPVPGGLDIQQLYWLSQLTH 497

QY 434 GVTQLGFVYLDRLDSLFINGVAPQNLISIRGEYQINFHIVNWNLSNPDPTSSEYITLLRDIQ 493
DB 498 GVTQLGFVYLDRLDSLFINGVAPQNLISIRGEYQINFHIVNWNLSNPDPTSSEYITLLRDIQ 557

QY 494 DKVTTLTKGSQLHDTFRFCLVTNLTMDSVLVTVKALFSSNLDPSLVQVFLDKTLNASFH 553
DB 558 DKVTTLTKGSQLHDTFRFCLVTNLTMDSVLVTVKALFSSNLDPSLVQVFLDKTLNASFH 617

QY 554 WLGSYQQLVDLHVTEMSSVYQPTSSSTQHFYLNFTITNLPYSQDKAQCCTTNYQNRK 613
DB 618 WLGSYQQLVDLHVTEMSSVYQPTSSSTQHFYLNFTITNLPYSQDKAQCCTTNYQNRK 677

QY 614 NIEDALNQLFNSSIKSYFSDQVSTFRSVNRRHHTGVDLSLNFSPILARRVDRVAIYEEF 673
DB 678 NIEDALNQLFNSSIKSYFSDQVSTFRSVNRRHHTGVDLSLNFSPILARRVDRVAIYEEF 737

QY 674 LRMRNGTQLQNFTLDRSSVLVDGYSPPNRNEPLTGNS 710
DB 738 LRMRNGTQLQNFTLDRSSVLVDGYSPPNRNEPLTGNS 774

RESULT 2

US-09-667-857-389
; Sequence 389, Application US/09667857
; Patent No. 6695664
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary Richard
; APPLICANT: Reed, Steven G.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C5
; CURRENT APPLICATION NUMBER: US/09/667, 857
; CURRENT FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 389
; LENGTH: 833
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-667-857-389

Query Match 92.9%; Score 3663; DB 2; Length 833;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 FTHRSSVSTTSTPGTPTVYLKASKTPASIFGPSAASHLLILFTLFTITNLYEENWPG 73
DB 78 FTHRSSVSTTSTPGTPTVYLKASKTPASIFGPSAASHLLILFTLFTITNLYEENWPG 137

QY 74 SRKFNTERVQLGLRLPLFKNTSVGLYSGRLTLRPEKDGATGVDACITHRPDTGP 133
DB 138 SRKFNTERVQLGLRLPLFKNTSVGLYSGRLTLRPEKDGATGVDACITHRPDTGP 197

QY 134 GLDREQLYLELSQTHSITELGPTTLDRDSLYNGFTHRSSVPTTSGVSEEPFTLNFT 193
DB 198 GLDREQLYLELSQTHSITELGPTTLDRDSLYNGFTHRSSVPTTSGVSEEPFTLNFT 257

QY 194 INNLYRMADMGQPSGLKFNITDNNMKHLLSPLFORSSIGARYTCRVIALRSVNGAETR 253
DB 258 INNLYRMADMGQPSGLKFNITDNNMKHLLSPLFORSSIGARYTCRVIALRSVNGAETR 317

QY 254 VDLCTYLQPLSGPLPIKQVFHLSQTHGITRLGYSYLDKSLYLYNGNEPDPDEPPT 313
DB 318 VDLCTYLQPLSGPLPIKQVFHLSQTHGITRLGYSYLDKSLYLYNGNEPDPDEPPT 377

QY 314 TPKPATTFLPPLSEATTAMGYHLKTLTINFTISNLQYSPDMGKSATFNSSTEGVLQHLR 373
DB 378 TPKPATTFLPPLSEATTAMGYHLKTLTINFTISNLQYSPDMGKSATFNSSTEGVLQHLR 437

QY 374 PLFOKSSMGPPYLGCOLISLRPEKDGATGVDTTCTVHPDPVPGGLDIQQLYWLSQLTH 433
DB 438 PLFOKSSMGPPYLGCOLISLRPEKDGATGVDTTCTVHPDPVPGGLDIQQLYWLSQLTH 497

QY 434 GVTQLGFVYLDRLDSLFINGVAPQNLISIRGEYQINFHIVNWNLSNPDPTSSEYITLLRDIQ 493
DB 498 GVTQLGFVYLDRLDSLFINGVAPQNLISIRGEYQINFHIVNWNLSNPDPTSSEYITLLRDIQ 557

QY 494 DKVTTLTKGSQLHDTFRFCLVTNLTMDSVLVTVKALFSSNLDPSLVQVFLDKTLNASFH 553
DB 558 DKVTTLTKGSQLHDTFRFCLVTNLTMDSVLVTVKALFSSNLDPSLVQVFLDKTLNASFH 617

QY 554 WLGSTYQLVDIHVTEMESSYQPTSSSTQHFYLNFTITNLPSYQDKAQPGTTNYQRNKR 613
Db 618 WLGSTYQLVDIHVTEMESSYQPTSSSTQHFYLNFTITNLPSYQDKAQPGTTNYQRNKR 677
QY 614 NIEDALNQLFRNSSIKSYFSDCQVSTFRSPVNRHHTGVDLSLNCNFSPLARRVDRVAIYEFP 673
Db 678 NIEDALNQLFRNSSIKSYFSDCQVSTFRSPVNRHHTGVDLSLNCNFSPLARRVDRVAIYEFP 737
QY 674 LRMRNTRGTLQNFNFTLDRSSVLVDGYSPNRNEPLTGNS 710
Db 738 LRMRNTRGTLQNFNFTLDRSSVLVDGYSPNRNEPLTGNS 774

RESULT 3
US-10-198-053-389
; Sequence 389, Application US/10198053
; Patent No. 6858710
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hill, Paul
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C9
; CURRENT APPLICATION NUMBER: US/10/198,053
; CURRENT FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 624
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 389
; LENGTH: 833
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-198-053-389

Query Match 92.9%; Score 3663; DB 2; Length 833;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 FTHRSSVSTSTPGTPTVYLGASKTPASIFGSPAASHLLILFTNLFTITNLRYEENWPG 73
Db 78 FTHRSSVSTSTPGTPTVYLGASKTPASIFGSPAASHLLILFTNLFTITNLRYEENWPG 137

QY 74 SRKFNTTERTVLOGLLRPLFKNTSVGLYSGCRITLLRPEKDGATGVDICTHRPDTGP 133
Db 138 SRKFNTTERTVLOGLLRPLFKNTSVGLYSGCRITLLRPEKDGATGVDICTHRPDTGP 197

QY 134 GLDREQLYLELSQTHSITELGPTTLDRLDLSYNGFTHRSSVPTTSTGVVSEPPFTLNFT 193
Db 198 GLDREQLYLELSQTHSITELGPTTLDRLDLSYNGFTHRSSVPTTSTGVVSEPPFTLNFT 257

QY 194 INNLRYMADMGQPSGLKFNITDNVMKHLSPFORSSLGARYTGCRIALRSVKNGAETR 253
Db 258 INNLRYMADMGQPSGLKFNITDNVMKHLSPFORSSLGARYTGCRIALRSVKNGAETR 317

QY 254 VDLCCTYLQPLSGPLPIKQVFHELSSQTHGIRLGPYSLDKDSLYLNGVNEPDPPEPT 313
Db 318 VDLCCTYLQPLSGPLPIKQVFHELSSQTHGIRLGPYSLDKDSLYLNGVNEPDPPEPT 377

QY 314 TPKPATTFPLPPLSEATTAMGYHLKTLTNFTISNLOYSMDMGKGSATFNSRGLVQLHLR 373
Db 378 TPKPATTFPLPPLSEATTAMGYHLKTLTNFTISNLOYSMDMGKGSATFNSRGLVQLHLR 437

QY 374 PLFOKSSMGPFYLGCOLISLRPEKDGATGVDICTHRPDPVPGGLDIOQLYWELSOLTH 433
Db 438 PLFOKSSMGPFYLGCOLISLRPEKDGATGVDICTHRPDPVPGGLDIOQLYWELSOLTH 497

QY 434 GVTQLGFYVLDRLDLSLFIINGYAPQNLISIRGEYQINFIHVNWNLSPDPPTSSSEYITLLRDIO 493
Db 498 GVTQLGFYVLDRLDLSLFIINGYAPQNLISIRGEYQINFIHVNWNLSPDPPTSSSEYITLLRDIO 557

QY 494 DKVTTLTKGSQLHDTFRFCLVNTLMDSVLTVKALFSSNLDPSLVEQVFLDKTLNASFH 553

Db 558 DKVTTLTKGSQLHDTFRFCLVNTLMDSVLTVKALFSSNLDPSLVEQVFLDKTLNASFH 617
QY 554 WLGSTYQLVDIHVTEMESSYQPTSSSTQHFYLNFTITNLPSYQDKAQPGTTNYQRNKR 613
Db 618 WLGSTYQLVDIHVTEMESSYQPTSSSTQHFYLNFTITNLPSYQDKAQPGTTNYQRNKR 677
QY 614 NIEDALNQLFRNSSIKSYFSDCQVSTFRSPVNRHHTGVDLSLNCNFSPLARRVDRVAIYEFP 673
Db 678 NIEDALNQLFRNSSIKSYFSDCQVSTFRSPVNRHHTGVDLSLNCNFSPLARRVDRVAIYEFP 737
QY 674 LRMRNTRGTLQNFNFTLDRSSVLVDGYSPNRNEPLTGNS 710
Db 738 LRMRNTRGTLQNFNFTLDRSSVLVDGYSPNRNEPLTGNS 774

RESULT 4
US-09-827-271-389
; Sequence 389, Application US/09827271
; Patent No. 6962980
; GENERAL INFORMATION:
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.462C6
; CURRENT APPLICATION NUMBER: US/09/827,271
; CURRENT FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 389
; LENGTH: 833
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-827-271-389

Query Match 92.9%; Score 3663; DB 2; Length 833;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 FTHRSSVSTSTPGTPTVYLGASKTPASIFGSPAASHLLILFTNLFTITNLRYEENWPG 73
Db 78 FTHRSSVSTSTPGTPTVYLGASKTPASIFGSPAASHLLILFTNLFTITNLRYEENWPG 137

QY 74 SRKFNTTERTVLOGLLRPLFKNTSVGLYSGCRITLLRPEKDGATGVDICTHRPDTGP 133
Db 138 SRKFNTTERTVLOGLLRPLFKNTSVGLYSGCRITLLRPEKDGATGVDICTHRPDTGP 197

QY 134 GLDREQLYLELSQTHSITELGPTTLDRLDLSYNGFTHRSSVPTTSTGVVSEPPFTLNFT 193
Db 198 GLDREQLYLELSQTHSITELGPTTLDRLDLSYNGFTHRSSVPTTSTGVVSEPPFTLNFT 257

QY 194 INNLRYMADMGQPSGLKFNITDNVMKHLSPFORSSLGARYTGCRIALRSVKNGAETR 253
Db 258 INNLRYMADMGQPSGLKFNITDNVMKHLSPFORSSLGARYTGCRIALRSVKNGAETR 317

QY 254 VDLCCTYLQPLSGPLPIKQVFHELSSQTHGIRLGPYSLDKDSLYLNGVNEPDPPEPT 313
Db 318 VDLCCTYLQPLSGPLPIKQVFHELSSQTHGIRLGPYSLDKDSLYLNGVNEPDPPEPT 377

QY 314 TPKPATTFPLPPLSEATTAMGYHLKTLTNFTISNLOYSMDMGKGSATFNSRGLVQLHLR 373
Db 378 TPKPATTFPLPPLSEATTAMGYHLKTLTNFTISNLOYSMDMGKGSATFNSRGLVQLHLR 437

QY 374 PLFOKSSMGPFYLGCOLISLRPEKDGATGVDICTHRPDPVPGGLDIOQLYWELSOLTH 433
Db 438 PLFOKSSMGPFYLGCOLISLRPEKDGATGVDICTHRPDPVPGGLDIOQLYWELSOLTH 497

QY 434 GVTQLGFYVLDRLDLSLFIINGYAPQNLISIRGEYQINFIHVNWNLSPDPPTSSSEYITLLRDIO 493
Db 498 GVTQLGFYVLDRLDLSLFIINGYAPQNLISIRGEYQINFIHVNWNLSPDPPTSSSEYITLLRDIO 557

QY 494 DKVTTLTKGSQLHDTFRFCLVNTLMDSVLTVKALFSSNLDPSLVEQVFLDKTLNASFH 553

```
Db 558 DKVTTYKGSQSLHDTFRFCLVTNLTWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASPH 617
QY 554 WLGSYQLVDIHVTMESSYQPTSSSTQHLYNFTTNLPSQDKAQPGTNTYQNRK 613
Db 618 WLGSYQLVDIHVTMESSYQPTSSSTQHLYNFTTNLPSQDKAQPGTNTYQNRK 677
QY 614 NIEDALNQLFRNSSIKSYFSDCOVSTFRSVPNRHHTGVDSLCLNFSPLARRVDRVAIYEEF 673
Db 678 NIEDALNQLFRNSSIKSYFSDCOVSTFRSVPNRHHTGVDSLCLNFSPLARRVDRVAIYEEF 737
QY 674 LRMTRNGTQLQNFLLDRSSVLVDGYSPNNEPLTGN 710
Db 738 LRMTRNGTQLQNFLLDRSSVLVDGYSPNNEPLTGN 774

RESULT 5
US-09-404-879A-312
; Sequence 312, Application US/09404879A
; Patent No. 6468546
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C2
; CURRENT APPLICATION NUMBER: US/09/404,879A
; CURRENT FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 393
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 312
; LENGTH: 914
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-404-879A-312

Query Match 92.9%; Score 3663; DB 2; Length 914;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 FTHRSSVSTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWPG 73
Db 159 FTHRSSVSTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWPG 218
QY 74 SRKENTERVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRPDPGTP 133
Db 219 SRKENTERVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRPDPGTP 278
QY 134 GLDREQLYLELSQLTHSITELGPYTLDRDSLTVNGFTTHRSSVPTTSTGVVSEEPFTLNFT 193
Db 279 GLDREQLYLELSQLTHSITELGPYTLDRDSLTVNGFTTHRSSVPTTSTGVVSEEPFTLNFT 338
QY 194 INNLRYMADMGQPSGLKFNITDNVMKHLSPFORSSIGARYTCGRVIALRSVKGAE 253
Db 339 INNLRYMADMGQPSGLKFNITDNVMKHLSPFORSSIGARYTCGRVIALRSVKGAE 398
QY 254 VDLCTYLOPLSGPLPKQVFEHLSQTHGTRIGPYSLDKSLYLNGYNPEGDEPPT 313
Db 399 VDLCTYLOPLSGPLPKQVFEHLSQTHGTRIGPYSLDKSLYLNGYNPEGDEPPT 458
QY 314 TPKPATTFLPPLSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATNSTEGVLQHLR 373
Db 459 TPKPATTFLPPLSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATNSTEGVLQHLR 518
QY 374 PLFKQSSMGPPYLGQSLSLRPEKDGATGVDTTCTTHPDPVGPGLDIQQLYWELSQLTH 433
Db 519 PLFKQSSMGPPYLGQSLSLRPEKDGATGVDTTCTTHPDPVGPGLDIQQLYWELSQLTH 578
QY 434 GVTQLGFVYLDRLDSLFINGYAPQNLISIRGEYQINFIHVNWNLSPDPPTSSEYITLLRDIQ 493
Db 579 GVTQLGFVYLDRLDSLFINGYAPQNLISIRGEYQINFIHVNWNLSPDPPTSSEYITLLRDIQ 638
QY 494 DKVTTYKGSQSLHDTFRFCLVTNLTWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASPH 553

Db 639 DKVTTYKGSQSLHDTFRFCLVTNLTWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASPH 698
QY 554 WLGSYQLVDIHVTMESSYQPTSSSTQHLYNFTTNLPSQDKAQPGTNTYQNRK 613
Db 699 WLGSYQLVDIHVTMESSYQPTSSSTQHLYNFTTNLPSQDKAQPGTNTYQNRK 758
QY 614 NIEDALNQLFRNSSIKSYFSDCOVSTFRSVPNRHHTGVDSLCLNFSPLARRVDRVAIYEEF 673
Db 759 NIEDALNQLFRNSSIKSYFSDCOVSTFRSVPNRHHTGVDSLCLNFSPLARRVDRVAIYEEF 818
QY 674 LRMTRNGTQLQNFLLDRSSVLVDGYSPNNEPLTGN 710
Db 819 LRMTRNGTQLQNFLLDRSSVLVDGYSPNNEPLTGN 855

RESULT 6
US-09-338-933-312
; Sequence 312, Application US/09338933
; Patent No. 6488931
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer Lynn
; APPLICANT: King, Gordon E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF
; FILE OF INVENTION: OVARIAN CANCER
; FILE REFERENCE: 210121.462C1
; CURRENT APPLICATION NUMBER: US/09/338,933
; CURRENT FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 312
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 312
; LENGTH: 914
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-338-933-312

Query Match 92.9%; Score 3663; DB 2; Length 914;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 FTHRSSVSTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWPG 73
Db 159 FTHRSSVSTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWPG 218
QY 74 SRKENTERVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRPDPGTP 133
Db 219 SRKENTERVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRPDPGTP 278
QY 134 GLDREQLYLELSQLTHSITELGPYTLDRDSLTVNGFTTHRSSVPTTSTGVVSEEPFTLNFT 193
Db 279 GLDREQLYLELSQLTHSITELGPYTLDRDSLTVNGFTTHRSSVPTTSTGVVSEEPFTLNFT 338
QY 194 INNLRYMADMGQPSGLKFNITDNVMKHLSPFORSSIGARYTCGRVIALRSVKGAE 253
Db 339 INNLRYMADMGQPSGLKFNITDNVMKHLSPFORSSIGARYTCGRVIALRSVKGAE 398
QY 254 VDLCTYLOPLSGPLPKQVFEHLSQTHGTRIGPYSLDKSLYLNGYNPEGDEPPT 313
Db 399 VDLCTYLOPLSGPLPKQVFEHLSQTHGTRIGPYSLDKSLYLNGYNPEGDEPPT 458
QY 314 TPKPATTFLPPLSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATNSTEGVLQHLR 373
Db 459 TPKPATTFLPPLSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATNSTEGVLQHLR 518
QY 374 PLFKQSSMGPPYLGQSLSLRPEKDGATGVDTTCTTHPDPVGPGLDIQQLYWELSQLTH 433
Db 519 PLFKQSSMGPPYLGQSLSLRPEKDGATGVDTTCTTHPDPVGPGLDIQQLYWELSQLTH 578
QY 434 GVTQLGFVYLDRLDSLFINGYAPQNLISIRGEYQINFIHVNWNLSPDPPTSSEYITLLRDIQ 493
Db 579 GVTQLGFVYLDRLDSLFINGYAPQNLISIRGEYQINFIHVNWNLSPDPPTSSEYITLLRDIQ 638
QY 494 DKVTTYKGSQSLHDTFRFCLVTNLTWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASPH 553
```

Db 639 DKVTLYKGSQHDHTRFCLVNTLMDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFH 698
Qy 554 WLSTYQLVDIHVTEMESSVYQPTSSSTQHFYLNFTITNLPSQDKAQPCTTNYQNRK 613
Db 699 WLSTYQLVDIHVTEMESSVYQPTSSSTQHFYLNFTITNLPSQDKAQPCTTNYQNRK 758
Qy 614 NIEDALNQLFRNSIKSYFSDCOVSTFRSPVNRHHTGVDSLCNFSPLARRVDRVAIYEEF 673
Db 759 NIEDALNQLFRNSIKSYFSDCOVSTFRSPVNRHHTGVDSLCNFSPLARRVDRVAIYEEF 818
Qy 674 LRMRNGTQQLNQFTLDRSSVLVDGYSNREPLTNS 710
Db 819 LRMRNGTQQLNQFTLDRSSVLVDGYSNREPLTNS 855
RESULT 7
US-09-667-857-312
; Sequence 312, Application US/09667857
; Patent No. 6699664
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary Richard
; APPLICANT: Reed, Steven G.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C5
; CURRENT APPLICATION NUMBER: US/09/667,857
; CURRENT FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 312
; LENGTH: 914
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-667-857-312

Query Match 92.9%; Score 3663; DB 2; Length 914;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 14 FTHRSSVSTSTPGTPTVYLKASKTPASIFGSPAASHLLILFTLNTITNLRYEENWPG 73
Db 159 FTHRSSVSTSTPGTPTVYLKASKTPASIFGSPAASHLLILFTLNTITNLRYEENWPG 218
Qy 74 SRKFNTTERTVLOGLLRPLFNTSVGPLYSGCRLLTLRPEKGEATGVDAICTHRPDPGP 133
Db 219 SRKFNTTERTVLOGLLRPLFNTSVGPLYSGCRLLTLRPEKGEATGVDAICTHRPDPGP 278
Qy 134 GLDREQLYLELSQTHSITELGPYTLDRDLSYNGFTHRSSVPTTSTGVVSEEPFTLNFT 193
Db 279 GLDREQLYLELSQTHSITELGPYTLDRDLSYNGFTHRSSVPTTSTGVVSEEPFTLNFT 338
Qy 194 INNLRYMADMGQPSLKFNITDNVMKHLSPFORSSLGARYTGCRIALRSVKNCAETR 253
Db 339 INNLRYMADMGQPSLKFNITDNVMKHLSPFORSSLGARYTGCRIALRSVKNCAETR 398
Qy 254 VDLCTYLOPLSGPLPIKQVPHLSQOQTHGTRGLPYSLDKSLYNGNBPDPPT 313
Db 399 VDLCTYLOPLSGPLPIKQVPHLSQOQTHGTRGLPYSLDKSLYNGNBPDPPT 458
Qy 314 TPKPATTFPLPPLSEATTAMGYHLKTLTILNFTISNLQYSPDMKGKSGATFNSTEGVLOHLR 373
Db 459 TPKPATTFPLPPLSEATTAMGYHLKTLTILNFTISNLQYSPDMKGKSGATFNSTEGVLOHLR 518
Qy 374 PLFOKSMGPFYLGCOLISLRPEKGAATGVDTCTTYHPPDVPGLDIOQLYWELSQLTH 433

Db 519 PLFOKSMGPFYLGCOLISLRPEKGAATGVDTCTTYHPPDVPGLDIOQLYWELSQLTH 578
Qy 434 GVTOLGFVLDRLSLFNGVAPQNLSTIRGEVQNFHIVNNLSNPDPTSSSEYITLLRDIO 493
Db 579 GVTOLGFVLDRLSLFNGVAPQNLSTIRGEVQNFHIVNNLSNPDPTSSSEYITLLRDIO 638
Qy 494 DKVTLYKGSQHDHTRFCLVNTLMDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFH 553
Db 639 DKVTLYKGSQHDHTRFCLVNTLMDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFH 698
Qy 554 WLSTYQLVDIHVTEMESSVYQPTSSSTQHFYLNFTITNLPSQDKAQPCTTNYQNRK 613
Db 699 WLSTYQLVDIHVTEMESSVYQPTSSSTQHFYLNFTITNLPSQDKAQPCTTNYQNRK 758
Qy 614 NIEDALNQLFRNSIKSYFSDCOVSTFRSPVNRHHTGVDSLCNFSPLARRVDRVAIYEEF 673
Db 759 NIEDALNQLFRNSIKSYFSDCOVSTFRSPVNRHHTGVDSLCNFSPLARRVDRVAIYEEF 818
Qy 674 LRMRNGTQQLNQFTLDRSSVLVDGYSNREPLTNS 710
Db 819 LRMRNGTQQLNQFTLDRSSVLVDGYSNREPLTNS 855
RESULT 8
US-10-198-053-312
; Sequence 312, Application US/10198053
; Patent No. 6858710
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hill, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C9
; CURRENT APPLICATION NUMBER: US/10/198,053
; CURRENT FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 624
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 312
; LENGTH: 914
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-198-053-312

Query Match 92.9%; Score 3663; DB 2; Length 914;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 14 FTHRSSVSTSTPGTPTVYLKASKTPASIFGSPAASHLLILFTLNTITNLRYEENWPG 73
Db 159 FTHRSSVSTSTPGTPTVYLKASKTPASIFGSPAASHLLILFTLNTITNLRYEENWPG 218
Qy 74 SRKFNTTERTVLOGLLRPLFNTSVGPLYSGCRLLTLRPEKGEATGVDAICTHRPDPGP 133
Db 219 SRKFNTTERTVLOGLLRPLFNTSVGPLYSGCRLLTLRPEKGEATGVDAICTHRPDPGP 278
Qy 134 GLDREQLYLELSQTHSITELGPYTLDRDLSYNGFTHRSSVPTTSTGVVSEEPFTLNFT 193
Db 279 GLDREQLYLELSQTHSITELGPYTLDRDLSYNGFTHRSSVPTTSTGVVSEEPFTLNFT 338
Qy 194 INNLRYMADMGQPSLKFNITDNVMKHLSPFORSSLGARYTGCRIALRSVKNCAETR 253
Db 339 INNLRYMADMGQPSLKFNITDNVMKHLSPFORSSLGARYTGCRIALRSVKNCAETR 398
Qy 254 VDLCTYLOPLSGPLPIKQVPHLSQOQTHGTRGLPYSLDKSLYNGNBPDPPT 313
Db 399 VDLCTYLOPLSGPLPIKQVPHLSQOQTHGTRGLPYSLDKSLYNGNBPDPPT 458
Qy 314 TPKPATTFPLPPLSEATTAMGYHLKTLTILNFTISNLQYSPDMKGKSGATFNSTEGVLOHLR 373
Db 459 TPKPATTFPLPPLSEATTAMGYHLKTLTILNFTISNLQYSPDMKGKSGATFNSTEGVLOHLR 518

QY	374	PLFQKSSMGPFYVLCQGLISLRPEKGAATGVDTTCTTHPDVPGGLDIQQLYWELSQLTH	433
DB	519	PLFQKSSMGPFYVLCQGLISLRPEKGAATGVDTTCTTHPDVPGGLDIQQLYWELSQLTH	578
QY	434	GVTLQGFVYVLDRLDSLFINGYAPQNLISIRGEYQINFIHVNWNLSPDPPTSSEYITLLRDIQ	493
DB	579	GVTLQGFVYVLDRLDSLFINGYAPQNLISIRGEYQINFIHVNWNLSPDPPTSSEYITLLRDIQ	638
QY	494	DKVTLLYKGSQGLHDFRCLVNLTMDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASPH	553
DB	639	DKVTLLYKGSQGLHDFRCLVNLTMDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASPH	698
QY	554	WLGSTYQLVDIHVTEMESVYQPTSSSTQHFYLNFTIITNLPYSQKAOPTGTTNYQRNR	613
DB	699	WLGSTYQLVDIHVTEMESVYQPTSSSTQHFYLNFTIITNLPYSQKAOPTGTTNYQRNR	758
QY	614	NIEDALNQLFRNSSIKSYFSDCQVSTFRSVPNRHHGTGVDLNCNFSPLARRVDRVAIYEEF	673
DB	759	NIEDALNQLFRNSSIKSYFSDCQVSTFRSVPNRHHGTGVDLNCNFSPLARRVDRVAIYEEF	818
QY	674	LRMTRNGTQLQNFTRDRSSVLVDGYSPNRNEPLTGNS	710
DB	819	LRMTRNGTQLQNFTRDRSSVLVDGYSPNRNEPLTGNS	855
RESULT 9			
US-10-198-053-478			
; Sequence 478, Application US/10198053			
; Patent No. 6858710			
; GENERAL INFORMATION:			
; APPLICANT: Bangur, Chaitanya S.			
; APPLICANT: Retter, Marc W.			
; APPLICANT: Fanger, Gary R.			
; APPLICANT: Hill, Paul			
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY			
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER			
; FILE REFERENCE: 210121.462C9			
; CURRENT APPLICATION NUMBER: US/10/198,053			
; CURRENT FILING DATE: 2002-07-17			
; NUMBER OF SEQ ID NOS: 624			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 478			
; LENGTH: 914			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-10-198-053-478			
Query Match 92.9%; Score 3663; DB 2; Length 914;			
Best Local Similarity 99.9%; Pred. No. 0;			
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
QY	14	FTHRSSVSTTSTPGTPTVYLGASKTPASIFGSPSAASHLLILFTLNTITNLYEENMWP	73
DB	159	FTHRSSVSTTSTPGTPTVYLGASKTPASIFGSPSAASHLLILFTLNTITNLYEENMWP	218
QY	74	SRKFNTTERRVLOGLRLPFLKNTSVGCLTLRLPEKGEATGVDICTHRDPDPTGP	133
DB	219	SRKFNTTERRVLOGLRLPFLKNTSVGCLTLRLPEKGEATGVDICTHRDPDPTGP	278
QY	134	GLDREQLYLELSQTHSITELGPYTLDRDSLNYNGFTHRSSVPTTSTGVVSEEPFLNFT	193
DB	279	GLDREQLYLELSQTHSITELGPYTLDRDSLNYNGFTHRSSVPTTSTGVVSEEPFLNFT	338
QY	194	INNLRVYMDMGQPGSLKFNITDNVVKHLLSPLFORSSLGARYTGCRVIALRSYKNGAETR	253
DB	339	INNLRVYMDMGQPGSLKFNITDNVVKHLLSPLFORSSLGARYTGCRVIALRSYKNGAETR	398
QY	254	VDLLCTYLOPLSGPLPIKQVPHLSQOOTHGITRLGYSLDKDSLNYNGFPGDPDEPPT	313
DB	399	VDLLCTYLOPLSGPLPIKQVPHLSQOOTHGITRLGYSLDKDSLNYNGFPGDPDEPPT	458
QY	314	TPKPATTFPLPLSEATTAMGYHLKTLTNTITNLTISNLOQSPDMGKGSATFNSTEGVLOHLR	373

Db 459 TPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQVSPDMGKGSATFNSTEGVLOHLR 518
Qy 374 PLFKSMGPFYLGCCQLISLRPEKGAATGVDITCTYHPDPVGPGLDIOQLYWELSLTH 433
Db 519 PLFKSMGPFYLGCCQLISLRPEKGAATGVDITCTYHPDPVGPGLDIOQLYWELSLTH 578
Qy 434 GVTOLGPFYLDRLDLSLFGINGVAPQNLISIRGEYQINPHIVNMNLSNPDPPTSSEYITLLRDIQ 493
Db 579 GVTOLGPFYLDRLDLSLFGINGVAPQNLISIRGEYQINPHIVNMNLSNPDPPTSSEYITLLRDIQ 638
Qy 494 DKVTLLYKGSQSLHDTFRFCLVTLNLTWDSVLVTKALFSSNLDPSLVEQVFLDKTLNASFH 553
Db 639 DKVTLLYKGSQSLHDTFRFCLVTLNLTWDSVLVTKALFSSNLDPSLVEQVFLDKTLNASFH 698
Qy 554 WLGSTYQLVDIHVTEMESVYQPTSSSSTQHFYLNFTITNLPSQKAQPGTTNYQRNKR 613
Db 699 WLGSTYQLVDIHVTEMESVYQPTSSSSTQHFYLNFTITNLPSQKAQPGTTNYQRNKR 758
Qy 614 NIEDALNQLFRNSIISYFSDCQVSTFRSPVNRHHTGVDSLCNFSPLARRVDRVAIYEEF 673
Db 759 NIEDALNQLFRNSIISYFSDCQVSTFRSPVNRHHTGVDSLCNFSPLARRVDRVAIYEEF 818
Qy 674 LRMRNGTQLOQNFTRDRSSVLVDGYSNRPNEPLTGS 710
Db 819 LRMRNGTQLOQNFTRDRSSVLVDGYSNRPNEPLTGS 855

RESULT 11
US-10-198-053-595
; Sequence 595, Application US/10198053
; Patent No. 6858710
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hill, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C9
; CURRENT APPLICATION NUMBER: US/10/198,053
; CURRENT FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 624
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 595
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 177, 335, 523, 618, 663, 875, 961, 1001, 1441, 1555, 1560,
; LOCATION: 1563, 1574, 1585, 2065, 2070, 2683, 2990, 3269, 3381, 3401
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-198-053-595

Query Match 92.5%; Score 3651; DB 2; Length 3451;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 694; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 14 FTHRSSVSTSTGPTPVYLGASKTPASIFGPSAASHLLILFTLNTITNLRYEENWPG 73
Db 2696 FTHRSSVSTSTGPTPVYLGASKTPASIFGPSAASHLLILFTLNTITNLRYEENWPG 2755
Qy 74 SRKFNTTVERVLOGLLRPLFNTSVGPLYSGCRITLLRPEKDGATGVDAICTHRPPTGP 133
Db 2756 SRKFNTTVERVLOGLLRPLFNTSVGPLYSGCRITLLRPEKDGATGVDAICTHRPPTGP 2815
Qy 134 GLDREQLYLSQTHSITELGPTTLDRLDLSLVNGFTHRSSVPTTSTGVVSEBPFILNFT 193
Db 2816 GLDREQLYLSQTHSITELGPTTLDRLDLSLVNGFTHRSSVPTTSTGVVSEBPFILNFT 2875
Qy 194 INNLRYMADMGQPSLKFNTIDNMVKHLLSPLFQRSSLGARYTGCRIALRSYKGAETR 253
Db 2876 INNLRYMADMGQPSLKFNTIDNMVKHLLSPLFQRSSLGARYTGCRIALRSYKGAETR 2935

Qy 254 VDLCTLYQLPSGPGLPKIQVFHELSSQTHGITRLGPFSLDKOSLYLNGYNEPDEPPT 313
Db 2936 VDLCTLYQLPSGPGLPKIQVFHELSSQTHGITRLGPFSLDKOSLYLNGYNEPDEPPT 2995
Qy 314 TPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQVSPDMGKGSATFNSTEGVLOHLR 373
Db 2996 TPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQVSPDMGKGSATFNSTEGVLOHLR 3055
Qy 374 PLFKSMGPFYLGCCQLISLRPEKGAATGVDITCTYHPDPVGPGLDIOQLYWELSLTH 433
Db 3056 PLFKSMGPFYLGCCQLISLRPEKGAATGVDITCTYHPDPVGPGLDIOQLYWELSLTH 3115
Qy 434 GVTOLGPFYLDRLDLSLFGINGVAPQNLISIRGEYQINPHIVNMNLSNPDPPTSSEYITLLRDIQ 493
Db 3116 GVTOLGPFYLDRLDLSLFGINGVAPQNLISIRGEYQINPHIVNMNLSNPDPPTSSEYITLLRDIQ 3175
Qy 494 DKVTLLYKGSQSLHDTFRFCLVTLNLTWDSVLVTKALFSSNLDPSLVEQVFLDKTLNASFH 553
Db 3176 DKVTLLYKGSQSLHDTFRFCLVTLNLTWDSVLVTKALFSSNLDPSLVEQVFLDKTLNASFH 3235
Qy 554 WLGSTYQLVDIHVTEMESVYQPTSSSSTQHFYLNFTITNLPSQKAQPGTTNYQRNKR 613
Db 3236 WLGSTYQLVDIHVTEMESVYQPTSSSSTQHFYLNFTITNLPSQKAQPGTTNYQRNKR 3295
Qy 614 NIEDALNQLFRNSIISYFSDCQVSTFRSPVNRHHTGVDSLCNFSPLARRVDRVAIYEEF 673
Db 3296 NIEDALNQLFRNSIISYFSDCQVSTFRSPVNRHHTGVDSLCNFSPLARRVDRVAIYEEF 3355
Qy 674 LRMRNGTQLOQNFTRDRSSVLVDGYSNRPNEPLTGS 710
Db 3356 LRMRNGTQLOQNFTRDRSSVLVDGYSNRPNEPLTGS 3392

RESULT 12
US-10-198-053-458
; Sequence 458, Application US/10198053
; Patent No. 6858710
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hill, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C9
; CURRENT APPLICATION NUMBER: US/10/198,053
; CURRENT FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 624
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 458
; LENGTH: 1148
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-198-053-458

Query Match 92.3%; Score 3642; DB 2; Length 1148;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 694; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 14 FTHRSSVSTSTGPTPVYLGASKTPASIFGPSAASHLLILFTLNTITNLRYEENWPG 73
Db 393 FTHRSSVSTSTGPTPVYLGASKTPASIFGPSAASHLLILFTLNTITNLRYEENWPG 452
Qy 74 SRKFNTTVERVLOGLLRPLFNTSVGPLYSGCRITLLRPEKDGATGVDAICTHRPPTGP 133
Db 453 SRKFNTTVERVLOGLLRPLFNTSVGPLYSGCRITLLRPEKDGATGVDAICTHRPPTGP 512
Qy 134 GLDREQLYLSQTHSITELGPTTLDRLDLSLVNGFTHRSSVPTTSTGVVSEBPFILNFT 193
Db 513 GLDREQLYLSQTHSITELGPTTLDRLDLSLVNGFTHRSSVPTTSTGVVSEBPFILNFT 572
Qy 194 INNLRYMADMGQPSLKFNTIDNMVKHLLSPLFQRSSLGARYTGCRIALRSYKGAETR 253

Db 573 INNLRYADMGQSGSLKFNITDNVKKHLLSPLFORSSLGARYTGCVRVIALRSVKNGAETR 632
Qy 254 VDLCTYLQPLSGPLPIKQVHLSQTHGIRLPGYSLDKSLYNGNBPDEPPT 313
Db 633 VDLCTYLQPLSGPLPIKQVHLSQTHGIRLPGYSLDKSLYNGNBPDEPPT 692
Qy 314 TPXPATTFPLPPLSEATTAMGYHLKTLTLNFTISNLOYSPDMGKGSATFNSTEGVLOHLLR 373
Db 693 TPXPATTFPLPPLSEATTAMGYHLKTLTLNFTISNLOYSPDMGKGSATFNSTEGVLOHLLR 752
Qy 374 PLFOKSSMGPFYLGCOLISLRPEKDGAAATGVDITCTYHPDPVGPGLDIQOLYWELSOLTH 433
Db 753 PLFOKSSMGPFYLGCOLISLRPEKDGAAATGVDITCTYHPDPVGPGLDIQOLYWELSOLTH 812
Qy 434 GVTQLGFYVLDRLDSLFNGVAPQNLISIRGEYQINFHIVNNLSNPDPSTSEYITLLRDIQ 493
Db 813 GVTQLGFYVLDRLDSLFNGVAPQNLISIRGEYQINFHIVNNLSNPDPSTSEYITLLRDIQ 872
Qy 494 DKVTTLKGSQSLHDTFRFCLVTNLTMDSVLVTKALFSSNLDPSLVEQVFLDKTLNASPH 553
Db 873 DKVTTLKGSQSLHDTFRFCLVTNLTMDSVLVTKALFSSNLDPSLVEQVFLDKTLNASPH 932
Qy 554 WLGSYQVLDIHVTEMESVYQPTSSSTQHFYLNFTITNLPSQDKAQPGTTNYQRNKR 613
Db 933 WLGSYQVLDIHVTEMESVYQPTSSSTQHFYLNFTITNLPSQDKAQPGTTNYQRNKR 992
Qy 614 NIEDALNQLFRNSSIKSYFSDCQVSTFRSVPNRHHTGVDLSLGNFSPPLARRVDRVAIYEEF 673
Db 993 NIEDALNQLFRNSSIKSYFSDCQVSTFRSVPNRHHTGVDLSLGNFSPPLARRVDRVAIYEEF 1052
Qy 674 LRMTNGTQLONFTLDRSSVLVDGYSNRPNEPLTGNS 710
Db 1053 LRMTNGTQLONFTLDRSSVLVDGYSNRPNEPLTGNS 1089

RESULT 13

US-10-198-053-479

; Sequence 479, Application US/10198053

; Patent No. 6858710

; GENERAL INFORMATION:

; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: Retter, Marc W.

; APPLICANT: Fanger, Gary R.

; APPLICANT: Hill, Paul

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER

; FILE REFERENCE: 210121.462C9

; CURRENT APPLICATION NUMBER: US/10/198.053

; CURRENT FILING DATE: 2002-07-17

; NUMBER OF SEQ ID NOS: 624

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 479

; LENGTH: 1148

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-198-053-479

Query Match 92.3%; Score 3642; DB 2; Length 1148;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 694; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 14 FTHRSSVSTTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENMWPG 73
Db 393 FTHRSSVSTTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENMWPG 452
Qy 74 SRKENTTERTVQLGLLRPLFKNTSVGPLYSGRLTLRLPEKDGATGVDAICTHRPDPDTPG 133
Db 453 SRKENTTERTVQLGLLRPLFKNTSVGPLYSGRLTLRLPEKDGATGVDAICTHRPDPDTPG 512
Qy 134 GLDREQLYLELSQTHSITELGPYTLDRDSLRYNGFTHRSSVPTTSTGVSEEPFTLNFT 193
Db 513 GLDREQLYLELSQTHSITELGPYTLDRDSLRYNGFTHRSSVPTTSTGVSEEPFTLNFT 572

Qy 194 INNLRYADMGQSGSLKFNITDNVKKHLLSPLFORSSLGARYTGCVRVIALRSVKNGAETR 253
Db 573 INNLRYADMGQSGSLKFNITDNVKKHLLSPLFORSSLGARYTGCVRVIALRSVKNGAETR 632
Qy 254 VDLCTYLQPLSGPLPIKQVHLSQTHGIRLPGYSLDKSLYNGNBPDEPPT 313
Db 633 VDLCTYLQPLSGPLPIKQVHLSQTHGIRLPGYSLDKSLYNGNBPDEPPT 692
Qy 314 TPXPATTFPLPPLSEATTAMGYHLKTLTLNFTISNLOYSPDMGKGSATFNSTEGVLOHLLR 373
Db 693 TPXPATTFPLPPLSEATTAMGYHLKTLTLNFTISNLOYSPDMGKGSATFNSTEGVLOHLLR 752
Qy 374 PLFOKSSMGPFYLGCOLISLRPEKDGAAATGVDITCTYHPDPVGPGLDIQOLYWELSOLTH 433
Db 753 PLFOKSSMGPFYLGCOLISLRPEKDGAAATGVDITCTYHPDPVGPGLDIQOLYWELSOLTH 812
Qy 434 GVTQLGFYVLDRLDSLFNGVAPQNLISIRGEYQINFHIVNNLSNPDPSTSEYITLLRDIQ 493
Db 813 GVTQLGFYVLDRLDSLFNGVAPQNLISIRGEYQINFHIVNNLSNPDPSTSEYITLLRDIQ 872
Qy 494 DKVTTLKGSQSLHDTFRFCLVTNLTMDSVLVTKALFSSNLDPSLVEQVFLDKTLNASPH 553
Db 873 DKVTTLKGSQSLHDTFRFCLVTNLTMDSVLVTKALFSSNLDPSLVEQVFLDKTLNASPH 932
Qy 554 WLGSYQVLDIHVTEMESVYQPTSSSTQHFYLNFTITNLPSQDKAQPGTTNYQRNKR 613
Db 933 WLGSYQVLDIHVTEMESVYQPTSSSTQHFYLNFTITNLPSQDKAQPGTTNYQRNKR 992
Qy 614 NIEDALNQLFRNSSIKSYFSDCQVSTFRSVPNRHHTGVDLSLGNFSPPLARRVDRVAIYEEF 673
Db 993 NIEDALNQLFRNSSIKSYFSDCQVSTFRSVPNRHHTGVDLSLGNFSPPLARRVDRVAIYEEF 1052
Qy 674 LRMTNGTQLONFTLDRSSVLVDGYSNRPNEPLTGNS 710
Db 1053 LRMTNGTQLONFTLDRSSVLVDGYSNRPNEPLTGNS 1089

RESULT 14

US-09-827-271-458

; Sequence 458, Application US/09827271

; Patent No. 6962980

; GENERAL INFORMATION:

; APPLICANT: Retter, Marc W.

; APPLICANT: Fanger, Gary R.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER

; FILE REFERENCE: 210121.462C6

; CURRENT APPLICATION NUMBER: US/09/827.271

; CURRENT FILING DATE: 2001-04-04

; NUMBER OF SEQ ID NOS: 461

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 458

; LENGTH: 1148

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-827-271-458

Query Match 92.3%; Score 3642; DB 2; Length 1148;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 694; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 14 FTHRSSVSTTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENMWPG 73
Db 393 FTHRSSVSTTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENMWPG 452
Qy 74 SRKENTTERTVQLGLLRPLFKNTSVGPLYSGRLTLRLPEKDGATGVDAICTHRPDPDTPG 133
Db 453 SRKENTTERTVQLGLLRPLFKNTSVGPLYSGRLTLRLPEKDGATGVDAICTHRPDPDTPG 512
Qy 134 GLDREQLYLELSQTHSITELGPYTLDRDSLRYNGFTHRSSVPTTSTGVSEEPFTLNFT 193
Db 513 GLDREQLYLELSQTHSITELGPYTLDRDSLRYNGFTHRSSVPTTSTGVSEEPFTLNFT 572

QY 194 INNLRYMADMGQPGSLKFNITDNVMKHLSPFORSSLGARYTGCRRVIALRSVKNAGETR 253
Db 573 INNLRYMADMGQPGSLKFNITDNVMKHLSPFORSSLGARYTGCRRVIALRSVKNAGETR 632
QY 254 VDLCTYLQPLSGPGLPIKQVPHLSQOHTGIRLGPYSLDKDSLYLNGYNEPGDEPPT 313
Db 633 VDLCTYLQPLSGPGLPIKQVPHLSQOHTGIRLGPYSLDKDSLYLNGYNEPGDEPPT 692
QY 314 TPKPATTFPLPPLSEATTAMGYHLKTLTINFTISNLQYSPDMGKGSATFNSSTEGVLOHLR 373
Db 693 TPKPATTFPLPPLSEATTAMGYHLKTLTINFTISNLQYSPDMGKGSATFNSSTEGVLOHLR 752
QY 374 PLFQKSSMGPFYLGCCQLISLRPEKOGAATGVDTCCTTHPDVPGGLDIQOLYWELSLTH 433
Db 753 PLFQKSSMGPFYLGCCQLISLRPEKOGAATGVDTCCTTHPDVPGGLDIQOLYWELSLTH 812
QY 434 GVTOLGFYVLDRLSLFINGYAPQNLISIRGEYQINPHI VNMNLSNPDPSTSEYITLLRDIQ 493
Db 813 GVTOLGFYVLDRLSLFINGYAPQNLISIRGEYQINPHI VNMNLSNPDPSTSEYITLLRDIQ 872
QY 494 DKVTLYKGSQSLHDTFRCLVTNLTWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFH 553
Db 873 DKVTLYKGSQSLHDTFRCLVTNLTWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFH 932
QY 554 WLGSTYQVLDIHTVEMESSYVQPTSSSTQHFYLPNFTITNLPSYQDKAOPGTTNYQRNKR 613
Db 933 WLGSTYQVLDIHTVEMESSYVQPTSSSTQHFYLPNFTITNLPSYQDKAOPGTTNYQRNKR 992
QY 614 NIEDALNQLFRNSSIKSYFSDCQVSTFRSPVNRHHTGVDSLNCNFSPLARRVDRVAIYEEF 673
Db 993 NIEDALNQLFRNSSIKSYFSDCQVSTFRSPVNRHHTGVDSLNCNFSPLARRVDRVAIYEEF 1052
QY 674 LRMTNGTQLOQNTFLDRSSVLVDGYSPNRNEPLTGNS 710
Db 1053 LRMTNGTQLOQNTFLDRSSVLVDGYSPNRNEPLTGNS 1089

RESULT 15

US-10-198-053-459
; Sequence 459, Application US/10198053
; Patent No. 6858710
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hill, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C9
; CURRENT APPLICATION NUMBER: US/10/198,053
; CURRENT FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 624
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 459
; LENGTH: 1156
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-198-053-459

Query Match 92.3%; Score 3642; DB 2; Length 1156;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 694; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 14 FTHRSSVSTSTPGTPTVYLGAASKTPASIFGSAASHLLILFTLNFTITNLRYEENWPG 73
Db 401 FTHRSSVSTSTPGTPTVYLGAASKTPASIFGSAASHLLILFTLNFTITNLRYEENWPG 460
QY 74 SRKFNTTERRVLOGLLRPLFKNTSVGLYSGRLLTLRPEKOGATGVDAICTHRPDPGP 133
Db 461 SRKFNTTERRVLOGLLRPLFKNTSVGLYSGRLLTLRPEKOGATGVDAICTHRPDPGP 520
QY 134 GLDREQLYLELSQTHSITELGPYTLDRSLYNGFTHRSSVPTTSTGVVSEBFTLNFT 193

Db 521 GLDREQLYLELSQTHSITELGPYTLDRSLYNGFTHRSSVPTTSTGVVSEBFTLNFT 580
QY 194 INNLRYMADMGQPGSLKFNITDNVMKHLSPFORSSLGARYTGCRRVIALRSVKNAGETR 253
Db 581 INNLRYMADMGQPGSLKFNITDNVMKHLSPFORSSLGARYTGCRRVIALRSVKNAGETR 640
QY 254 VDLCTYLQPLSGPGLPIKQVPHLSQOHTGIRLGPYSLDKDSLYLNGYNEPGDEPPT 313
Db 641 VDLCTYLQPLSGPGLPIKQVPHLSQOHTGIRLGPYSLDKDSLYLNGYNEPGDEPPT 700
QY 314 TPKPATTFPLPPLSEATTAMGYHLKTLTINFTISNLQYSPDMGKGSATFNSSTEGVLOHLR 373
Db 701 TPKPATTFPLPPLSEATTAMGYHLKTLTINFTISNLQYSPDMGKGSATFNSSTEGVLOHLR 760
QY 374 PLFQKSSMGPFYLGCCQLISLRPEKOGAATGVDTCCTTHPDVPGGLDIQOLYWELSLTH 433
Db 761 PLFQKSSMGPFYLGCCQLISLRPEKOGAATGVDTCCTTHPDVPGGLDIQOLYWELSLTH 820
QY 434 GVTOLGFYVLDRLSLFINGYAPQNLISIRGEYQINPHI VNMNLSNPDPSTSEYITLLRDIQ 493
Db 821 GVTOLGFYVLDRLSLFINGYAPQNLISIRGEYQINPHI VNMNLSNPDPSTSEYITLLRDIQ 880
QY 494 DKVTLYKGSQSLHDTFRCLVTNLTWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFH 553
Db 881 DKVTLYKGSQSLHDTFRCLVTNLTWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFH 940
QY 554 WLGSTYQVLDIHTVEMESSYVQPTSSSTQHFYLPNFTITNLPSYQDKAOPGTTNYQRNKR 613
Db 941 WLGSTYQVLDIHTVEMESSYVQPTSSSTQHFYLPNFTITNLPSYQDKAOPGTTNYQRNKR 1000
QY 614 NIEDALNQLFRNSSIKSYFSDCQVSTFRSPVNRHHTGVDSLNCNFSPLARRVDRVAIYEEF 673
Db 1001 NIEDALNQLFRNSSIKSYFSDCQVSTFRSPVNRHHTGVDSLNCNFSPLARRVDRVAIYEEF 1060
QY 674 LRMTNGTQLOQNTFLDRSSVLVDGYSPNRNEPLTGNS 710
Db 1061 LRMTNGTQLOQNTFLDRSSVLVDGYSPNRNEPLTGNS 1097

RESULT 16

US-09-827-271-459
; Sequence 459, Application US/09827271
; Patent No. 6962980
; GENERAL INFORMATION:
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C6
; CURRENT APPLICATION NUMBER: US/09/827,271
; CURRENT FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 459
; LENGTH: 1156
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-827-271-459

Query Match 92.3%; Score 3642; DB 2; Length 1156;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 694; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 14 FTHRSSVSTSTPGTPTVYLGAASKTPASIFGSAASHLLILFTLNFTITNLRYEENWPG 73
Db 401 FTHRSSVSTSTPGTPTVYLGAASKTPASIFGSAASHLLILFTLNFTITNLRYEENWPG 460
QY 74 SRKFNTTERRVLOGLLRPLFKNTSVGLYSGRLLTLRPEKOGATGVDAICTHRPDPGP 133
Db 461 SRKFNTTERRVLOGLLRPLFKNTSVGLYSGRLLTLRPEKOGATGVDAICTHRPDPGP 520
QY 134 GLDREQLYLELSQTHSITELGPYTLDRSLYNGFTHRSSVPTTSTGVVSEBFTLNFT 193

```

Db 521 GLDREQLYELSLQTHSITELGPTTLDRSLYNGFTHRSSVPTTSTGVSEBPTLNFT 580
Qy 194 INNLRYMADMGQPGSLKFNITDNVMKHLSPFORSSLGARYTGCRRVIALRSVKNGAETR 253
Db 581 INNLRYMADMGQPGSLKFNITDNVMKHLSPFORSSLGARYTGCRRVIALRSVKNGAETR 640
Qy 254 VDLCTYQLPSGPGPLIKOVFHELSSQTHGITRLGYSLDKSLYNGNEPDPBPPT 313
Db 641 VDLCTYQLPSGPGPLIKOVFHELSSQTHGITRLGYSLDKSLYNGNEPDPBPPT 700
Qy 314 TPXPATTFPLPSEATTAMGYHLKTLTINFTISNLQYSPDMGKGSATFNSSTEGVLQHLR 373
Db 701 TPXPATTFPLPSEATTAMGYHLKTLTINFTISNLQYSPDMGKGSATFNSSTEGVLQHLR 760
Qy 374 PLFKSSMGPFYLGCOLISLRPEKGAATGVDTTCTYHPDPVPGGLDIQOLYWELSLQTH 433
Db 761 PLFKSSMGPFYLGCOLISLRPEKGAATGVDTTCTYHPDPVPGGLDIQOLYWELSLQTH 820
Qy 434 GVTOLGYPVLDRLSLFNGYAPQNLSIRGEYQINFHIVNNLSNPDPTSSEYITLLRDIO 493
Db 821 GVTOLGYPVLDRLSLFNGYAPQNLSIRGEYQINFHIVNNLSNPDPTSSEYITLLRDIO 880
Qy 494 DKVTTLKGSQQLHDTFRFCLVTNLTMDSVLVTKALFSSNLDPSLVEQVFLDKTLNASFH 553
Db 881 DKVTTLKGSQQLHDTFRFCLVTNLTMDSVLVTKALFSSNLDPSLVEQVFLDKTLNASFH 940
Qy 554 WLGSTYQLVDIHVTEMESVYQPTSSSTQHFYLNFTITNLPSYQDKAQPGTTNYQRNKR 613
Db 941 WLGSTYQLVDIHVTEMESVYQPTSSSTQHFYLNFTITNLPSYQDKAQPGTTNYQRNKR 1000
Qy 614 NIEDALNQLFRNSSIKYFSDCQVSTFRSPNRRHTGVDLSLCPNPLARRVDRVAIYEEF 673
Db 1001 NIEDALNQLFRNSSIKYFSDCQVSTFRSPNRRHTGVDLSLCPNPLARRVDRVAIYEEF 1060
Qy 674 LRMTNRGTQLQNFLLDRSSVLVDGYSNRRNEPLTGN 710
Db 1061 LRMTNRGTQLQNFLLDRSSVLVDGYSNRRNEPLTGN 1097

```

RESULT 17

US-09-404-879A-388

; Sequence 388, Application US/09404879A

; Patent No. 6468546

; GENERAL INFORMATION:

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: King, Gordon E.

; APPLICANT: Algate, Paul A.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER

; FILE REFERENCE: 210121.462C2

; CURRENT APPLICATION NUMBER: US/09/404,879A

; CURRENT FILING DATE: 1999-09-24

; NUMBER OF SEQ ID NOS: 393

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 388

; LENGTH: 772

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-404-879A-388

Query Match 80.8%; Score 3189; DB 2; Length 772;

Best Local Similarity 100.0%; Pred. No. 1.8e-282;

Matches 605; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 FTHRSSVTTSTPGTPTVILGASKTPASIFGPSAASHLLILFTLNFTITNLRYENMWPG 73

Db 159 FTHRSSVTTSTPGTPTVILGASKTPASIFGPSAASHLLILFTLNFTITNLRYENMWPG 218

Qy 74 SRKFNTERVQLGLRLPLFKNTSVGLYSGCRLTLRLPEKGEATGVDAICTHRPDPTGP 133

Db 219 SRKFNTERVQLGLRLPLFKNTSVGLYSGCRLTLRLPEKGEATGVDAICTHRPDPTGP 278

```

Qy 134 GLDREQLYELSLQTHSITELGPTTLDRSLYNGFTHRSSVPTTSTGVSEBPTLNFT 193
Db 279 GLDREQLYELSLQTHSITELGPTTLDRSLYNGFTHRSSVPTTSTGVSEBPTLNFT 338
Qy 194 INNLRYMADMGQPGSLKFNITDNVMKHLSPFORSSLGARYTGCRRVIALRSVKNGAETR 253
Db 339 INNLRYMADMGQPGSLKFNITDNVMKHLSPFORSSLGARYTGCRRVIALRSVKNGAETR 398
Qy 254 VDLCTYQLPSGPGPLIKOVFHELSSQTHGITRLGYSLDKSLYNGNEPDPBPPT 313
Db 399 VDLCTYQLPSGPGPLIKOVFHELSSQTHGITRLGYSLDKSLYNGNEPDPBPPT 458
Qy 314 TPXPATTFPLPSEATTAMGYHLKTLTINFTISNLQYSPDMGKGSATFNSSTEGVLQHLR 373
Db 459 TPXPATTFPLPSEATTAMGYHLKTLTINFTISNLQYSPDMGKGSATFNSSTEGVLQHLR 518
Qy 374 PLFKSSMGPFYLGCOLISLRPEKGAATGVDTTCTYHPDPVPGGLDIQOLYWELSLQTH 433
Db 519 PLFKSSMGPFYLGCOLISLRPEKGAATGVDTTCTYHPDPVPGGLDIQOLYWELSLQTH 578
Qy 434 GVTOLGYPVLDRLSLFNGYAPQNLSIRGEYQINFHIVNNLSNPDPTSSEYITLLRDIO 493
Db 579 GVTOLGYPVLDRLSLFNGYAPQNLSIRGEYQINFHIVNNLSNPDPTSSEYITLLRDIO 638
Qy 494 DKVTTLKGSQQLHDTFRFCLVTNLTMDSVLVTKALFSSNLDPSLVEQVFLDKTLNASFH 553
Db 639 DKVTTLKGSQQLHDTFRFCLVTNLTMDSVLVTKALFSSNLDPSLVEQVFLDKTLNASFH 698
Qy 554 WLGSTYQLVDIHVTEMESVYQPTSSSTQHFYLNFTITNLPSYQDKAQPGTTNYQRNKR 613
Db 699 WLGSTYQLVDIHVTEMESVYQPTSSSTQHFYLNFTITNLPSYQDKAQPGTTNYQRNKR 758
Qy 614 NIEDA 618
Db 759 NIEDA 763

```

RESULT 18

US-09-667-857-388

; Sequence 388, Application US/09667857

; Patent No. 6699664

; GENERAL INFORMATION:

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: King, Gordon E.

; APPLICANT: Algate, Paul A.

; APPLICANT: Fling, Steven P.

; APPLICANT: Retter, Marc W.

; APPLICANT: Fanger, Gary Richard

; APPLICANT: Reed, Steven G.

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Carter, Darrick

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER

; FILE REFERENCE: 210121.462C5

; CURRENT APPLICATION NUMBER: US/09/667,857

; CURRENT FILING DATE: 2000-09-20

; NUMBER OF SEQ ID NOS: 455

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 388

; LENGTH: 772

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-667-857-388

Query Match 80.8%; Score 3189; DB 2; Length 772;

Best Local Similarity 100.0%; Pred. No. 1.8e-282;

Matches 605; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 FTHRSSVTTSTPGTPTVILGASKTPASIFGPSAASHLLILFTLNFTITNLRYENMWPG 73

Db 159 FTHRSSVTTSTPGTPTVILGASKTPASIFGPSAASHLLILFTLNFTITNLRYENMWPG 218

Qy 74 SRKFNTERVQLGLRLPLFKNTSVGLYSGCRLTLRLPEKGEATGVDAICTHRPDPTGP 133

Db 219 SRKFNTERVQLGLRPLFKNTSVGLYSGCRLLRPEKDGATGDAICTHRPDTGP 278
Qy 134 GLDREQLYLELSQTHSITELGPTTLDRLDSLYVNGFTHRSSVPTTSTGVVSEBPTLNFT 193
Db 279 GLDREQLYLELSQTHSITELGPTTLDRLDSLYVNGFTHRSSVPTTSTGVVSEBPTLNFT 338
Qy 194 INNRYMADMGQPSGLKFNITDNVMKHLSPFORSSIGARYTCRCVIALRSVKNGAETR 253
Db 339 INNRYMADMGQPSGLKFNITDNVMKHLSPFORSSIGARYTCRCVIALRSVKNGAETR 398
Qy 254 VDLCTVLPGLSGPLPIKOVFHELSTOOTHGITRLGYSLDKDSLILNGYNEPGDEPPT 313
Db 399 VDLCTVLPGLSGPLPIKOVFHELSTOOTHGITRLGYSLDKDSLILNGYNEPGDEPPT 458
Qy 314 TPKPATTFLPPLSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATFNSSTEGVLQHLR 373
Db 459 TPKPATTFLPPLSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATFNSSTEGVLQHLR 518
Qy 374 PLFOKSMGPFYLGCOLISLRPEKDGAAATGDTTCTYHPDPVGPGLDIQQLYWELSOLTH 433
Db 519 PLFOKSMGPFYLGCOLISLRPEKDGAAATGDTTCTYHPDPVGPGLDIQQLYWELSOLTH 578
Qy 434 GVTOLGFVLDRLDSLFINGVAPQNLSIRGEVQINFIHVNWNLSPDPPTSSEYITLLRDIQ 493
Db 579 GVTOLGFVLDRLDSLFINGVAPQNLSIRGEVQINFIHVNWNLSPDPPTSSEYITLLRDIQ 638
Qy 494 DKVTLLYKGSQQLHDTFRFCVLTNLTMDSVLVTKALFSSNLDPSLVQVFLDKTINASPH 553
Db 639 DKVTLLYKGSQQLHDTFRFCVLTNLTMDSVLVTKALFSSNLDPSLVQVFLDKTINASPH 698
Qy 554 WLASTYQLVDIHVTEMESVYQPTSSSTQHFYLNFTITNLPSYQDKAQPQTNYQRNKR 613
Db 699 WLASTYQLVDIHVTEMESVYQPTSSSTQHFYLNFTITNLPSYQDKAQPQTNYQRNKR 758
Qy 614 NIEDA 618
Db 759 NIEDA 763

RESULT 19

US-10-198-053-388
; Sequence 388, Application US/10198053
; Patent No. 6858710
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Bangur, Marc W.
; APPLICANT: Ratter, Gary R.
; APPLICANT: Hill, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C9
; CURRENT APPLICATION NUMBER: US/10/198,053
; CURRENT FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 624
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 388
; LENGTH: 772
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-198-053-388

Query Match 80.8%; Score 3189; DB 2; Length 772;
Best Local Similarity 100.0%; Pred. No. 1.8e-282;
Matches 605; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 FTHRSSVSTSTPGTPTVYLGAASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWPG 73
Db 159 FTHRSSVSTSTPGTPTVYLGAASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWPG 218
Qy 74 SRKFNTERVQLGLRPLFKNTSVGLYSGCRLLRPEKDGATGDAICTHRPDTGP 133
Db 219 SRKFNTERVQLGLRPLFKNTSVGLYSGCRLLRPEKDGATGDAICTHRPDTGP 278

Qy 134 GLDREQLYLELSQTHSITELGPTTLDRLDSLYVNGFTHRSSVPTTSTGVVSEBPTLNFT 193
Db 279 GLDREQLYLELSQTHSITELGPTTLDRLDSLYVNGFTHRSSVPTTSTGVVSEBPTLNFT 338
Qy 194 INNRYMADMGQPSGLKFNITDNVMKHLSPFORSSIGARYTCRCVIALRSVKNGAETR 253
Db 339 INNRYMADMGQPSGLKFNITDNVMKHLSPFORSSIGARYTCRCVIALRSVKNGAETR 398
Qy 254 VDLCTVLPGLSGPLPIKOVFHELSTOOTHGITRLGYSLDKDSLILNGYNEPGDEPPT 313
Db 399 VDLCTVLPGLSGPLPIKOVFHELSTOOTHGITRLGYSLDKDSLILNGYNEPGDEPPT 458
Qy 314 TPKPATTFLPPLSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATFNSSTEGVLQHLR 373
Db 459 TPKPATTFLPPLSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATFNSSTEGVLQHLR 518
Qy 374 PLFOKSMGPFYLGCOLISLRPEKDGAAATGDTTCTYHPDPVGPGLDIQQLYWELSOLTH 433
Db 519 PLFOKSMGPFYLGCOLISLRPEKDGAAATGDTTCTYHPDPVGPGLDIQQLYWELSOLTH 578
Qy 434 GVTOLGFVLDRLDSLFINGVAPQNLSIRGEVQINFIHVNWNLSPDPPTSSEYITLLRDIQ 493
Db 579 GVTOLGFVLDRLDSLFINGVAPQNLSIRGEVQINFIHVNWNLSPDPPTSSEYITLLRDIQ 638
Qy 494 DKVTLLYKGSQQLHDTFRFCVLTNLTMDSVLVTKALFSSNLDPSLVQVFLDKTINASPH 553
Db 639 DKVTLLYKGSQQLHDTFRFCVLTNLTMDSVLVTKALFSSNLDPSLVQVFLDKTINASPH 698
Qy 554 WLASTYQLVDIHVTEMESVYQPTSSSTQHFYLNFTITNLPSYQDKAQPQTNYQRNKR 613
Db 699 WLASTYQLVDIHVTEMESVYQPTSSSTQHFYLNFTITNLPSYQDKAQPQTNYQRNKR 758
Qy 614 NIEDA 618
Db 759 NIEDA 763

RESULT 20

US-09-827-271-388
; Sequence 388, Application US/09827271
; Patent No. 6962980
; GENERAL INFORMATION:
; APPLICANT: Ratter, Marc W.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C6
; CURRENT APPLICATION NUMBER: US/09/827,271
; CURRENT FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 388
; LENGTH: 772
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-827-271-388

Query Match 80.8%; Score 3189; DB 2; Length 772;
Best Local Similarity 100.0%; Pred. No. 1.8e-282;
Matches 605; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 FTHRSSVSTSTPGTPTVYLGAASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWPG 73
Db 159 FTHRSSVSTSTPGTPTVYLGAASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWPG 218
Qy 74 SRKFNTERVQLGLRPLFKNTSVGLYSGCRLLRPEKDGATGDAICTHRPDTGP 133
Db 219 SRKFNTERVQLGLRPLFKNTSVGLYSGCRLLRPEKDGATGDAICTHRPDTGP 278
Qy 134 GLDREQLYLELSQTHSITELGPTTLDRLDSLYVNGFTHRSSVPTTSTGVVSEBPTLNFT 193
Db 279 GLDREQLYLELSQTHSITELGPTTLDRLDSLYVNGFTHRSSVPTTSTGVVSEBPTLNFT 338

Mon Mar 20 08:49:44 2006

QY	194	INNLRVWADMGQPSLKFNITDNNMKHLISPLFORSSLGARYTGCVRVIALRSVKNGAETR	253
Db	339	INNLRVWADMGQPSLKFNITDNNMKHLISPLFORSSLGARYTGCVRVIALRSVKNGAETR	398
QY	254	VDLLCTYLOPLSGPLPIKQVHELHQSQTHGITRLGPYSLDKDSLYLNGYNEPGDEPPT	313
Db	399	VDLLCTYLOPLSGPLPIKQVHELHQSQTHGITRLGPYSLDKDSLYLNGYNEPGDEPPT	458
QY	314	TPKPATTFPLPPLSEATTAMGYHUKTULNFTISNLOQSPDMGKGSATFNSTEGVLOHLLR	373
Db	459	TPKPATTFPLPPLSEATTAMGYHUKTULNFTISNLOQSPDMGKGSATFNSTEGVLOHLLR	518
QY	374	PLFKQSSMGPFYLGCCQLISLRPEKDGAAATGVDTTCTYHPDPVGPGLDIQOLYWELSQLTH	433
Db	519	PLFKQSSMGPFYLGCCQLISLRPEKDGAAATGVDTTCTYHPDPVGPGLDIQOLYWELSQLTH	578
QY	434	GVTQLGFVLDRLDSLFINGYAPQNLISIRGEYQINFHIVNWNLSNPDPTSSEYITLLRDIQ	493
Db	579	GVTQLGFVLDRLDSLFINGYAPQNLISIRGEYQINFHIVNWNLSNPDPTSSEYITLLRDIQ	638
QY	494	DKVTTLYKGSQQLHDTFRFCLVTNLTMDSVLTVKALFSSNLDPSLVEQVFLDKTLNASFH	553
Db	639	DKVTTLYKGSQQLHDTFRFCLVTNLTMDSVLTVKALFSSNLDPSLVEQVFLDKTLNASFH	698
QY	554	WLGSTYQLOVDIHVTMESSVYQPTSSSSSTOFHFLNFTITNL.PYSODKAQPGTTNYQRNKR	613
Db	699	WLGSTYQLOVDIHVTMESSVYQPTSSSSSTOFHFLNFTITNL.PYSODKAQPGTTNYQRNKR	758
QY	614	NIEDA 618	
Db	759	NIEDA 763	

Search completed: March 20, 2006, 07:31:33
Job time : 43.8343 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 20, 2006, 07:29:34 ; Search time 27.2939 Seconds
(without alignments)
2636.859 Million cell updates/sec

Title: US-10-687-035-1
Perfect score: 3945
Sequence: 1 AQAQARRARTKLFTHRSSV.....QKLISEEDLNMGTGHHHHH 748

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : PIR 80:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	144.5	3.7	1408	2 H69068	cell surface glyco
2	135.5	3.4	1117	2 S63399	probable membrane
3	123.5	3.1	2477	2 S14428	fibronectin precu
4	122	3.1	631	2 I52257	episialin - mouse
5	121.5	3.1	1475	2 S42718	nuclear pore compl
6	121.5	3.1	2471	2 T42977	large tegument pro
7	121.5	3.1	5005	2 P82884	hypothetical prote
8	121	3.1	1131	2 T41144	hypothetical serin
9	118	3.0	532	2 T34235	hypothetical prote
10	117.5	3.0	1377	2 A38926	DNA-binding protei
11	116	2.9	1848	2 A41140	cellulose-binding
12	115.5	2.9	1474	2 F69009	probable membrane
13	115	2.9	888	2 A54280	cell differentiat
14	114.5	2.9	709	2 A35364	carcinoembryoni
15	113.5	2.9	855	2 T07015	Cf-4A protein - to
16	113.5	2.9	1004	2 B25039	outer cell wall pr
17	113.5	2.9	1369	2 T17504	hypothetical prote
18	113.5	2.9	3344	2 JQ1899	genome polyprotein
19	113.5	2.9	5762	2 A41819	proline-rich pepti
20	112.5	2.9	838	2 S38156	hypothetical prote
21	112.5	2.9	948	2 T11678	hypothetical prote
22	112.5	2.9	1348	2 AH1115	cell surface prote
23	112.5	2.9	4936	2 A28515	hypothetical prote
24	112	2.8	643	2 S55593	membrane protein S
25	112	2.8	3587	2 T31075	tyrosidine synthet
26	111.5	2.8	919	2 S45889	probable regulator
27	111.5	2.8	1622	2 AB1717	probable cell surf
28	111	2.8	1777	2 T34369	hypothetical prote
29	111	2.8	2386	1 FNHU	fibronectin precu

30	110.5	2.8	530	2 A39344	tumor-associated m
31	110.5	2.8	1778	2 JT0382	apolipoprotein B -
32	110.5	2.8	2508	2 S61441	surface-associated
33	110	2.8	628	1 A39262	transcription fact
34	110	2.8	1128	2 A49960	bud emergence prot
35	110	2.8	1349	2 A11476	cell surface prote
36	110	2.8	3131	2 T39553	vacuolar protein a
37	109.5	2.8	1268	1 A39640	neural cell adhesi
38	109	2.8	989	2 I56333	apolipoprotein B -
39	109	2.8	998	2 C75489	conserved hypothet
40	108.5	2.8	504	2 D97302	hypothetical prote
41	108.5	2.8	504	2 T33485	hypothetical prote
42	108.5	2.8	537	2 A35400	surface protein T6
43	108.5	2.8	776	2 A82787	tonB-dependent rec
44	108.5	2.8	1040	2 D88568	protein ZK757.3 [1
45	108.5	2.8	1113	2 H84105	hypothetical prote
46	108.5	2.8	1642	2 T19130	hypothetical prote
47	108	2.7	609	2 T25120	hypothetical prote
48	108	2.7	628	1 A33333	transcription fact
49	108	2.7	630	1 A46149	transcription fact
50	108	2.7	709	2 T28712	hypothetical prote
51	108	2.7	1035	2 T23165	hypothetical prote
52	108	2.7	1037	2 S37879	nuclear pore prote
53	108	2.7	1084	2 B64088	hemoglobin-binding
54	108	2.7	3603	1 D69681	peptide synthetase
55	107.5	2.7	661	2 S21221	hemocyanin chain c
56	107.5	2.7	934	2 G86548	polymorphic outer
57	107.5	2.7	934	2 A72075	polymorphic membra
58	107.5	2.7	952	2 D81593	ascites sialoglyco
59	107.5	2.7	1630	2 A53577	probable cell-adhe
60	107.5	2.7	2140	2 T18543	hypothetical prote
61	107	2.7	611	2 B71220	probable serine-th
62	107	2.7	664	2 C70584	hypothetical prote
63	107	2.7	771	2 T34376	protein-tyrosine-p
64	107	2.7	1118	1 A49724	probable membrane
65	107	2.7	1609	2 S23345	hypothetical prote
66	106.5	2.7	967	2 S66852	hypothetical prote
67	106.5	2.7	1301	2 S18118	apoptosis signal-r
68	106.5	2.7	1379	2 JCS778	tenascin precursor
69	106.5	2.7	1810	1 A32230	probable exported
70	106	2.7	777	2 AE0462	hypothetical prote
71	106	2.7	821	2 T41364	hypothetical prote
72	106	2.7	1298	2 A64157	probable membrane
73	106	2.7	1636	2 S60403	probable membrane
74	105.5	2.7	853	2 T17461	penicillin-binding
75	105.5	2.7	916	2 F97053	disease resistance
76	105.5	2.7	1163	2 I56126	lymphocyte functi
77	105.5	2.7	1250	2 B81339	probable restricti
78	105.5	2.7	1679	2 T30271	surface protein -
79	105.5	2.7	1695	2 A56921	kinesin family pro
80	105.5	2.7	1962	2 A36334	lactocepin (EC 3.4
81	105	2.7	1770	2 S56221	hypothetical prote
82	104.5	2.6	872	2 T50369	probable serine/th
83	104.5	2.6	2829	2 I48569	apolipoprotein B -
84	104.5	2.6	2710	2 A37052	toxin A - Clostrid
85	104	2.6	446	2 A27424	tubulin beta chain
86	104	2.6	562	2 AD0074	probable hemolysin
87	104	2.6	621	2 S73155	hypothetical prote
88	104	2.6	624	2 S44938	nitrogen permease
89	104	2.6	701	2 A11501	internalin protein
90	104	2.6	845	2 T07039	Hcr9-0 protein - t
91	104	2.6	952	2 T50451	hypothetical coile
92	104	2.6	1093	2 B86748	hypothetical prote
93	104	2.6	1522	2 T39371	transcription regu
94	104	2.6	1824	2 S68553	surface layer prot
95	104	2.6	3124	2 A40020	collagen alpha 1(X
96	103.5	2.6	449	1 UBCKBA	tubulin beta chain
97	103.5	2.6	555	2 T00778	probable tRNA aden
98	103.5	2.6	792	2 S03232	hypothetical prote
99	103.5	2.6	952	2 JC7227	ent-kaurane syntha
100	103.5	2.6	977	2 T16232	hypothetical prote

ALIGNMENTS

RESULT 1

H69068
cell surface glycoprotein (s-layer protein) related protein - Methanobacterium thermoaut
C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: H69068
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiawani, N.
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: func
A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Accession: H69068
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-1408 <MTH>
A;Cross-references: UNIPROT:O27557; UNIPARC:UPI0000066761; GB:AE000911; GB:AE000666; NID
A;Experimental source: strain Delta H
C;Genetics:
A;Gene: MTH1513
A;Start codon: TTG

Query Match 3.7%; Score 144.5; DB 2; Length 1408;
Best Local Similarity 20.1%; Pred. No. 0.19; Mismatches 258; Indels 269; Gaps 40;
Matches 157; Conservative 99;
QY 58 NFTITNLRYBENMWPGRKFNNT---ERVQLGLRLPLFKNTSVGPLYSGCRLTLRLPEKD 114
DB 444 NFTVT-----PDACKNKLGLSDGLTRFPFIISNIVTPL----- 480
QY 115 GEATGVDAICTHRPDPGGLDRQLYLEL-SOLTHSITELGPVTLDRDLYNGFTHRS 173
DB 481 -----NGTGP-----LVTLRGNITCGDSTGWYRLD---LYNGY--RT 515
QY 174 SVPTTSYGVSEEBFTLNFTI-----NNLRVMDMGQ 205
DB 516 AGKWEVGSLETFEPFEFTFLRNSRAYSVGNPPATRVVFLGLIIPENLRVTPSGGQ 575
QY 206 PGSLEKFINDNVMMKHLSPFORSLGARVTGCRVIALRSVKGAEATRV----- 254
DB 576 E-PLKVNVTADLVNYGDLPSYRAEL---YIDGVLLDSRVNVNASSRTTVSNRLLAAG 631
QY 255 --DLLCTYLP-----LSGGLPLIKQVHLSQTHG-----ITRL--GPYSLDK 295
DB 632 LYEITINDLEPELVVMEGKFIYEN--FTLTQSGAAPTIVTVSAMITNIDSNPRSYTA 689
QY 296 DSYLYNG-----YNEPGDPEPTPKPATTFPLPSEATTANGYH---LKLTL-LNF 343
DB 690 -TIYVNGVPDHTKVLNTPGES---TVPFSTIILPDRGLYTISLNNVSGTVRVLSANF 745
QY 344 TISNLQYSPDMGKGSATFNSTEGVLQHLRLPLFOKSSMGPPFLGCQLISLRPEKDGAAATG 403
DB 746 TLSNVTSPVEGKSPLVNVTVAIV-----RNGDLAG 777
QY 404 VDTTCTYHPDPVPGFLDIQQLYWELSQLTHGVTLQGFVYLDRLDRLFNGYAPQNLSTIGE 463
DB 778 -DPAVTLVLDVA-----WETRTVS-----VPGKSSVLVS--FKKELAPFGE 816
QY 464 YQINFHI---VNNWLSNPDPTSSSYIILLRDIQDKVTLYKGSQHLHTFRCL-VTN--- 516
DB 817 YRLNLSGTDVIRVLEPDPFITGF-----NVTFTVGTGAPL--SVRASLVNTPHD 865
QY 517 -----LTWDSVLVTVKALFSSNLPDLSLVEQVFLDKLTNANSPHWLGL----- 556
DB 866 LVIGFTARLAVDGVVQENIV---SLSPGETREIATMGTLTPGNHTVGINEFSKIVRLR 922
QY 557 -STYQLVDIHTVMESSYQP-----TSSSSQHFVYNFT-----ITNLPSYQDKAQGT 605
DB 923 PASITLSDLRVT--PSSGFSPLTITATATARTGEVDGNYTAVLYINGLAVDKKNVTGVA 980

RESULT 2

S63399
probable membrane protein YNR067c - yeast (Saccharomyces cerevisiae)
N;Alternate names: Hypothetical protein N3547
C;Species: Saccharomyces cerevisiae
C;Date: 27-Apr-1996 #sequence_revision 03-May-1996 #text_change 09-Jul-2004
C;Accession: S63399
R;Duesterhoeft, A.; Floeth, M.; Pritz, C.; Heuss-Neitzel, D.; Hilbert, H.; Moestl, D.
submitted to the Protein Sequence Database, April 1996
A;Reference number: S62944
A;Accession: S63399
A;Molecule type: DNA
A;Residues: 1-1117 <DUE>
A;Cross-references: UNIPROT:P53753; UNIPARC:UPI000013BACB; EMBL:Z71682; NID:GL302597; PI1
A;Experimental source: strain S288C
C;Genetics:
A;Gene: MIPS:YNR067c
A;Cross-references: SGD:S0005350
A;Map position: 14R
C;Keywords: transmembrane protein
F;6-22/Domain: transmembrane #status predicted <TM>

Query Match 3.4%; Score 135.5; DB 2; Length 1117;
Best Local Similarity 21.1%; Pred. No. 0.56;
Matches 156; Conservative 94; Mismatches 255; Indels 233; Gaps 39;
QY 4 PARRARKLFTHRSSVSSTSTPGTPTVYLG-----SKTPAS--IFGSAASHL 51
DB 206 PSYSSQETKIIP--SSLTNKKIYITISVRTNAATATGEDSFIASTPASSTLFPSPSTQD 263
QY 52 LILFTNFTNLRYBEN---MWPGRKFNFTERV-----LQGLRLPL 91
DB 264 LVQ-TLASTAGAPYNSRTOITLSFSVLSYTSPIYPSNITENGSSPSLSSTVSPV 322
QY 92 FKNTSVGLYSGCRLTLRLPEKDEATGVDAICTHRPDPGGLDRQLYLELS-QLTHS 150
DB 323 YPSSSTGNIL---LSSLFSTVDSSSS-----PVSSTLD--TIYVSSSQATIS 365
QY 151 ITELGPVTLDRDLYNGFTHRSVPTSTGVVSEEBFTLNFTINNLRVMDMGQPSGLX 210
DB 366 SSSSSRQTKTSS-----SLSTSTSTATTENSSTT--TIVNLFNAVSTDEPPTV- 414
QY 211 FNITDNVMMKHLSPFORSLGARVTGCRVIALRSVKGAEATRVLDLCTVQLPSGLPL 270
DB 415 FDRSPNPM-----SLADGVSN-----DGP-IQ 435
QY 271 IKQVFHBL---SQOTHGITRLGPYSLDK-----DSLYNGINEPPEPDEPP 312
DB 436 TNKFTYTNLVGSGESPAF--VYPVSLWKYTSYSGYFAVQHTTVDOYSGYDSSGNAEYL 493
QY 313 TTPKPAATFPLPSEATTANGYHLKTLNFTISNLOQYSPDMGKGSATFNSTEGVL----- 368
DB 494 VNP-----LGIHVVFSAFNSFDSMTMQVDEMTLSSTRVVLSESN 533
QY 369 ---QHLLRLPLFOKSSMGPPFLGCQLISLRPEKDGAAATGVDTTCTYHPDPVPGFLDIQQLY 425
DB 534 DSSNLYEIPLVQ--GMG-FATGIYHGLN-AKIGSSVGFNTIVSESSNLAQGI-----LK 585
QY 426 WELSQTLGHVTLQGFVYLDRLDRLFNGYAPQNLSTIRGEYQINFH-----IVNNWLSNPD 479

Db 843 -VYSPSEGSSTELNLPETANSV-----TSLD-----QPQ-VQYNNITIVAVE 893
QY 220 --HLLSPLF-QRSLSG-----ARYTGRVIALRSVKNAGT--RVLLCT 259
Db 884 ENQESTPVFIQOETGTPVPRSDVPAKDLQFVEVTDVKVTIMWTPPNSAVTGYRVDVLPV 943
QY 260 YLQPLSGPLPI-KQVFHELSSQOHTGIT---RLGPYSLDKDSLVLNGYNEPQDEP--- 311
Db 944 NLGEHGORLVRNRTFAEVTGLSPGVYLFKVFANVHOGRESKPLTAQOITKLDAPNLQ 1003
QY 312 ---PTTPKPAATFLPP-----LSEATTAMG-----YHLKTLTLNFTISNLQVSPDMG- 355
Db 1004 FVNETDRTVLVWTPPRARIAGYRLTVGLTRGGQPKQYVGNPMAKYPRLNLPQGSSEYTV 1063
QY 356 ----KGSATFNSTEGVLQHLRPLFOKSSMGPF-----YHLCQQLISL 393
Db 1064 TLMVAVKNGQSPKATGVFT-TLOPL---RSIPPYNTVEVTTIVITWTPAPRIGFKL-GV 1118
QY 394 RPEKDGAAATGVDTTCTVHPDPVGPGLDIQQLYXWELSQLTHGVTLQGPYVL-----DRD 446
Db 1119 RPSGGAPREVTS-----DSGSIV--VSLTTPGVY--YTIQVLRDQGERD 1162
QY 447 SLFINGYA-----PQNLISIRGEYQINPHIVNNLS-NPD-----PTSSEYITLLRD 491
Db 1163 APIVNRVVTPLSPTNLHLEANPDTGVLTVSWERSTTPDITGYRIITTTPTNGQOQTALRE 1222
QY 492 IQDKVTLTKGSLDTRFCLVTN-----LTMSVLTVTK-----ALFSSNL---DPSIV 539
Db 1223 V-----VHADQSCSTFENRPNPGLYVSVYTVKDKESAPISDTVPEVPQLT 1270
QY 540 EQVFLDKT-LNASPHW--LGSTYQLVDIHVTEMESS---VYOPTSSSTQHFYLNFTIT 592
Db 1271 DLSEVDITDSIGLWTPLNSS-TIIGYRITVNAAGEIPIFEDFVDSVGY-----YTVT 1325
QY 593 NLPYSQDKAOPGTTNYQRNKNI-----EDALNQLFRNSSI-----KSYFSDCQVSTF 640
Db 1326 GL-----EPG-IDYDISVITLINGGESAPTTLTQQTAVPPPTDLRTNIGPDMTRVTV 1377
QY 641 RSVPNRHHTGVDSLCNFSPLARRVDRVAIYEEFLRMTNGTQLON-----FTLDRSSVL 694
Db 1378 APPPSIELTNL--LVRYSPVKNEED---VAELSTSPSDNAVLTNLLPGTEYLVSVSSV- 1431
QY 695 VDGYSFNRNPLQNSADIQHSGRSSIEGPR-PEQKLISEDLNMB-----TGH-- 743
Db 1432 ---YEQHESILRGRQ-----KTGLDSTGDFDSSDVANSFTVHWVAPRATIGYII 1480
QY 744 -HHHH 748
Db 1481 RHHAH 1486
RESULT 4
I52257
A:Species: Mus musculus (house mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C:Accession: I52257; I65210
R;Vos, H.L.; De Vries, Y.; Hilkens, J.
Biochem. Biophys. Res. Commun. 181, 121-130, 1991
A:Title: The mouse epistatin (Muc1) gene and its promoter. Rapid evolution of the repeti
A:Reference number: I52257; MUID:92068178; PMID:1958179
A:Accession: I52257
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-631 <RES>
A:Cross-references: UNIPROT:Q02496; UNIPARC:UPI000002A11B; GB:M77226; NID:g199835; PIDN:
A:Accession: I65210
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-631 <RES>
A:Cross-references: UNIPARC:UPI000002A11B; GB:M84683; NID:g199842; PIDN:AAA39756.1; PID:
C:Genetics:
A:Gene: Muc1

A;Introns: 20/1; 454/3; 472/2; 517/1; 557/3; 607/3
Query Match 3.1%; Score 122; DB 2; Length 631;
Best Local Similarity 21.4%; Pred. No. 1.9;
Matches 122; Conservative 55; Mismatches 207; Indels 186; Gaps 26;
QY 89 RPLFKNITGVPLYSGLRLLRPEKDGATGVDAICTHRPDPPTGPGDLRQLYLELSQLT 148
Db 58 RPPGDSTS-SPVQSSTSSPATRAPEDSTSTAV-LSGTSSPATAP-----VNSASSPVA 109
QY 149 HSTELGPLYTLDRD---SLYVNGFTHRSSVPTTSTGVSEEPFLTNLTNNLYMADMGQ 205
Db 110 HGTSTPATSTLSKDSNSPVVHSGT--SSAPATTAPVDS---TSPVHVGHTSSPATSP 163
QY 206 PGSKLNITDNNVKKHLLSPLFORSSILGARVTCRVLALRSVKNGAETRVLLCTYLOPLS 265
Db 164 PGD-----STSSPDHSSSTSSPATRAPEDSTSTAV-----LS 194
QY 266 GPGLP--IKQVFHELSSQOHTGITRLGYPYSLDKDSLVLNGYNEP---GPDEPPTPKPAT 319
Db 195 GTSSPATAPVDSTSPVAHDDTSSPATSLSEDSA-----SSPVAHGGTSSPATSPLRDS 249
QY 320 TFLPPLSEATTAMGYHLKT-----LTNFTISNLQYSPDMKGSATFNSTE 365
Db 250 TSSPVHSSASI---QNIKTTSLASTPDHNGTSVTTTSSALGATSPDHSGTSTTTNSSE 306
QY 366 GVLQHLRLPLFOKSSMGPFYVLCQLISLRPEKGAATGVDTTCTYHPDPVPGP-LDIQQL 424
Db 307 SVL--ATTPLY--SSM-PF-----STTKVSGSALIPDHNGSSVLPTSSV 346
QY 425 YWELSQLTHGVTLQGFVFLDRDSLFIINGYAPQNLISIRGEYQINPHIVNNLSNPDPTSSSE 484
Db 347 LGSATSLVNTSAIATTPVS-----NGTQP---SVPSQYPV-----SPTMATSS 388
QY 485 YITLRRDIQDKVTTLKYGSQLHDTFRFCLVTNLTMSVLTVKALPSSNLDPSLVEQVFL 544
Db 389 HSTI-----ASSSYSTVTF-----STFSSSPQL----- 414
QY 545 DKTINASFWLGSYQLVDIHVTEMESSVYQPTSSSTQHFYLNFTITNLPYSQDKAOPG 604
Db 415 --SVGSVF-----FFLSFYQNHPFNSSLEDDPS 440
QY 605 TTNVQRNKRNIEDALNQLFRN-----SSIK 629
Db 441 SNTYQELKRNISGLFQIFNGDFLGISSIK 470
RESULT 5
S42718
nuclear pore complex protein nup153 - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S42718; S37477
R;McMorrow, I.; Bastos, R.; Horton, H.; Burke, B.
Biochim. Biophys. Acta 1217, 219-223, 1994
A:Title: Sequence analysis of a cDNA encoding a human nuclear pore complex protein, hnup
A:Reference number: S42718; MUID:94154002; PMID:8110839
A:Accession: S42718
A:Molecule type: mRNA
A:Residues: 1-1475 <MCM>
A:Cross-references: UNIPROT:P49790; UNIPARC:UPI000012FC15; EMBL:Z25535; NID:g406224; PID

Query Match 3.1%; Score 121.5; DB 2; Length 1475;
Best Local Similarity 19.4%; Pred. No. 8.1;
Matches 86; Conservative 57; Mismatches 162; Indels 139; Gaps 17;
QY 7 RARTRKLFTHRSSVSTSTP-----GTPVTYVLGASKTPASIFGPSAASHLLILFTLNFT 60
Db 351 QAKREKVDQVPPVQRLMTPKVSIATNRSVYFKPSLTPSG-----EFR 394
QY 61 ITNLR-----YEENWPGSRKFNTERVLOGLRLPLFKNTSVGPLYSGRLTLRPE 112
Db 395 KTNQRIDNKCSTGYEKNTPGQNR-----EQRESGFSYPNFS-----LPA 434


```
Db 932 -----NSDDNHVLDSQKT-----PGFSTPKASFDLVSVTASDVVDANKVNSVHIVI 979
Qy 444 DRDLFLNGYAPQNLSSIRGBYQI---NFHIVNNWLSNPD-----479
Db 980 NNDGTSLNKCAKIVYNDGEHDLVNNFVNLVNGVNEYDFNLDDLKHNRISYFKKLIYTE 1039
Qy 480 PTSSEY-ITLRLDIQKVITYLKGSLQHDTRFCLVTLNLTWDSVLVTVKALFSSNL-----534
Db 1040 PNQNDYKFSFLNN--QKITNTFKTASVNE-----QLTIDTKLVRKP---DSNLKIN 1086
Qy 535 -----DP-----SLVEQVFLDKTLNAGFHWLG-----STVQLVDIHHVTEWESSVYQ 575
Db 1087 LKQINDPNDFLEQDSILEITFDEKDKTTHNVIGKINVDANNKNTLEFSEVENTNFKIQ 1146
Qy 576 PTSSSSQHFYLNFTINLRY-SDKAQPGTT-NYQNKKNIEDALNQLFRNSIKSYFS 633
Db 1147 P-----NHKYI---VDNINATQNKIQPANAISNNNSKNSIYDASS---NPSKILSFTN 1194
Qy 634 DCQVSTER-SVNPBHHTGVDSLCLNFSPLAR-----RVDRAIYEEFLEMTENGTLQONFT 687
Db 1195 ELFVNNINVAQPN-----TLNPTASIDVELKSSQNLKDDQYLALYIDNNHOKIW 1245
Qy 688 LDRSSVLVDGYSNPNRPLETGNSSADIQH 715
Db 1246 SDIASV-----NNVDLAH 1258

RESULT 8
T41144
hypothetical serine rich protein - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T41144; T41591
R;Hilbert, H.; Duesterhoeft, A.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, October 1998
A;Reference number: Z21973
A;Accession: T41144
A;Status: translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-1131 <HIL>
A;Cross-references: UNIPROT:Q74851; UNIPARC:UPI000006A713; EMBL:AL031907; NID:g3766362;
A;Experimental source: strain 972h-; cosmid c18
R;Murphy, L.; Harris, D.; Iyne, M.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, September 1998
A;Reference number: Z21968
A;Accession: T41591
A;Status: translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 44-1131 <MUR>
A;Cross-references: UNIPARC:UPI0000161F34; EMBL:AL031543; NID:g4239667; PIDN:CAA20837.1;
A;Experimental source: strain 972h-; cosmid c74
C;Comment: For a possible alternative initiator product, see PIR:T42367.
C;Genetics:
A;Gene: SPCC74.07C; SPDB:SPCC18.01C
A;Map position: 3
C;Keywords: alternative initiators

Query Match 3.1%; Score 121; DB 2; Length 1131;
Best Local Similarity 18.6%; Pred. No. 5.7;
Matches 161; Conservative 130; Mismatches 353; Indels 222; Gaps 30;
Qy 2 AQPARRARTKLFTHRSVSTSTPGTPVYLGASKTPASIFGFSASHLILFTLFTI 61
Db 341 ASSSSSSASATATSAESSIAT--SPITSSSNVSVSISTSSMDSSGAVSSYVVOGSLASII 398
Qy 62 TNLAYENMWPGRKENTERVQLGLRPLPKNTSVGLYSGCLTLRLRPEKDEATGVD 121
Db 399 S-----NAYTATSKSLNGSVTLASPTSSSTFTVSL-----LRRSIDGSASSS 445
Qy 122 ---AICTHRPDPTGFLDREQLYLELSQLTSHSITELGPLYTLDRDSLTVNGFTHRSSVPTT 178
Db 446 ASLAVPTVSSSTTG-----SLHYK-TTTTVMVTEVFTRYLGDDSTPVTs----SSIFST 494
```

```
Qy 179 ST-----GVVSEEPFTLNFTINNRYMADMGPGSLKFNITDNVMKLLSPLFOR 228
Db 495 ATBATTSVQTSSAIIQSSSTSIQSSSVYASSTGALSNSLSSTSSVSTSYINPASS 554
Qy 229 SSLGARYTGRVIALRSVKNAGETRVDLLCTYLQPLSGFGLPIKQVHFELSQOHTGIRL 288
Db 555 SVYASSTEALSNLSSTSSAST-----SYIPSASSSVYEVASNSDDYVQTVSSITAS 608
Qy 289 GPYSLDKSL-----YLNG-----YNEGPDEPPTTPKATFLPPLSEATAMG 333
Db 609 GTTSTSEIVSTPASNTGSLNGTSSFNVSNGPSSSQTTPTSSSITGSQLKETSSP 668
Qy 334 YHLKTLTANFTIQLQYSPDMGKGSATFNS-----TEGVLOH 370
Db 669 AYVS--TVSTSSVD-----SSSTYNSSTGSSSDSQSPSGTTSYSDPTTITSEVSI 720
Qy 371 LLRPLFKSMGPFYLGCLILSRPEKGAATGVTCTTVHPDPVGPGLDIOQLYWELSQ 430
Db 721 LSSPTSMQSSVS-----RPOSSGDASGNT-----IFTSISQ 752
Qy 431 LTHGVTLQGFVLDRLSFLNGYAPQNLSTIRGEYQINFHIV-----NMNLSNP 478
Db 753 SSDGET--SGYTSSNSNQNSASEPQTAFPTSSSSATPTITQSSISTSVSSQSSMSSYS 810
Qy 479 DPTSSEVITLRLDIQDKV-----TTLYKGSQHLDTFRFCLV 514
Db 811 SPISNSVTSSTSIISIIASSSVTSIPSSIIASSFDFDASGFTSYNGTKAGSSSFALA 870
Qy 515 TNLTMDSVLTVKALFSSNLDPQLVQVFLDKTLN-----ASFHWLGSTYQLVDI 564
Db 871 SNESGA-----SDVLSSTIAKPTPKFSTNSGTSYSIPSSSRNEGTTSSYNNI 921
Qy 565 HVTEWESSVQV--TSSSSSTQHFLNFTTNLPYSQDKAQPQGTNVQRKNKNIEDALNQL 622
Db 922 TVT---SSTLKPSTSVSTASSIASSSNTLS---TEPKTFS---SSSTLSESISI 972
Qy 623 FRN-----SSIKSVFSDCQVSTFRSPVN--RHHTGVDSLCLNFSPLARR-----663
Db 973 NTNSLTVPKPESSLSSTSTGLTSSSTIPSTSESESEASSTSSASKRSSSTSLVQSN 1032
Qy 664 -VDRVAIYEBF-----LRMTRNGTQLQNFPLDRSSVLVDGYSPNRPETLGNs-----710
Db 1033 PVKTVVSLSEYKFTTSKISLVKNPTKTYTVDVETNVVQTHTVSVYEHSTSYTWVHTTL 1092
Qy 711 ---ADQHSGRSLEGPREFEQLIS 733
Db 1093 YEYADVEASTKSTSEPSAKSKRNAVS 1118

RESULT 9
T34235
hypothetical protein F22A3.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T34235
R;Hallsworth, K.
submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid F22A3.
A;Reference number: Z21492
A;Accession: T34235
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-532 <HAL>
A;Cross-references: UNIPROT:Q19695; UNIPARC:UPI000017B91C; EMBL:U41547; PIDN:AAA83194.1;
C;Genetics:
A;Gene: CESP:F22A3.1
A;Introns: 55/1; 99/1; 148/3; 176/3; 190/1; 239/1; 303/1; 331/3; 357/1; 391/1; 511/1;
P;446-527/Domain: ets DNA-binding domain homology <ETS>

Query Match 3.0%; Score 118; DB 2; Length 532;
Best Local Similarity 20.5%; Pred. No. 2.7;
Matches 101; Conservative 59; Mismatches 171; Indels 162; Gaps 25;
```


QY 102 SGRLTLRLPEK-----DGEATGVDAICTHRDPTGPGLDRE 138
DB 267 LNFNFSAGNPKRLVITVVDTPFVAVTATIGKVQVNAGETVAVPNLTKVP---AAGLATI 323
QY 139 QLVLELSQLTHSITE-----LGPVTLDRDLSLY-- 165
DB 324 ELPLTFDSASLEVSITAGDIVLNPVSFSTVSGSTIKLLFLDDTLGSLIITKGVFAT 383
QY 166 -----VNGFTHR-SSVPTTSGV-----SSEPFTLNTINNLRYMADMGQPGSLKFN 212
DB 384 ITFKAKAITGTAKVTSVKLAGTPVGDQAOQEKPCAVN-----PGVITIN 429
QY 213 ITDNVKKHLLSPFORSSLAGRYGCRVIALRSVKN-----GAETRVDLLCTYLOPLS--- 265
DB 430 PIDNRMQISVG-----TATVKAIGEIAAPVTLTSPSTGIATAEAQVSFDTLLLEVASVTA 485
QY 266 -----GP-----GLPIKOVFHELSQOHTGIRLGPYSKDKSLYLNQYNEPGPDEP 311
DB 486 GDIVLNTVNFSTVNGVNIKLLPLD-----DTLGSQLISKDGVFVT-INPKAKAVT 536
QY 312 PTPKPAATLPLPSEATTAMGYHLKTLTLNFTNISNLQYSPDMGKGSATFNSTEGVLOHL 371
DB 537 STVTPTVTSCTPVFADGTLAEVQSKT-----AAGSVTINIGDPILEPT 580
QY 372 LRPL---FQKSSMGPFYLGQILSLRPEKGAATGVDTTCTYHPDPVPGGLDIQOQLWEL 428
DB 581 ISPVATATFDKK-----APADVATTMT----- 601
QY 429 SOLTHGVTLQFYVLDRLDLSLFIINGYAPQNLIS--IRGEYQINFHIV----- 471
DB 602 -----LNGYTFNGITGLTSDYSISGNVVKLSQAYLAKQPVGD 640
QY 472 --NMNLSNPPT-SSYITLRLDIQDKVT-----TLYKG-----SQL 505
DB 641 TLTFENFNGNKATATAKLWISKAPKTATVATVATVAGTAVPVTLSNVSGISTAE 700
QY 506 HDPRFCL--VTNLTMDSVLVTKALPSSNLDPSLVEQVFLDKTLNASFWHLGTYQLVD 563
DB 701 QLSFDATLLEVVSTAGDIVLNPVSFVNGVSTIKLLFLDDTLGSLISKDGVFATIN 760
QY 564 IHVTESSVYQPTSSSTQHFYLNFTITNLPY 596
DB 761 PKASVTSTVTPVKVSGTPV-ADGTLAELSY 792

RESULT 12
F69009
probable membrane protein MTH1074 - Methanobacterium thermoautotrophicum (strain Delta H
C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: F69009
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiواني, N.
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: func
A;Reference number: A69000; MUID:98037514; PMID:9371463
C;Accession: F69009
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-1474 <MTH>
A;Cross-references: UNIPROT:O27146; UNIPARC:UPI00000666BF; GB:AE000878; GB:AE000666; NID
A;Experimental source: strain Delta H
C;Genetics:
A;Gene: MTH1074
C;Keywords: duplication

Query Match 2.9%; Score 115.5; DB 2; Length 1474;
Best Local Similarity 20.5%; Pred. No. 21;
Matches 158; Conservative 92; Mismatches 306; Indels 215; Gaps 38;
QY 26 PGFTPT-VYLGASKTPASIFGSPASASHLLILFTLN-FTITNLRYEENMWPGRKFNTERV 83

DB 393 PNNATGVYVTDLLPPQLSPFVSASASRGIVNSTTGIWITIGNLEYFETV-----TLNITATV 447
QY 84 LQGLLRPLFKNTSVGLYSCRLT--LLRPEKGEATGVDAICTHRDPTGPGLDREQLY 141
DB 448 -----TATGAIVNNANVTGDVDFDM---ANNYASAAALNSPPASDLTIDK--- 489
QY 142 LELSOLTHSITEGLPYTLDRDLSLVNGFTHRSRVPTTSTGVSEEPF----- 188
DB 490 -----SVNPEPY-VGENIQYITVSNRG--PDNAGVVVEDVLPAGLIPISATPSK 538
QY 189 -----TLNF-TINNLRYMADMGQPGSLK--FNITDNVKKHLLSPF-----ORSS 230
DB 539 GSYVMGTWVNGTILNLEIATLTIIARVNATGSLTNFANIT-----SPNFDPNPNNN 590
QY 231 LGARYTCRCVIALRSVKNGBATVD-----LLCTYLOPLSGPGLPIKOVFHE-LSQQ 281
DB 591 DTAEWGIPVADLLIVKQVSDPRPDYGVSVVTFVAVTNLGPNSNATGVTVTDILSPGLVYL 650
QY 282 THGITRLGPYSLDKDSLNGYNEPGDEPTTPKPAATLPLPSEATTAMGYHLKTLTL 341
DB 651 SHVTQ-GTYNATTGVWYIGALNY-----AASALMNLTVLNTTGDSSNTV-- 695
QY 342 NFTISNLQYSPDMGKGSAA--TFNSTEGVLOHLRLPFPKSSMGPFYLGCOLISLRPEKQ 399
DB 696 --SVTGNRDPDRTNDAVSTLNAVSADLS-----IQKTV-----RPVINN 735
QY 400 AATGVDTCTYHPDPVPGGLDI--QQLYWELSQLTHGVTLQFGY-----VLDRLSLFINGY 453
DB 736 GETATFVIVRNAGDPTPSNVVSDLLPAGLSISYITVTOGSNTTGTGWSVGLPALFQ 795
QY 454 APQNLISIRGE--YQINFHIVNMNLSNPDPSTSEYITLL-----RDIQDKVTVLYKGS 503
DB 796 ATTLVVRATQAGFTN--IVNVSSELPDPLPGNDVAVTVDRPSADVKTITVSNAP 853
QY 504 QLHDTFRFCL--VTNLTMDSVLVTKALPSSNLDPSLVEQVFLDKTLNASFWHLGTYQLV 562
DB 854 DFGDTVVFYITVNLGPDATV-----RT----- 878
QY 563 DIHVTESSVYQPTSSSTQHFYLNFTITNLPYSQKAPQGTNYQNKENIEDALNQL 622
DB 879 ---VDTMPSGLVYQSHSASAGIVFVEFNV---WTVDSLAPGASE-TLNTITVLVNATGGM 930
QY 623 FRNSSIKSYSDCOVSTFRSPVNRHHTGVDSLNCNFSPLARRVDRVAIVAEELRMTNGTQ 682
DB 931 INTVSVTSTEYDPLT-----NNHAG--LLN---AEAVADIAVQKTVLLFPINNGQ 977
QY 683 LQNFLLDRSSVLVDGYSNPRNEPLTGNAD-----IQHSGGRSSLEG 724
DB 978 ITNFT-----VTVTNNGFN--DATGVAVTDLPPGLGLLSHSASQGTFFAG 1020

RESULT 13
A54280
cell differentiation protein LagC precursor - slime mold (Dictyostelium discoideum)
N;Alternate names: loose aggregate C
C;Species: Dictyostelium discoideum
C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004
C;Accession: A54280
R;Dynes, J.L.; Clark, A.M.; Shaulesky, G.; Kuspa, A.; Loomis, W.F.; Firtel, R.A.
Genes Dev. 8, 948-958, 1994
A;Title: LagC is required for cell-cell interactions that are essential for cell-type dif
A;Reference number: A54280; MUID:95011593; PMID:7926779
C;Accession: A54280
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-888 <DYN>
A;Cross-references: UNIPROT:P42523; UNIPARC:UPI000012E1FF; GB:U09478; NID:9495172; PIDN:
A;Note: authors translated the codon TCA for residue 34 as Leu
C;Genetics:
A;Gene: lagC
C;Superfamily: Dictyostelium discoideum cell differentiation protein LagC.
C;Keywords: transmembrane protein

Query Match 2.9%; Score 115; DB 2; Length 888;
Best Local Similarity 19.6%; Pred. No. 10;
Matches 157; Conservative 109; Mismatches 235; Indels 298; Gaps 47;

QY 110 RPEKGE--ATG-----VDAICTHRP-----DPT-----GPGLD 136
DB 130 KPTSGEDIVITGYSYLRFGPNFLINSIDVNRPFVVKGNFSPDSCNNITVTFPPGSG 189
QY 137 REQLYELSLQTHSITELG---PYTLD-----RDSLXYNG---FTHRSSVPT 177
DB 190 KFLYYD-----ETGNPVPFYSVESPIISSVSDSKQIITINGDNFFTKDLVKV 240
QY 178 TSGVSWSEEPFTLNFTI-----NNLRVMDMGQPSLKFNTI----- 214
DB 241 SPDGI--DQD--NFIIIVNHKIQVNNYRV---DPGPMVNIITVEVSIENKVIHCP 291
QY 215 -----DNVWKHL-----LSPILFORSSLGARTGCRVIALRSVKG 249
DB 292 PAITISISSVSNHLDGIVTIKGBKSLSTLYLTPSI---TIGDKY-----VLIKSTTE 343
QY 250 AETRVLLCTYLQPLSGPLPIKQVFI-----ELSQOHTGI----- 285
DB 344 LEKLD-----ANELGKLPVNNVFGGCDSTSPNGVSFTYNIPTLSRGSYSNGIVTLIG 398
QY 286 TRIGPYSLDKDSIYLANG-----YNEPGDPEPTTPKPATTFPLPLSEAT-----TAM 332
DB 399 TNLGTNNESSIQYGDIGKNTNISQFNVSSDE-----KSVTFELPHLRCSFNINFTRS 453
QY 333 GYHLKTLTLNFTIS--NLOVSPDMKGSATFNSTEGVLHLLRPLFOKSMGPPYLCOLI 391
DB 454 GITAKTLSIASLVNVRPTV-----SNGIL-----NIEIYMDCTIS 493
QY 392 SLRPE-----KOGAATGVDTCTVHPDPVPGPLDIQQLYWELSLQTHGVTO 437
DB 494 SSAPSTVGDSSASPCSPSSNSSSYETTC---PTPYGTGIN-KQPIFKINSET----- 544
QY 438 LGPYVLDRLSLFINGYAP---QNLISIRGE-YQINPHIVNNLS-----NPDPTSSSY 485
DB 545 -----VSDQFS-----YAPPEVENRTISDDGTNIELHGNNGFNSTSLIKVYNGSDISSE- 594
QY 486 IYLLRDIQD-----KVTLYK-----GSLQHDHTFPLC-----VTNLTMDSV----- 522
DB 595 ---IOLEDHQTLIKILDSYENGPIINITVDGNTMDSLFLYTLPPVIYRITNKDKTLACG 651
QY 523 -LVTVKALFSSNLDPSLVQVFLDKTLNASFWLGSYQLVDIVHVTMESSYQPT----- 577
DB 652 GLITVS---GKNLLTSDKBKVNKNKNTTVFAQDEKILIVRDSRSSLFVTTFIGV 708
QY 578 -SSSSQHFYLNFTINLPSYQDKAOPGTNTYQNRKNRTIEDALNQLFRNSSIKSYFS--- 633
DB 709 RSGPSTLYIKPMISEIPTIENKIEGILAIIRG-YSTDIILNASLTVSSETVPLSCNL 767
QY 634 DCQVS-----TFRVPRNHHHTGVDSL-CNFSPLARRVDRVAIYEEFLMRTRNGLO- 684
DB 768 ECLSPNEILDSDSETNITNSNTDCLSCHSGSSVKNTSGV-----LYLLFNSTSFQY 821
QY 685 NFTLDRSSVLVDGYSNPN 703
DB 822 NVTIEEIKL-----SPSPN 835

RESULT 14
A35364
carcinoembryonic antigen-related protein (clone mCGM1) - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 17-Aug-1990 #sequence_revision 17-Aug-1990 #text_change 09-Jul-2004
C:Accession: A35364
R:Rebertus, S.; Lucas, K.; Thompson, J.A.; Zimmermann, W.
J. Biol. Chem. 265, 7872-7879, 1990
A:Title: cDNA and gene analyses imply a novel structure for a rat carcinoembryonic antigen
A:Reference number: A35364; MUID:90243655; PMID:2335509
A:Accession: A35364

A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-709 <REB>
A:Cross-references: UNIPROT:Q63111; UNIPARC:UPI00008E1AF; GB:M32474; NID:G203430; PIDN:1-709
C:Superfamily: carcinoembryonic antigen precursor amino-terminal homology <CEA1>
F;1-137/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEA1>
F;168-217/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEA2>
F;242-378/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEA3>
F;480-612/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEA3>
F;633-690/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEA3>

Query Match 2.9%; Score 114.5; DB 2; Length 709;
Best Local Similarity 20.0%; Pred. No. 7.6;
Matches 136; Conservative 80; Mismatches 263; Indels 201; Gaps 30;

QY 134 GLDREOLYELSLQTHSITELGTYLDRSLYNGFTHRSSVPTTSGVSEEPFTLNFT 193
DB 70 GLTNMISGLVALSYLTNNVTVTGPHSGRETLYNSGLMIQNTVTKDQTFY----- 120
QY 194 INNLRYMDMGQPSLKFNTITONVMKHLSPILFORSSLGARTGCRVIALRSVKGAE 253
DB 121 ---LRTISNHE-----IVSNTSLH-LHYVESTLTGCAATSAQ-LSIESVPTSISK 168
QY 254 VDLCTYLOPLSGPLP--IKQVFI-----ELSQOHTGIRL--GPYSLDKDSLY 299
DB 169 EGAL-----LLAHLNLPENLRATFWYKGAIVFKDLVARYVICTNSSVPCPAHSGRETMY 222
QY 300 LAG-----YNEPGDPEPTTPKPATTFPLPLSEATTAMGY-HLKTLLTNFTISNLOYS 354
DB 223 SNGSLQLQVTRNDAGFYTLKTLST-----DLKTEIAYVQLQVDFCFMSYAGPPTSAQL 276
QY 355 GKGSATFNSTEG---VLQHLRPP-----LFQKSSMGPFVLCQLSLRPEKD 398
DB 277 TVESAPTSVAEGASVLLLVNLPENLRATFWYKGVILFKDLEVARVYVICTNSSVLC 336
QY 399 GAATGVDTCTVHPDPVPGPLDIQQLYWELSLQTHGVTO--LGFYVLDRLSLFINGYAPQ 456
DB 337 GRET-----MYSNGLLQVTRNDAGFYTLRSLTSLDKAKV-- 373
QY 457 NLSIRGEYQINPHIVNNLSNPDPTSSSEYITLLRDIQDKVTT-LYKGSOLHDTFRCLVT 515
DB 374 ---VHVLQVN-----TSSCCDPLTPALLTI-----DPVPRHAKG----- 406
QY 516 NLTMDSVLVTKALFSSNLDPSLVQVFLDKTLNASFWLGSYQLVDIVHVTMESSY 572
DB 407 ---ESVLLQVR-----NLPEDL-----RMFIFKSVYTSQIKAIYSRAINY 446
QY 573 VYOPTSSSTQHFYLNFTINLPSYQDKAOPGTNTYQNRKNRTIEDALNQLFRNSSIKSYF 632
DB 447 VFRGPAHSGRETMYTNGSL---LLQDATEKDTGLY-----TLQIYRNFKIETAH 493
QY 633 SDCQVST-----FRSVPRNHHHTGVDSLCPNFSPLARRVDRVAIYEEFLMRTRNGT 681
DB 494 VQVSVHTCVHPSTTQQLVIESVPPNVVEGDVL-----LLVHNMP 534
QY 682 QLQNFPLDRSSVLVDGYSNPNRNEPITNGSADI--OHSGRSSSLEGPFEQKLISEDLNM 739
DB 535 NLOQSPWYKGVAVINRHEISRN-ITASNRTSLGPAHSGRETLYNSGLLHNAATEDNGL 593
QY 740 HT-----GHHHHHH 748
DB 594 YTLWTVNRHSETQGIHVH 613

RESULT 15
T07015
Cf-4A protein - tomato
C:Species: Lycopersicon esculentum (tomato)
C>Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
C:Accession: T07015
R:Rakken, F.B.; Schipper, D.; Nijkamp, H.J.; Hill, J.
Plant J. 14, 401-411, 1998
A:Title: Identification and De-tagged isolation of a new gene at the Cf-4 locus of tomato

A:Reference number: Z15863; MUID:98335213; PMID:9670557

A: Accession: T07015

A:Status: preliminary: translated from GB/EMBL/DBJ

A: Molecule type: DNA

A;Molecule type: DNA
A:Residues: 1-855 <TAK>

A/RES/RES: 1-833 <IAK>
A:Cross-references: UNTPROT:050024: UNTPARC:UPT0000009EC28: EMBL:Y12640: NID:e1289424: PT

A; CROSS-REFERENCES: UNIFAC: 030024; UNIFAC: 051000
A: Experimental source: strain Cf-4: isolate MM-Cf-4

A; Experiment
C: Genetics:

C;GeneticB:
A:Gene: CF-AA

A; Gene: C1-4A

Query Match	2.9%;	Score 113.5;	DB 2;	Length 855;
Best Local Similarity	19.6%;	Pred. NO. 12;		
Match 148.	Conservative	111.	Mismatches	209.
			Indels	293.
			Gaps	43.

54 LFTLNFTITNLRYEEN-----MWPGSRKFNTTERTVLO-----GLLRPLFKNTS 96

[illegible]

42 MFTTNPNASNYCYDRRTI.SWNKSTSCCSWDGVHCDETTGOVIELDLGCSOLOGKFHSNSS 101

DD 4Z MF IINFNABN ICIDRRKIBSNNNSI9CCSCWDBDVAHODDEITIGQVIBBWBBDCCOCCYXZT8044 "304555

Q: 97 VGRVYSCBPI.TV.I.BPEKNGEATGVMAICTHRRPDPGTGPGI.DREQI.VI.EI.SOL.THSTTEIGP 156

9/ VGFLYSGCRFLTLRFFENDGEAIGVDAICIAHREFDFIGFGLDREQDI DEFSQVHHSIETSEF 150
 :
 :

103 1 EOI SNT VBLD --- SSND ETC --- SPT SP --- KEGEESD1,TH --- 139

DB I02 L F Q T S N L K R L D L ----- S S N D F I G ----- S F I S P ----- K F G E F S D D I H ----- 13

Q: 157 YMI D-POST VAN/CEMURB C910/TTCSTC/12/SEP-----PETI.NET.T 194

QY 157 YTLD-RDSLYVNGFTHRSSVPITSTGVSEE-----PFTLNFTI 194

DATE	DESCRIPTION	AMOUNT	BALANCE
1/1/20	OPENING BALANCE		100.00
1/15/20	PAYROLL	50.00	50.00
1/20/20	RECEIVED	25.00	75.00
1/25/20	PAYROLL	50.00	25.00
1/30/20	RECEIVED	25.00	50.00
2/1/20	PAYROLL	50.00	0.00
2/15/20	RECEIVED	25.00	25.00
2/20/20	PAYROLL	50.00	0.00
2/25/20	RECEIVED	25.00	25.00
2/28/20	PAYROLL	50.00	0.00
3/1/20	RECEIVED	25.00	25.00
3/15/20	PAYROLL	50.00	0.00
3/20/20	RECEIVED	25.00	25.00
3/25/20	PAYROLL	50.00	0.00
3/30/20	RECEIVED	25.00	25.00
3/31/20	PAYROLL	50.00	0.00
4/1/20	RECEIVED	25.00	25.00
4/15/20	PAYROLL	50.00	0.00
4/20/20	RECEIVED	25.00	25.00
4/25/20	PAYROLL	50.00	0.00
4/30/20	RECEIVED	25.00	25.00
4/31/20	PAYROLL	50.00	0.00
5/1/20	RECEIVED	25.00	25.00
5/15/20	PAYROLL	50.00	0.00
5/20/20	RECEIVED	25.00	25.00
5/25/20	PAYROLL	50.00	0.00
5/30/20	RECEIVED	25.00	25.00
5/31/20	PAYROLL	50.00	0.00
6/1/20	RECEIVED	25.00	25.00
6/15/20	PAYROLL	50.00	0.00
6/20/20	RECEIVED	25.00	25.00
6/25/20	PAYROLL	50.00	0.00
6/30/20	RECEIVED	25.00	25.00
6/31/20	PAYROLL	50.00	0.00
7/1/20	RECEIVED	25.00	25.00
7/15/20	PAYROLL	50.00	0.00
7/20/20	RECEIVED	25.00	25.00
7/25/20	PAYROLL	50.00	0.00
7/30/20	RECEIVED	25.00	25.00
7/31/20	PAYROLL	50.00	0.00
8/1/20	RECEIVED	25.00	25.00
8/15/20	PAYROLL	50.00	0.00
8/20/20	RECEIVED	25.00	25.00
8/25/20	PAYROLL	50.00	0.00
8/30/20	RECEIVED	25.00	25.00
8/31/20	PAYROLL	50.00	0.00
9/1/20	RECEIVED	25.00	25.00
9/15/20	PAYROLL	50.00	0.00
9/20/20	RECEIVED	25.00	25.00
9/25/20	PAYROLL	50.00	0.00
9/30/20	RECEIVED	25.00	25.00
9/31/20	PAYROLL	50.00	0.00
10/1/20	RECEIVED	25.00	25.00
10/15/20	PAYROLL	50.00	0.00
10/20/20	RECEIVED	25.00	25.00
10/25/20	PAYROLL	50.00	0.00
10/30/20	RECEIVED	25.00	25.00
10/31/20	PAYROLL	50.00	0.00
11/1/20	RECEIVED	25.00	25.00
11/15/20	PAYROLL	50.00	0.00
11/20/20	RECEIVED	25.00	25.00
11/25/20	PAYROLL	50.00	0.00
11/30/20	RECEIVED	25.00	25.00
11/31/20	PAYROLL	50.00	0.00
12/1/20	RECEIVED	25.00	25.00
12/15/20	PAYROLL	50.00	0.00
12/20/20	RECEIVED	25.00	25.00
12/25/20	PAYROLL	50.00	0.00
12/30/20	RECEIVED	25.00	25.00
12/31/20	PAYROLL	50.00	0.00
1/1/21	RECEIVED	25.00	25.00
1/15/21	PAYROLL	50.00	0.00
1/20/21	RECEIVED	25.00	25.00
1/25/21	PAYROLL	50.00	0.00
1/30/21	RECEIVED	25.00	25.00
1/31/21	PAYROLL	50.00	0.00
2/1/21	RECEIVED	25.00	25.00
2/15/21	PAYROLL	50.00	0.00
2/20/21	RECEIVED	25.00	25.00
2/25/21	PAYROLL	50.00	0.00
2/28/21	RECEIVED	25.00	25.

DB 136 --LDLSDSNF-----TGVIPSEISHLSKTHVLRISDQYKLSLGGPHNFELLUL I/7

התאריך: 10.10.2019

[illegible]

Db 180 KNLTQLRELHLESVNISSTIPSNFSFHL-----TNLRLSYTELR-----218

1. **Introduction**
 2. **Background**
 3. **Methodology**
 4. **Results**
 5. **Discussion**
 6. **Conclusion**
 7. **References**
 8. **Appendix**
 9. **Figure 1**
 10. **Figure 2**
 11. **Figure 3**
 12. **Figure 4**
 13. **Figure 5**
 14. **Figure 6**
 15. **Figure 7**
 16. **Figure 8**
 17. **Figure 9**
 18. **Figure 10**
 19. **Figure 11**
 20. **Figure 12**
 21. **Figure 13**
 22. **Figure 14**
 23. **Figure 15**
 24. **Figure 16**
 25. **Figure 17**
 26. **Figure 18**
 27. **Figure 19**
 28. **Figure 20**
 29. **Figure 21**
 30. **Figure 22**
 31. **Figure 23**
 32. **Figure 24**
 33. **Figure 25**
 34. **Figure 26**
 35. **Figure 27**
 36. **Figure 28**
 37. **Figure 29**
 38. **Figure 30**
 39. **Figure 31**
 40. **Figure 32**
 41. **Figure 33**
 42. **Figure 34**
 43. **Figure 35**
 44. **Figure 36**
 45. **Figure 37**
 46. **Figure 38**
 47. **Figure 39**
 48. **Figure 40**
 49. **Figure 41**
 50. **Figure 42**
 51. **Figure 43**
 52. **Figure 44**
 53. **Figure 45**
 54. **Figure 46**
 55. **Figure 47**
 56. **Figure 48**
 57. **Figure 49**
 58. **Figure 50**
 59. **Figure 51**
 60. **Figure 52**
 61. **Figure 53**
 62. **Figure 54**
 63. **Figure 55**
 64. **Figure 56**
 65. **Figure 57**
 66. **Figure 58**
 67. **Figure 59**
 68. **Figure 60**
 69. **Figure 61**
 70. **Figure 62**
 71. **Figure 63**
 72. **Figure 64**
 73. **Figure 65**
 74. **Figure 66**
 75. **Figure 67**
 76. **Figure 68**
 77. **Figure 69**
 78. **Figure 70**
 79. **Figure 71**
 80. **Figure 72**
 81. **Figure 73**
 82. **Figure 74**
 83. **Figure 75**
 84. **Figure 76**
 85. **Figure 77**
 86. **Figure 78**
 87. **Figure 79**
 88. **Figure 80**
 89. **Figure 81**
 90. **Figure 82**
 91. **Figure 83**
 92. **Figure 84**
 93. **Figure 85**
 94. **Figure 86**
 95. **Figure 87**
 96. **Figure 88**
 97. **Figure 89**
 98. **Figure 90**
 99. **Figure 91**
 100. **Figure 92**
 101. **Figure 93**
 102. **Figure 94**
 103. **Figure 95**
 104. **Figure 96**
 105. **Figure 97**
 106. **Figure 98**
 107. **Figure 99**
 108. **Figure 100**
 109. **Figure 101**
 110. **Figure 102**
 111. **Figure 103**
 112. **Figure 104**
 113. **Figure 105**
 114. **Figure 106**
 115. **Figure 107**
 116. **Figure 108**
 117. **Figure 109**
 118. **Figure 110**
 119. **Figure 111**
 120. **Figure 112**
 121. **Figure 113**
 122. **Figure 114**
 123. **Figure 115**
 124. **Figure 116**
 125. **Figure 117**
 126. **Figure 118**
 127. **Figure 119**
 128. **Figure 120**
 129. **Figure 121**
 130. **Figure 122**
 131. **Figure 123**
 132. **Figure 124**
 133. **Figure 125**
 134. **Figure 126**
 135. **Figure 127**
 136. **Figure 128**
 137. **Figure 129**
 138. **Figure 130**
 139. **Figure 131**
 140. **Figure 132**
 141. **Figure 133**
 142. **Figure 134**
 143. **Figure 135**
 144. **Figure 136**
 145. **Figure 137**
 146. **Figure 138**
 147. **Figure 139**
 148. **Figure 140**
 149. **Figure 141**
 150. **Figure 142**
 151. **Figure 143**
 152. **Figure 144**
 153. **Figure 145**
 154. **Figure 146**
 155. **Figure 147**
 156. **Figure 148**
 157. **Figure 149**
 158. **Figure 150**
 159. **Figure 151**
 160. **Figure 152**
 161. **Figure 153**
 162. **Figure 154**
 163. **Figure 155**
 164. **Figure 156**
 165. **Figure 157**
 166. **Figure 158**
 167. **Figure 159**
 168. **Figure 160**
 169. **Figure 161**
 170. **Figure 162**
 171. **Figure 163**
 172. **Figure 164**
 173. **Figure 165**
 174. **Figure 166**
 175. **Figure 167**
 176. **Figure 168**
 177. **Figure 169**
 178. **Figure 170**
 179. **Figure 171**
 180. **Figure 172**
 181. **Figure 173**
 182. **Figure 174**
 183. **Figure 175**
 184. **Figure 176**
 185. **Figure 177**
 186. **Figure 178**
 187. **Figure 179**
 188. **Figure 180**
 189. **Figure 181**
 190. **Figure 182**
 191. **Figure 183**
 192. **Figure 184**
 193. **Figure 185**
 194. **Figure 186**
 195. **Figure 187**
 196. **Figure 188**
 197. **Figure 189**
 198. **Figure 190**
 199. **Figure 191**
 200. **Figure 192**
 201. **Figure 193**
 202. **Figure 194**
 203. **Figure 195**
 204. **Figure 196**
 205. **Figure 197**
 206. **Figure 198**
 207. **Figure 199**
 208. **Figure 200**
 209. **Figure 201**
 210. **Figure 202**
 211. **Figure 203**
 212. **Figure 204**
 213. **Figure 205**
 214. **Figure 206**
 215. **Figure 207**
 216. **Figure 208**
 217. **Figure 209**

QY 254 VDLLCTYLQPLSGPGLPIKQVFH-----ELSQQTHG--ITRLGPYSLDKDS-----LYLNG 302

Db 219 -----GVLPERVFHLSNLELDLSYNPQLTVRFPTIWNSSASLVKLYLSR 264

QY 303 YNEPG--PDEPPTTPKPAATFLPPLSEA-----TTAMGYHLKTLTLNFTISNLOQSPDMGK 356

Db 265 VNIAGNIPD-----SFSYLTALHELDVMVYTNLSGPIPKPL---WNLTNIE-SLDL-- 310

[illegible]

357 GSATFNSTEGVLOHLLRPLFOKSSMGPFYLGCOLISLRPEKGAATGVDTTCTYHPPVG 410

[illegible]

RESULT 16

RESUL
825039

BZ5039
outer cell wall protein precursor - *Bacillus brevis* (strain 47)

outer cell wall protein precursor - bacterial
N: Alternate names: S-layer protein QWP

N;Alternate names: S-layer
C:Species: Bacillus brevis

RESULT 17

TI17504
hypothetical protein A14r - Chlorella virus PBCV-1
C:Species: Chlorella virus PBCV-1
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: TI17504
R:Graves, M.V.; Van Etten, J.L.
submitted to the EMBL Data Library, May 1999
A:Reference number: Z18806
A:Accession: TI17504
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1369 <GRA>
A:Cross-references: UNIPROT:Q99349; UNIPARC:UPI00000F9125; EMBL:U42580; NID:94028896; PT
A:Experimental source: specific host Chlorella strain NC64A
C:Genetics:
A:Gene: A14r

Query Match 2.9%; Score 113.5; DB 2; Length 1369;
Best Local Similarity 21.3%; Pred. No. 26;
Matches 179; Conservative 116; Mismatches 352; Indels 193; Gaps 42;
QY 11 TKLTHRSVSTSTGTPVYLGASKTPASIRGPSA---ASHLLILF-----TL---NP 59
DB 281 TFFVNASHTTNTTNGTNTSNVASFNSVDSPENGNVRANTLTVTYANITGTLASGNV 340
QY 60 TITNRYENM--WPGSRKFNTHRVLOGLRLPLPKNTSV--GPLYSGCRLTLRLPEKDG 115
DB 341 AVGNLISADTSEFANITSTFTGLVNGNIITAAIGNVFLANVTANSLTL-----QSS 396
QY 116 EATGVDAICTHR-----PDTGGDLDEQLYLELSQTHSITELGPTTLD 160
DB 397 SSTAAASNVTTTWIQSTTSTSNVMTIGNITSGNVISSNAAYP-ANVISNTIITVMSAMTVS 455
QY 161 RSLVYN-----GPHTRSSVPTSGVSEBPFTLN-----PTINRLYMADM 203
DB 456 GNVSPGNGVFGNVGNTANITSTNGVSNVNLTSNVVNVVFCNASSVTANTLSIAUT 515
QY 204 G-----QPSLKFNTIDNVMKHLISPLFORSSL--GARYTGCRVIALRSVKNGAETRV 254
DB 516 GNTYVVSANTGLTANV-GNVFGTLTVGVANTVSMVSNALPANTAVSNLSNLTVT--- 572
QY 255 DILCTYLOPLSGPLPIKOVFHELSSQTHGTRGLPGYSLDKDLSLYNGYNEPGDEPPTT 314
DB 573 --ISSDISNISITGNTGNVF--AANIATIGTLTANVANVANVSNVAVNTSNIRTL 627
QY 315 PKPATTFPLPPLSEATMAYCHLKTTLNFTISNLQYSPDMGKGSATFNSTEGVQLHLRP 374
DB 628 ITGNANVSTTNSVITGGF--TITGNTISGLL--TSNVIAGNITWNTSNT-----T 676
QY 375 LF--QKSSMGPFYLG---CQLISLRPEKDG-----AATGVD 405
DB 677 LFTSNTSIANFAGMTAVNTIVSNLEIQGNSVITQTTPFKVTSVLLANVLPANTIIIS 736
QY 406 TTCTTHPDVGP-GLDIOOLYWELSQTHTGVTOFGYVYLDRLDLPIN-----GYAP-QNL 458
DB 737 NTFPTTANVVGNIISDIANI-----GIANVNF--LNTTDFAVNTANIVNYTPTSI 785
QY 459 SIRGEVQ-----INFHIVNMLNPDPTSSSEYITLLRDIQDKVTTLKGSQHLHTFPC 512
DB 786 NVTGMLTIGNANIVNFYATSANIVGNTANNNAVITFL-----TTPFYKSG----- 831
QY 513 LVTNLMTDSVLTVKALFSSNLDPSLVEQVFLDKTLNASEHFWLSTGYQLVDIHTVMESS 572
DB 832 -----TVSAGFTSIISANALSNVIVFGNLSANI-VSNLTLSNSINAVTFSN 878
QY 573 VY---OPTSSSTQHYLNFTITNLPYSDQ---KAQPGTNYQRNKNIEDALNQLFRNS 626
DB 879 VVNIQVSTSTGTLVNSINFNSVDVSGNVLVTRDVTTNITSVTIANIV--TFPSNV 936
QY 627 SIKSVFSDQVST-----FRSVP--NRHHTGVDSLCHNPSPLARRVDRVAIYEEFLR 675
DB 937 AIGNLISTRNLTAANLISSDLFNSGPGYTSQNVITIDL-NFT--AGNLGTVAARTTITT 993

QY 676

676 MTRNGTOLQNFLLDRSSVLVDGYSPNREPLTGN--SADIQHSGGRSSLSGPRFEOKLIS 733
DB 994 PTLFATDV-NFTQD---ALVAGELITQN--FYGNITSANI---GSRITIGNANVTQNTIT 1044

RESULT 18

QY1899
genome polyprotein - papaya ringspot virus
N:Contains: 46K protein; 63K protein; 6K protein; coat protein; cylindrical inclusion protein
C:Species: papaya ringspot virus, PRSV
C:Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 09-Jul-2004
C:Accession: QY1899; PQ0509; A56603; S24785; S35725
R:Yeh, S.D.; Jan, F.J.; Chiang, C.H.; Doong, T.J.; Chen, M.C.; Chung, P.H.; Bau, H.J.
J. Gen. Virol. 73, 2531-2541, 1992
A:Title: Complete nucleotide sequence and genetic organization of papaya ringspot virus F
A:Reference number: QY1899; MUID:93019006; PMID:1402799
A:Accession: QY1899
A:Molecule type: genomic RNA
A:Residues: 1-3344 <YEH1>
A:Cross-references: UNIPROT:Q01901; UNIPARC:UPI0000131E61; GB:S46722; NID:G258106; PIDN:1
A:Accession: PQ0509
A:Molecule type: protein
A:Residues: 548-554; 1402-1410 <YEH2>
A:Cross-references: UNIPARC:UPI000017874F; UNIPARC:UPI0000178750
R:Wang, C.H.; Yeh, S.D.
Arch. Virol. 127, 345-354, 1992
A:Title: Nucleotide sequence comparison of the 3'-terminal regions of severe, mild, and r
A:Reference number: A56603; MUID:93090098; PMID:1456896
A:Accession: A56603
A:Molecule type: genomic RNA
A:Residues: 2561-3344 <WAN>
A:Cross-references: UNIPARC:UPI0000170FCB; EMBL:X67672; NID:G62378; PIDN:CAA47904.1; PID
A:Experimental source: type P, strain HA
C:Superfamily: tobacco etch virus genome polyprotein
C:Keywords: ATP; coat protein; cylindrical inclusion protein; genome-linked protein; incl
F:1-547/Product: 63K protein #status predicted <PRO>
F:548-1004/Product: helper component-proteinase #status predicted <HCP>
F:1402-2036/Product: 46K protein #status predicted <PRT>
F:1402-2036/Product: cylindrical inclusion protein #status predicted <CIP>
F:1486-1493/Region: nucleotide-binding motif A (P-loop)
F:1571-1576/Region: nucleotide-binding motif B
F:1575-1578/Region: DXH motif
F:2037-2093/Product: 6K protein #status predicted <PRI>
F:2094-2520/Product: nuclear inclusion a protein #status predicted <NIA>
F:2521-3037/Product: nuclear inclusion b protein #status predicted <NIB>
F:3038-3344/Product: coat protein #status predicted <COP>
F:2156/Binding site: phosphoryl-RNA (Tyr) (covalent) #status predicted

Query Match 2.9%; Score 113.5; DB 2; Length 3344;

Best Local Similarity 19.0%; Pred. No. 1.1e+02;

Matches 133; Conservative 97; Mismatches 240; Indels 229; Gaps 33;

QY 175 VPTTSTGVSEBPFTLNFTINRLYMADMGPGLSKFNITDNVMKHLISPLFOR----- 228

DB 1634 VDNFTGANSD---VTFADNLVTVASYNEVDQLSKLSDK--GYLVTKIDGRIMKVGK 1688

QY 229 ---SSLGARYTGCRVIALRSVKNGAETRVLDLCTYLOPLSGPLPIKOVFHELSSQTH 282

DB 1689 TEISTSGTKFKKHFIATNIIENGVTLDIEAVIDFGMKV-PEMDSNRNIRYSKQAIISF 1747

QY 283 -HGTRILGPGYSLDKDLSLYN-GYNERGDEPPTTPKATTPPLPSEATTAMGYHLKTLT 340

DB 1748 GERQRLGRVRHREGIALRIGHTEKGQIEIPEWATSEAFI-----STYGLPVM 1799

QY 341 LNFTISNLQYSPDMGKGSATFNSTEGVQLHLRLPFQKSSMGPPFYLGQQLISLRPEKDG 400

DB 1800 HNVGLSLLK-----NCTVRQARTMQYELSPFTQN-----LVNF-----DG- 1836

QY 401 ATGVDTTCTTHPDVGPGLDITQQLYWEI-----SOLTHGVTOFGYVYLDRLDLPIN 451

DB 1837 -----TVHPK-----IDVLLRPYKLRDCEVRLSEAAIPIHGVSQI--WLSARDYEAVG 1881

Search completed: March 20, 2006, 07:36:24
Job time : 36.2939 secs

THIS PAGE BLANK (USPTO)

Result No.	Query			Description		
	Score	Match	Length	ID		
1	3658	92.7	1890	7	US-11-033-039-314	Sequence 314, Appl
2	166.5	4.2	308	7	US-11-046-456-6	Sequence 6, Appl
3	166.5	4.2	308	7	US-11-046-644-6	Sequence 6, Appl
4	134.5	3.4	98	6	US-10-952-535A-15	Sequence 15, Appl
5	134.5	3.4	123	6	US-10-952-535A-16	Sequence 16, Appl
6	134.5	3.4	155	6	US-10-952-535A-17	Sequence 17, Appl
7	130	3.3	401	6	US-10-949-720-419	Sequence 419, App
8	126.5	3.2	614	6	US-10-517-696-128	Sequence 128, App
9	119	3.0	957	7	US-11-108-172-1065	Sequence 1065, Ap
10	118.5	3.0	2223	7	US-11-193-561-2	Sequence 2, Appl
11	118.5	3.0	2223	7	US-11-193-771-2	Sequence 2, Appl
12	118.5	3.0	2223	7	US-11-193-789-2	Sequence 2, Appl
13	118.5	3.0	2223	7	US-11-193-806-2	Sequence 2, Appl
14	118.5	3.0	2223	7	US-11-193-857-2	Sequence 2, Appl
15	118.5	3.0	2421	7	US-11-193-561-17	Sequence 17, Appl
16	118.5	3.0	2421	7	US-11-193-771-17	Sequence 17, Appl
17	118.5	3.0	2421	7	US-11-193-789-17	Sequence 17, Appl
18	118.5	3.0	2421	7	US-11-193-806-17	Sequence 17, Appl
19	118.5	3.0	2421	7	US-11-193-857-17	Sequence 17, Appl
20	118.5	3.0	2477	7	US-11-193-561-15	Sequence 15, Appl
21	118.5	3.0	2477	7	US-11-193-771-15	Sequence 15, Appl
22	118.5	3.0	2477	7	US-11-193-789-15	Sequence 15, Appl
23	118.5	3.0	2477	7	US-11-193-806-15	Sequence 15, Appl
24	118.5	3.0	2477	7	US-11-193-857-15	Sequence 15, Appl
25	117	3.0	221	7	US-11-185-111-41	Sequence 41, Appl

; PRIOR APPLICATION NUMBER: US 60/539,605
; PRIOR FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: US 60/619,241
; PRIOR FILING DATE: 2004-10-15
; NUMBER OF SEQ ID NOS: 178
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 308
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: GIPF VSHis tag
US-11-046-644-6

Query Match 4.2%; Score 166.5; DB 7; Length 308;
Best Local Similarity 70.2%; Pred. No. 7.3e-06;
Matches 33; Conservative 1; Mismatches 10; Indels 3; Gaps 1;
QY 705 PLTGSADIQHSGRSLEGPRFEQKLISEEDLNM---HTGHHHHH 748
Db 262 PAKGNSADIQHSGRSLEGPRFEQKLISEEDLNM---HTGHHHHH 308

RESULT 4
US-10-952-535A-15
; Sequence 15, Application US/10952535A
; Publication No. US20050255113A1
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Messer, Anne
; APPLICANT: Lecerf, Jean-Michel
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING POLYPEPTIDE
; FILE REFERENCE: INR-004CP
; CURRENT APPLICATION NUMBER: US/10/952,535A
; PRIOR FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: 60/146,047
; PRIOR FILING DATE: 1999-07-27
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Construct
US-10-952-535A-15

Query Match 3.4%; Score 134.5; DB 6; Length 98;
Best Local Similarity 78.1%; Pred. No. 0.0005;
Matches 25; Conservative 1; Mismatches 5; Indels 1; Gaps 1;
QY 717 GGRSLEGPRFEQKLISEEDLNMHTGHHHHH 748
Db 68 GGSTMSRGP-PEQKLISEEDLNMHTGHHHHH 98

RESULT 5
US-10-952-535A-16
; Sequence 16, Application US/10952535A
; Publication No. US20050255113A1
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Messer, Anne
; APPLICANT: Lecerf, Jean-Michel
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING POLYPEPTIDE
; FILE REFERENCE: INR-004CP
; CURRENT APPLICATION NUMBER: US/10/952,535A
; PRIOR FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: 60/146,047
; PRIOR FILING DATE: 1999-07-27

; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Construct
US-10-952-535A-16

Query Match 3.4%; Score 134.5; DB 6; Length 123;
Best Local Similarity 78.1%; Pred. No. 0.00071;
Matches 25; Conservative 1; Mismatches 5; Indels 1; Gaps 1;
QY 717 GGRSLEGPRFEQKLISEEDLNMHTGHHHHH 748
Db 93 GGSTMSRGP-PEQKLISEEDLNMHTGHHHHH 123

RESULT 6
US-10-952-535A-17
; Sequence 17, Application US/10952535A
; Publication No. US20050255113A1
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Messer, Anne
; APPLICANT: Lecerf, Jean-Michel
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING POLYPEPTIDE
; FILE REFERENCE: INR-004CP
; CURRENT APPLICATION NUMBER: US/10/952,535A
; PRIOR FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: 60/146,047
; PRIOR FILING DATE: 1999-07-27
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Construct
US-10-952-535A-17

Query Match 3.4%; Score 134.5; DB 6; Length 155;
Best Local Similarity 78.1%; Pred. No. 0.001;
Matches 25; Conservative 1; Mismatches 5; Indels 1; Gaps 1;
QY 717 GGRSLEGPRFEQKLISEEDLNMHTGHHHHH 748
Db 125 GGSTMSRGP-PEQKLISEEDLNMHTGHHHHH 155

RESULT 7
US-10-949-720-419
; Sequence 419, Application US/10949720
; Publication No. US20050249736A1
; GENERAL INFORMATION:
; APPLICANT: Kraenoperov, Valery
; APPLICANT: Zozulya, Sergey
; APPLICANT: Kertesz, Nathalie
; APPLICANT: Reddy, Ramachandra
; APPLICANT: Gill, Parkash
; TITLE OF INVENTION: POLYPEPTIDE COMPOUNDS FOR INHIBITING
; FILE REFERENCE: VASG-P02-002
; CURRENT APPLICATION NUMBER: US/10/949,720
; PRIOR FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: US 60/454,432
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60/454,300

Mon Mar 20 08:49:44 2006

QY 375 LFOKSSMGPEYLGQQLISLRPEKGAATGVDITCTYHPDPVGPGLDIOQLYWEISQLTHG 434
Db 214 PAKST--PFSIPSHSDTFTTLASHSTKTDASSTH-STVPP-----LTSSNHS 260
QY 435 VTQLGFVYLDRLDSIFINGYAPQNLISIRGEYOINPHVN--WNLSNPDPSTSEYITLLARDI 492
Db 261 T-----SPQLSTGVSVFFLSFHSINLQFNSSLESDPSTDYQELORDI 302
QY 493 QDKVTIYK-----GS---OLHDTFRFCLVT-----N 516
Db 303 SEMFLOIYKGGFLGLSNIKFRPGSVVQVLTAFREGTINVHDVETQPNQYKTEASRYN 362
QY 517 LTMDSVLTV-----KALFSSNLDPSLVEQVFLDKTLNASFWHLG----- 556
Db 363 LTISDVSLLIGGGERRRYRAMVSAT---GILGAWAGKGGVSEWMLGIENGVLILAGVV 419
QY 557 -----STYQLVDIHVTEMESVYOPTSSSTQHYFLNFTINLPYS 597
Db 420 VALAEVPLCTRVEAPDASSTHSTVPLTSSNHSST-SFQLSTGVSVFFLSFHSINLQFN 478
QY 598 QDKAOPGTNTYORKNRTIEDALNQL 622
Db 479 SLEDPSTDYQELORDISEDVSDV 503

RESULT 9

US-11-108-172-1065
; Sequence 1065, Application US/11108172
; Publication No. US20050260177A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Smith, Carole L.
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C15
; CURRENT APPLICATION NUMBER: US/11/108,172
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 10/025,380
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: US 09/922,217
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 09/833,263
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US 09/649,811
; PRIOR FILING DATE: 2000-08-28
; PRIOR APPLICATION NUMBER: US 09/609,448
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 09/575,251
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/519,444
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: US 09/504,629
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: US 09/480,321
; PRIOR FILING DATE: 2000-01-10
; PRIOR APPLICATION NUMBER: US 09/476,296
; PRIOR FILING DATE: 1999-12-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1130

QY 632 FSDCQSVIFRSVP-----NRHHTGVDLSLNCNFSPLARR---VDRVAYIER----- 672
Db 251 FEFVNVTTDREVPVPAVDIRVTRSSPSSLSLAWAVPRAPSGAWLDYEVKYEKGAEGPSS 310
QY 673 --FLMRTRNGTOLQNFLLDR--SSVLVD-----GYSP-----NRNEPLTGNADIQHSGG 718
Db 311 VFPLKTSNRAELRG--LXRGASYLVQVRARGSEAGYGPFGQEHHSQTQLDSEGWREOQG 368
QY 719 RSSLEGPRFEQKLISEEDLNM---HTGHHHHH 748
Db 369 RSSLEGPRFEQKIPNPLILGLDSTRGHHHHH 401

RESULT 8

US-10-517-696-128
; Sequence 128, Application US/10517696
; Publication No. US20060051759A1
; GENERAL INFORMATION:
; APPLICANT: diadexus, Inc.
; APPLICANT: Salceda, Susana
; APPLICANT: Macina, Roberto A.
; APPLICANT: Turner, Leah R.
; APPLICANT: Liu, Yongming
; APPLICANT: Sun, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and Pa
; FILE REFERENCE: DEX-0432
; CURRENT APPLICATION NUMBER: US/10/517,696
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: US 60/389,327
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 171
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 128
; LENGTH: 614
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-517-696-128
Query Match 3.2%; Score 126.5; DB 6; Length 614;
Best Local Similarity 19.5%; Pred. No. 0.037;
Matches 110; Conservative 63; Mismatches 223; Indels 169; Gaps 19;
QY 151 ITELGPYTLDRSLYVNGFTHRSSVP-----TTSTGVVSEEPFTLNFTINNLYRYMADMGQ 205
Db 15 LTVLTATAPKATVVTGCHASSSTPGGKEKTSATQSSVPSTERNKAVMTSSVLSHS 74
QY 206 PGSLEKFNIDNMVKKHLLSLFORSSLGARYTGCVRVALRSVKNAGTRVDLLCTYLQPLS 265
Db 75 PGS--GSSITQGDVTLAPATEPASGSAATWGQDVTSV-----PVT 113
QY 266 GPGLPIKQVHELUSQOOTHGILRGLPSYLDKDSLILYNGYNEGP-----DBPPTT 314
Db 114 RPAL-----GSTTPPAHDVTSAPD-----NKPAPGSTAPPAGVTSAPDIR 154
QY 315 PKPATTFPLPSEATTAMGVHLKATLTINFTISNLQYSPDMKGSATFNSTEGVLQHLRP 374
Db 155 PAFPGST-APPAGVTSAPDNRPALGSTAPPVHNVTASGSGASGASTLVHNGTSARATTT 213

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1065
; LENGTH: 957
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-108-172-1065

Query Match      3.0%; Score 119; DB 7; Length 957;
Best Local Similarity 19.0%; Pred. No. 0.29;
Matches 146; Conservative 81; Mismatches 269; Indels 280; Gaps 31;

QY 17 RSSVSTSTGCTPTVYLGASTPASIFGSAASHLLILFTLNFTITNLRYYEENWPGSRK 76
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 20 QESTASHSSPGSTDTLLSPGSTASSLGPESTTP-----HSGPGSTE 61
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 77 F-----NTTERTVQLLRPLFKNTSVGLYSGCRLTLRP-----EKDGEATGVDAICTHR 127
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 62 TTLPLPDNTTASGLLEASTPVHSSIT-----GSPHTTSLPAGSTTRQGESITTSQS-WPNS 113
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 128 PDPTGGLDREQLYLELSQJTHSITELGPTVTLDRDSLYVNG-----FTHRSSVPT 177
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 114 KDITPAPPTTTSAPVELSTTSHGSPSSTPTTHFSASSTTLGRGEESTTVHSSPVATATTP 173
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 178 -----TSTGVVSEEPFTLNITNLRMYADMGPGLKFNITDNV-----MK 219
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 174 SPARSTTSGLVEE-----STTHSSPGSTQTMHFPESDTTSGRGEESTTSHSST 223
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 220 HLLS-----PLFORSSIGAR-----YTCGRVI 241
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 224 HTISSAPSTTSALVEETSTHSSPGSTATTTHFPDSDSTTSGRSEESTASHNQATGIVL 283
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 242 ALRSVRN---GAETRVLLCTYLQPLSGGLPIKQVPHLSQOQTHGITRLGYSLOKDSL 298
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 284 PARSTTVLLGEESTTSPISGSMETALPG-----STTTPGLS-----EKSTT 326
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 299 YLNGYNEPGDEPTTPKPAITFLPPLS-EATTAMGYHLKTLTLNFTISNLQYSPDMGKG 357
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 327 F-----HSSPRSPATLSPASTTSSGVSSEESTTSHSRPGSTHTTAPDSTT--TPGLSRH 379
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 358 SATFNSTEGVQLHLLRPLFKNSMGPPYLGCLISLRPEKDGATGVDITCTVHPDP--- 414
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 380 STTSHSPGSDTITLLPASTTTS-GP-----SQBSTTSHSPGST 418
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 415 ---VGPGLDIQQLYWELSQLTHGVTQLGFGYVLDRLDLSLFGYAPONLSIRGEYQINFHIV 471
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 419 DTALSPG-----STTALSF-----QBSTTTFH-- 440
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 472 NWNLSPDPTSSBYITLLRDIQKVYLYKGSQQLHDTFRCLVTNLTMDSVLTVVALFS 531
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 441 ---SSP---GSTHTTLFPDSTTSSGIVEASTRVHS-----STGSPRTTLLSP--A 481
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 532 SNLDPSLVEQVFLDKTLNAGFHWLGSYQLVDIHVTEMESSVYQPTSSSTQHLYLFT- 590
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 482 SSTSPGLQGESTAFQTHPASTHTTPSPATAPVEE-STYTHRSPESTTTHFPASST 540
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 591 -----ITNLYSQDKAQPG- 604
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 541 SCHSEKSTIHFSSPDASGTTSPSAHSTTSGRGEESTTSRISPGSTEITTLPGS--TTTPGL 598
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 605 ---TTNYQRKNRIEDALNQLFRNSSIKSYFSDCQVSTFRSVNRRHHTGVDSLCNFSF 659
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 599 SEASTTFYSPRSPPTTLLSP-----ASMTSLGVGEESTTSRSPQSGSTHVSPTASTTTP 652

RESULT 10
US-11-193-561-2
; Sequence 2, Application US/11193561
; Publication No. US20060024757A1
; GENERAL INFORMATION:
; APPLICANT: Husea, Robert
; APPLICANT: Shorter, Simon
; TITLE OF INVENTION: Detection of Oncofetal Fibronectin for Selection of Concepti
; FILE REFERENCE: 17101-080001/831
```

```
Db 1070 ---YVTGTL-----EPG-IDYDISVITLNGESAPTTLTQCTAVPPPTDLRFTNIGP 1118
Qy 638 STFRS--VPMRHTGVDLSNFSPLARRVDAIYEFELMRNGTOLQ-----FTLD 689
Db 1119 DTRVVTWAPPSPIDLTNLFVRYSPVKNED---VAELSISSPSONAVVLTLLPGTEYVVS 1175
Qy 690 RSSVLVDGYSFNRNEPLTGNADIQHSGRSSLEGPFEQKLISEEDLNH-----T 741
Db 1176 VSSV---YQHESTPLRG-----RQKTGLDSTGIDFSD--ITANSFTVHWIAPRATIT 1224
Qy 742 GHHHHH 748
Db 1225 GYRIRHH 1231

RESULT 11
US-11-193-771-2
; Sequence 2, Application US/11193771
; Publication No. US20060024722A1
; GENERAL INFORMATION:
; APPLICANT: Fisher-Colbrige, Mark
; APPLICANT: Hickok, Durlin
; APPLICANT: LaPointe, Jerome P.
; TITLE OF INVENTION: Samples for Detection of Oncofetal Fibronectin and uses thereof
; FILE REFERENCE: 17101-027001/828
; CURRENT APPLICATION NUMBER: US/11/193,771
; CURRENT FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: 60/592,823
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,803
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,825
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,804
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,824
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 2223
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-193-771-2

Query Match 3.0%; Score 118.5; DB 7; Length 2223;
Best Local Similarity 18.9%; Pred. No. 1.2;
Matches 171; Conservative 126; Mismatches 313; Indels 297; Gaps 46;

Qy 19 SVSTSTPGTPTVVLGAS-----KTPASIFGSPASASHLLILFTLFTNLTNRYE---- 67
Db 445 TTTSTPTVNTVTGETTPTSPPLVATSESVTEITASSFVSVWSASDVTSGFRVEYELS 504
Qy 68 -----ENMPGSKFKNTTERTVLQGLLRPLPKNTSVGLPGYSGCKRLT 107
Db 505 BEGDEPQVLDLPSTATSVNIPLDLPGRKYIVNVVQISEDGQSLILSTS----- 553
Qy 108 LLRPEKDEAGTVDAICTRPDPTGPGDLRDLRYLSQLTHSITELGPTVTLDRDSLY-- 165
Db 554 -----QTTPADA---PDPTVDQDDTSIVVRWSRQAPIT---GYRI---VYSP 594
Qy 166 -VNGFTRSSVPTSTGTVSEPTFLNTFTNNLRVMDMGOPGSLKFNITDNVM---KHL 221
Db 595 SVEGSSTELNLPETANSV-----TLSDL-----QPG-VQVNIITVAYEENQES 636
Qy 222 LSPLFORSSLG-----ARYTCRVIALRSVKNGAET--RVLLCTYLOPL 264
Db 637 TPVVIQQTGTGPRSDTVPSRDLQFVEVTVKVTIMTTPPESAVTGYRVDVIVNLPGE 696
Qy 265 SGPGLPV-KQVFHELSSQTHGIT---RLGPTSLDKOSLYLNGYNEPGDEP-----PT 313
Db 697 HGQRLPISRNTFAEVTGLSPGVTYVYKVFVAVSHGRESKPLTAQQTTLKLDAPTNLQFVNET 756
```

```
Qy 314 TPKPATTFLPPLSEATTAMGYHLKTLTILNFTISNLOVSPDMKGSATFNSTEGVLOHLR 373
Db 757 DSTVIVRWTTPPRAQIT---GYRL-TVGLTERGQPROY-----NVGPSVSKYPLR 801
Qy 374 PLPQSKSMGFYLGCOLISLRPEKOG-AATGVDTTCTYHPDPVPGGLDIOQLWELSQLT 432
Db 802 NLQPASE---YTVSLVAIKGNQESPKATGVFTT-----LQPGSSIPPYNTVEVTETT 849
Qy 433 HGVY---QLGF-----YVL-----DR 445
Db 850 IVITWTAPRIGFKLGVPRPSQGGEAPREVTSDSGSIVVSGLTGPGVEVYVYTIQVLRDQER 909
Qy 446 DSLFINGYA---PONLSIRGEYQINFHVNNWNLNPDPTSEYITLLRDIQDKVVTLY 500
Db 910 DAFIVNKVVTPLSPPTNLHLEANPDGVLTVSWERSTTPTDITGYRIT-----TTPT 960
Qy 501 KGSQ-----LHDTFRFCVLVNTLT-----MDSVLVTVKALFSS 532
Db 961 NGQGGNSLEEVVHADQSSCTFDNLSPGLEYNVSVYTVKDDKESVPISDTIPEV----- 1014
Qy 533 NLDPSLVEQVFLDKT-LNASFWH--LGSTYQLVDIHWTEMES-----VYQPTSSSSQHF 585
Db 1015 ---PQLTDLSFVDITDSSIGLRWTPLNSS-TIIGYRITVVAAGEGIDIFSDVDSVGY- 1069
Qy 586 YLNFITINLPYSQDKAQPGTNTYQNRKNI-----EDALNQLFRNSSIKS---YFSDCQV 637
Db 1070 ---YVTGTL-----EPG-IDYDISVITLNGESAPTTLTQCTAVPPPTDLRFTNIGP 1118
Qy 638 STFRS--VPMRHTGVDLSNFSPLARRVDAIYEFELMRNGTOLQ-----FTLD 689
Db 1119 DTRVVTWAPPSPIDLTNLFVRYSPVKNED---VAELSISSPSONAVVLTLLPGTEYVVS 1175
Qy 690 RSSVLVDGYSFNRNEPLTGNADIQHSGRSSLEGPFEQKLISEEDLNH-----T 741
Db 1176 VSSV---YQHESTPLRG-----RQKTGLDSTGIDFSD--ITANSFTVHWIAPRATIT 1224
Qy 742 GHHHHH 748
Db 1225 GYRIRHH 1231
```

```
RESULT 12
US-11-193-789-2
; Sequence 2, Application US/11193789
; Publication No. US20060024723A1
; GENERAL INFORMATION:
; APPLICANT: Husea, Robert
; APPLICANT: Fisher-Colbrige, Mark
; APPLICANT: LaPointe, Jerome
; APPLICANT: Senyei, Andrew
; APPLICANT: Shorter, Simon
; TITLE OF INVENTION: Methods for detecting Oncofetal Fibronectin
; FILE REFERENCE: 17101-029001/830
; CURRENT APPLICATION NUMBER: US/11/193,789
; CURRENT FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: 60/592,823
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,803
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,825
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,804
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,824
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 2223
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-193-789-2
```



```
Query Match      3.0%; Score 118.5; DB 7; Length 2223;
Best Local Similarity 18.9%; Pred. No. 1.2;
Matches 171; Conservative 126; Mismatches 313; Indels 297; Gaps 46;

; Publication No. US20060024724A1
; GENERAL INFORMATION:
; APPLICANT: Hussa, Robert
; APPLICANT: Fisher-Colbrie, Mark
; APPLICANT: Lapointe, Jerome
; APPLICANT: Shorter, Simon
; TITLE OF INVENTION: Oncofetal Fibronectin as a Marker for Health and Disease
; FILE REFERENCES: 17101-028001/829
; CURRENT APPLICATION NUMBER: US/11/193,806
; CURRENT FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: 60/592,823
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,803
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,825
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,804
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,824
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 2223
; TYPE: PNT
; ORGANISM: Homo Sapiens
; US-11-193-806-2

Query Match      3.0%; Score 118.5; DB 7; Length 2223;
Best Local Similarity 18.9%; Pred. No. 1.2;
Matches 171; Conservative 126; Mismatches 313; Indels 297; Gaps 46;

QY 19 SVSTTSPGTPVYLKAS-----KTPASIFGSAASHLLILFTLNFTINLYE----- 67
DB 445 TTTSTSTPVTNTVTGETTFPSPLVATSEVTEITASSFVSVWSASDVTGSRVVELS 504
QY 68 -----ENMPPGSRKENTTERTVLQGLLRPLFKNTSVGPLYSGRLT 107
DB 505 BEGDEPOYLDLPSTATSVNIPDLPGKVIYVNVQISEDEQSILSTS----- 533
QY 108 LLRPEKDGATGDAICTHRPDPTGPGDLREQLYLELSQTHSITELGPTVTLDRDLSY-- 165
DB 554 -----QTAPDA-----PPDPTVDQDDTSLVVRWSRPOAPIT---GYRI---VYSP 594
QY 166 -VNGFTHRSSVPTTSTGVVSEEPFTLNFTINLYMADMGQPSGLKFNITDNVM---KHL 221
DB 595 SVSGSSTELNLPETANSV-----TLSDL-----QPG-VQYNITIYAVEENQES 636
QY 222 LSPLFQRSSLG-----ARYTGCVRVIALRSVKNQAEF---RVDLLCTVYLQPL 264
DB 637 TPVVIQOETTGTPRSPTVPSRDLQFVEVTDVKVTIMTPPEASVATGYRVDVIPNLPGE 696
QY 265 SGGLPI-KQVFHELSSQTHGIT---RLGPLYLDKDSLVLNGYNEPGDPEP-----PT 313
DB 697 HGQRLPISRTNFAEVTGLSPGVTYFKVFAVSHGRESKPLTAQOTTKLDAPTMLQFVNET 756
QY 314 TKPATTFLPPLSEATTAMGYHLKTLTNTLNLYSPDMGKGSATFSTEGVLOHLR 373
DB 757 DSTVLVRWTFPPRAQIT---GYRL-TVGLTRGQPRQY-----NVGPSVSKYPLR 801
QY 374 PLFQKSSMGFFYLGCOLISLRPEKDG-AATGVDITCTYHPDPVPGGLDIOQLYWELSQLT 432
DB 802 NLQPAE-----YTVSLVAIKGNQESPKATGVFTT-----LQPGSSIPPYNTEVETT 849
QY 433 HGVY-----QLGF-----YVL-----DR 445
DB 850 IVITWTPAPRIGPKLGVRSQGEAPREVTSDSGSIIVSGLTPGVEVYTIQVLRDQER 909
QY 446 DSLFINGYA-----PONLSIRGEYQINFHIVNNLSNPDPSTSEYITLLARDIOQKVTLY 500
DB 910 DAPIVNVKVTPLSPPTNLHLEANPDGVLTVSWERSTTPDITGYRIT-----TTPT 960
QY 501 KGSQ-----LHDTFRFCLVNLNLT-----MDSVLVTVKALFSS 532
DB 961 NQOQNSLEEVVHADQSSCTFDNLSPGLEYNVSVYTVKDKESVPISDTIIPV----- 1014
QY 533 NLDPQLVEQVFLDKT-LNASFWH--LGSTYQVLDIHVTEMSS-----VYQPTSSSTQHF 585
DB 1015 ---PQLTDLFSVDITDSSIGLRTWPLNSS-TIIGYRITVVAAGEGIPEDFVDSVGY- 1069
QY 586 YLNFTITNLYPSQDKAQPGTNTYQNKENT-----EDALNQLFRNSSIKS-----YFSDCQV 637
DB 1070 ---YTVTGL-----EPG-IDYDISVITLINGESAPTTLTQQTAPPPPTDLRFTNIGP 1118
QY 638 STFRS--VPNRHTGVDSLCNFGSLARRVDRVAIYEFBLMTNGTQLOQ-----FTLD 689
DB 1119 DTRKVTWAPPSPSIDLTLNLYRVPKNEED---VAELISISPSDNVAVLTLPGTEYVVS 1175
QY 690 RSSVLDGYSPNRNEPTGNASADIOHSGRSSLEGPRFEOKLI SEEDLNH-----T 741
DB 1176 VSSV-----YEQHESHTPLRG-----RQKTGLDSTPGIDFSD--ITANSFTVHWIAPRATIT 1224
QY 742 GHHHHH 748
DB 1225 GYRIHH 1231

RESULT 13
US-11-193-806-2
; Sequence 2, Application US/11193806
```

```
Db 961 NGQGNLSLEEVHADQSSCTFDNLSPGLEYNVSVYTVKDKESVPISDIIPEV----- 1014
Qy 533 NLDPSLVEQVFLDKT-LNASFHW--LGSTYQLVDIIVHTEMESS-----VYOPTSSSTQHF 585
Db 1015 ---PQLTDLSFVDITDSSIGLWTLNLS--TIIGYRITVVAAGEGIPEDFVDSSVGY- 1069
Qy 586 YLNFPTINLPYSQDKAOGTNTVORKNRI-----EDALNOLFNSSIKS-----YFSDCQV 637
Db 1070 ---YTVTGL-----EPG-IDYDISVITLINGSAPTTLTQCTAVPPPTDLRFTNIGP 1118
Qy 638 STFRS--VPRNHTGVDSLCLNCFSPFLARRVDRVAIYEEFLMRTRNGTQLON-----FTLD 689
Db 1119 DTRVWAPPSSIDLTLNFLVRYSPVKNED---VAELISPSDNVAVLTLNLPTEYVVS 1175
Qy 690 RSSVLVDGYSNRPNEPLTGNASADIQHSGRSSLEGPREFEQLISEEDLNMH-----T 741
Db 1176 VSSV---YEQHESTPLRG-----RQKTGLDSTGIDFSD--ITANSFTVHWIAPRATIT 1224
Qy 742 GHHHHH 748
Db 1225 GYRIRHH 1231

RESULT 14
US-11-193-857-2
; Sequence 2, Application US/11193857
; Publication No. US20060024725A1
; GENERAL INFORMATION:
; APPLICANT: Husea, Robert
; APPLICANT: Fisher-Colbrie, Mark
; APPLICANT: Hickok, Durlin
; APPLICANT: LaPointe, Jerome P.
; TITLE OF INVENTION: Oncofetal Fibronectin as Marker for Pregnancy-Related Indications
; FILE REFERENCE: 17101-026001/827
; CURRENT APPLICATION NUMBER: US/11/193,857
; PRIOR FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: 60/592,823
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,803
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,825
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,804
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,824
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 2223
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-193-857-2

Query Match 3.0%; Score 118.5; DB 7; Length 2223;
Best Local Similarity 18.9%; Pred. No. 1.2;
Matches 171; Conservative 126; Mismatches 313; Indels 297; Gaps 46;

Qy 19 SVSTSTPTGTPTVLGLAS-----KTPASIFGPSAASHLLILFTLFTNLRYE--- 67
Db 445 TTTSTSTPTGTPTVLGLAS-----KTPASIFGPSAASHLLILFTLFTNLRYE--- 67
Qy 68 -----ENMPGSRKNTTERTVLQGLRLPLFKNTSVGLPYSGCKLT 107
Db 505 BEGDEPQYLDLPSTATSVNIPDPLPGRKYIVNVYQISEDGQSLTSTS----- 553
Qy 108 LLRPEKDEATGVAICTHRDPTGPGDLRQLVLELSQLTHTSITELGPTLDRDSL-- 165
Db 554 -----OTTAPDA-----PPDPTVDQVDDTSIVVWRSRPQAPIT---GYRI---VYSP 594
Qy 166 -VNGFTRSSVPTTSTGVVSEPTFTNLTNNRYMADMGPQGLSKFNITDNVM---KHL 221
```

```
Db 595 SVEGSSTELNLPETANSV-----TSLDL-----QPG-VQYNTITIYAVENQES 636
Qy 222 LSLPLFORSSIG-----ARYTGCKRVIALRSVKNGAET--RVDLLCTVLQPL 264
Db 637 TPVVIQETITGPRSDTVSPRDLQFVEDVKVTTIMWTTPPSAVTGYRVDVTPVNLPG 696
Qy 265 SGGLPI-KQVHELSSQOHTGIT--RLGPIYSLDKDLSLYLNGYNEPGDEP-----PT 313
Db 697 HGQLRPIRNTPAEVTGLSPGVYTFKFAVSHGRESKELTAQOQTKLDAPTNLQFVNET 756
Qy 314 TPKPATTFPLPSEATANGYHLKTLTINFTISNLOYSMDMGKSATFNSTEGVLQHLR 373
Db 757 DSTVLVRVTPPRAQIT---GYRL-TVGLTRRGQPROY-----NVGPSVKYPLR 801
Qy 374 PLPQKSSMGPPYLGCOLISLRPEKDG-AATGVDTTCTYHPDPVPGGLDIIQQLYWEISQLT 432
Db 802 NLQPAE-----YTVSLVAIKGNQSPKATGVFTT-----LQPGSSIPPYNTVETTT 849
Qy 433 HGVT---QLGF-----YVL-----DR 445
Db 850 IVITWTPAPRIGFKLGVPRPSQGGEAPREVTSDSGSIWVSGLTGPEVYVYTIQVLRDQER 909
Qy 446 DSLFINGYA-----PONLSIRGEYQINFHIVNWNLSNPDPSTSEYITLLRDIQDKVTTY 500
Db 910 DAPIVKNVVTPLSPPTNLHLNANPDGTGLTVSWERSTTTPDITGYRIT-----TTPT 960
Qy 501 KGSQ-----LHDTFRFCIVTNLT-----MDSVLVTVKALFSS 532
Db 961 NGQGNLSLEEVHADQSSCTFDNLSPGLEYNVSVYTVKDKESVPISDIIPEV----- 1014
Qy 533 NLDPSLVEQVFLDKT-LNASFHW--LGSTYQLVDIIVHTEMESS-----VYOPTSSSTQHF 585
Db 1015 ---PQLTDLSFVDITDSSIGLWTLNLS--TIIGYRITVVAAGEGIPEDFVDSSVGY- 1069
Qy 586 YLNFPTINLPYSQDKAOGTNTVORKNRI-----EDALNOLFNSSIKS-----YFSDCQV 637
Db 1070 ---YTVTGL-----EPG-IDYDISVITLINGSAPTTLTQCTAVPPPTDLRFTNIGP 1118
Qy 638 STFRS--VPRNHTGVDSLCLNCFSPFLARRVDRVAIYEEFLMRTRNGTQLON-----FTLD 689
Db 1119 DTRVWAPPSSIDLTLNFLVRYSPVKNED---VAELISPSDNVAVLTLNLPTEYVVS 1175
Qy 690 RSSVLVDGYSNRPNEPLTGNASADIQHSGRSSLEGPREFEQLISEEDLNMH-----T 741
Db 1176 VSSV---YEQHESTPLRG-----RQKTGLDSTGIDFSD--ITANSFTVHWIAPRATIT 1224
Qy 742 GHHHHH 748
Db 1225 GYRIRHH 1231

RESULT 15
US-11-193-561-17
; Sequence 17, Application US/11193561
; Publication No. US20060024757A1
; GENERAL INFORMATION:
; APPLICANT: Husea, Robert
; APPLICANT: Shorter, Simon
; TITLE OF INVENTION: Detection of Oncofetal Fibronectin for Selection of Concepti
; FILE REFERENCE: 17101-080001/831
; CURRENT APPLICATION NUMBER: US/11/193,561
; PRIOR FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: 60/592,823
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,803
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,825
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,804
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,824
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 39
```

SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 2421
; TYPE: PRN
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank NM 212475
; DATABASE ENTRY DATE: 2005-06-10
US-11-193-561-17

Query Match 3.0%; Score 118.5; DB 7; Length 2421;
Best Local Similarity 18.9%; Pred. No. 1.3;
Matches 171; Conservative 126; Mismatches 313; Indels 297; Gaps 46;

```
Qy 19 SVSTSTPGTPTVYLGA-----KTPASIFGPSAASHLLILFTLNFTITNRYE--- 67
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
698 TTSTSTPTVNTVGTTPSPPLVATSESVTEITASSFVSVVSASDITVSGFRVEYELS 757
Qy 68 -----ENMWPGRKNTTERTVLQGLLRPLFKNTSVGPLYSGCRLT 107
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
758 EGDPEQYLDLPSTATSVNIPDLLPGRKYVNVYQISEDEGEQSLILSTS----- 806
Qy 108 LLRPEKDGATGVDAICTHRPDPTGCLDREQLYLELSQLTHTSITELGPVTLDRDSLY-- 165
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
807 -----QTTAPDA-----PPDPTVDQVDDTSIVVRWSRPAQIT---GYRI----VYSP 847
Qy 166 -VNGFTHRSVPTTSTGVVSEEPFTLNFTINLRVMADMGPQGLSKFNITDNVM---KHL 221
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
848 SVESGSTELNLPETANSV-----TLSDL-----QPG-VQYNTIYAVEENQES 889
Qy 222 LSPLFORSISLG-----ARYTGCRIALRSVNGAET--RVDLLCTYLOPL 264
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
890 TPVVIQOETGTTPRSPTVPSRDLQFVETDVKTMTWTPPESAVTGYRVDVIPVNLPG 949
Qy 265 SGGLPI-KQVPELSQOHTGIT---RLGPYSLDKDSLYLNGYNEPCDPEP-----PT 313
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
950 HGQRLPISRTNFAEVTGLSPGVTYFKVFAVSHGRESKPLTAQOQTKLDAPTNLQFVNET 1009
Qy 314 TPKPATTFPLPPLSEATAMGYHLKTLTNFTISNLQVSPDMGKGSATFNSTEGVLOHLR 373
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1010 DSTVLVRWTPPRAQIT---GYRL-TVGLTRGQPRQY-----NVGPSVKYPLR 1054
Qy 374 PLFQKSMGPFYLGCOLISLRPEKOG--AATGVDTTCYHPDPVPGGLDIOQLWELSQLT 432
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1055 NLQPAE-----YTVSLVAIKGQESPKATGVFTT-----LQPGSSIPPYNTEVETT 1102
Qy 433 HGVT-----QLGF-----YVL-----DR 445
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1103 IVITWTPAPRIGKLGVRPSQCGEAPREVTSDSGSIWVSGLTGPEVYVYTIQVLRDQER 1162
Qy 446 DSLFINGYA-----PQNLISIRGEYQINFHIVNNLGNPDPTSSEYITLLRDIQKVTTL 500
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1163 DAPIVKNVTPLEPPTNLHLEANDPGVLTVSWEESTPTDITGYRIT-----TTPT 1213
Qy 501 KGSQ-----LHDTFRFCVLTNLT-----MDSVLTVTKALFSS 532
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1214 NGQQGNSLEEVVHADQSSCTFDNLSPGLEYNVSVYTVKDKESVPISDTIPEV----- 1267
Qy 533 NLDPISLVEQVFLDKT-LNASFWH--LGSTVQLVDIHVTESS-----VQPTSSSSTQHP 595
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1268 ---PQTLDSLFSVDITSSIGLRTPLNSS--TIIGYRITVVAAGEGIPFEDFVDSVGVY- 1322
Qy 586 YLNFITINLPYSQDKAQPGTNTYQNRKNI-----EDALNQLFNSSIKS-----YFSDCOV 637
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1323 ---YTVTGL-----EPG-IDYDISVITLNGESAPTTLTQOAVPPPTDLRFTNIGP 1371
Qy 638 STFRS--VPMRHTGVDSLNCNFPGLARRVDRVAIYEEFLMRNGTQLQN-----FTLD 689
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1372 DTKRVTWAPPSPSIDTLNFLVRYSPVKNED---VAELSISSPDNAVVLTNLLPGTEVYVS 1428
Qy 690 RSSVLVDGYSFNRNEPLTGNASDIQHSGRSSLEGPRFQKLISEEDLNWH-----T 741
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1429 VSSV-----YEQHSESTPLRG-----RQKTGLDSPTGIDFSD--ITANSFTVHWIAPRATIT 1477
```

Qy 742 GHHHHH 748
Db : : : : :
1478 GYRIRH 1484

RESULT 16

US-11-193-771-17
; Sequence 17; Application US/11193771
; Publication No. US20060024722A1
; GENERAL INFORMATION:
; APPLICANT: Fisher-Colbrie, Mark
; APPLICANT: Hickok, Durlin
; APPLICANT: LaPointe, Jerome P.
; TITLE OF INVENTION: Samples for Detection of Oncofetal Fibronectin and uses thereof
; FILE REFERENCE: 17101-027001/828
; CURRENT APPLICATION NUMBER: US/11/193, 771
; CURRENT FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: 60/592, 823
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592, 803
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592, 825
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592, 804
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592, 824
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 2421
; TYPE: PRN
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank NM 212475
; DATABASE ENTRY DATE: 2005-06-10
US-11-193-771-17

Query Match 3.0%; Score 118.5; DB 7; Length 2421;
Best Local Similarity 18.9%; Pred. No. 1.3;
Matches 171; Conservative 126; Mismatches 313; Indels 297; Gaps 46;

```
Qy 19 SVSTSTPGTPTVYLGA-----KTPASIFGPSAASHLLILFTLNFTITNRYE--- 67
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
698 TTSTSTPTVNTVGTTPSPPLVATSESVTEITASSFVSVVSASDITVSGFRVEYELS 757
Qy 68 -----ENMWPGRKNTTERTVLQGLLRPLFKNTSVGPLYSGCRLT 107
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
758 EGDPEQYLDLPSTATSVNIPDLLPGRKYVNVYQISEDEGEQSLILSTS----- 806
Qy 108 LLRPEKDGATGVDAICTHRPDPTGCLDREQLYLELSQLTHTSITELGPVTLDRDSLY-- 165
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
807 -----QTTAPDA-----PPDPTVDQVDDTSIVVRWSRPAQIT---GYRI----VYSP 847
Qy 166 -VNGFTHRSVPTTSTGVVSEEPFTLNFTINLRVMADMGPQGLSKFNITDNVM---KHL 221
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
848 SVESGSTELNLPETANSV-----TLSDL-----QPG-VQYNTIYAVEENQES 889
Qy 222 LSPLFORSISLG-----ARYTGCRIALRSVNGAET--RVDLLCTYLOPL 264
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
890 TPVVIQOETGTTPRSPTVPSRDLQFVETDVKTMTWTPPESAVTGYRVDVIPVNLPG 949
Qy 265 SGGLPI-KQVPELSQOHTGIT---RLGPYSLDKDSLYLNGYNEPCDPEP-----PT 313
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
950 HGQRLPISRTNFAEVTGLSPGVTYFKVFAVSHGRESKPLTAQOQTKLDAPTNLQFVNET 1009
Qy 314 TPKPATTFPLPPLSEATAMGYHLKTLTNFTISNLQVSPDMGKGSATFNSTEGVLOHLR 373
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1010 DSTVLVRWTPPRAQIT---GYRL-TVGLTRGQPRQY-----NVGPSVKYPLR 1054
Qy 374 PLFQKSMGPFYLGCOLISLRPEKOG--AATGVDTTCYHPDPVPGGLDIOQLWELSQLT 432
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1429 VSSV-----YEQHSESTPLRG-----RQKTGLDSPTGIDFSD--ITANSFTVHWIAPRATIT 1477
```

Db 1055 NLQASE-----YTVSLVAIKGQESPKATGVFTT-----LQPGSSIPPYNTEVTETT 1102
Qy 433 HGVT-----OLGF-----YVL-----DR 445
Db 1103 IVITWTPAPRIGFKLGVRPSQGGAPREVTSDSGSIIVVSGLTGCVYVYTIQVLRDQGER 1162
Qy 446 DSLFINGYA-----PQNLISIRGEVQINFHIVNNLSNPDPTSSSEYITLLRDIQDKVTTLY 500
Db 1163 DAPIVNVKVTPLSPPTNLHLEANDPTGVLTVSWERSTTDPITGYRIT-----TTPT 1213
Qy 501 KGSO-----LHDTFRFCIVTNLT-----MDSVLVTVKALFSS 532
Db 1214 NGQGNLSLEEVHADQSSCTFDNLSPGLEYNVSVYTVKDKESVPISDTIPEV-----1267
Qy 533 NLDPQLVEQVFLDKT-INASFWH--LGSTYQVLDIHTVEMESS-----VYQPTSSSSSTQHF 585
Db 1268 ---PQLTDLSEFVDITDSSIGLRWTPLNSS-TIIGYRITVVAAGGEGIFEDFVDSVGVY- 1322
Qy 586 YLNFITITNLPYSQDKAQPGTINYORKNRI-----EDALNOLFNRSSIKS-----YFSDQV 637
Db 1323 ---YTVTGL-----EPG-IDYDISVITLINGESAPTTLTQQTAVPPPTDLRFTNIGP 1371
Qy 638 STFRS--VPNRHHTGVDSLNCNFSPLARRVDRVAIYEEFLMRTRNGTOLQ-----FTLD 689
Db 1372 DTRVWTWAPPSIDLTVFLVRYSPVKNEED---VAELSISSDNNAVLTNLLPCTEYVVS 1428
Qy 690 RSSVLVDGYSPPNRNEPTTGNADIOHSGGRSSLEGPRFEQKLISEEDLNH-----T 741
Db 1429 VSSV---YEQHESSTPLRG-----RQKTGLDSTPTGIDFSD--ITANSFTVHWIAPRATIT 1477
Qy 742 GHHHHH 748
Db 1478 GYIRRH 1484

RESULT 17

US-11-193-789-17
; Sequence 17, Application US/11193789
; Publication No. US20060024723A1
; GENERAL INFORMATION:
; APPLICANT: Husse, Robert
; APPLICANT: Fisher-Colbrie, Mark
; APPLICANT: Lapointe, Jerome
; APPLICANT: Seney, Andrew
; APPLICANT: Shorter, Simon
; TITLE OF INVENTION: Methods for detecting Oncofetal Fibronectin
; FILE REFERENCE: 17101-029001/830
; CURRENT APPLICATION NUMBER: US/11/193,789
; CURRENT FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: 60/592,823
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,803
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,825
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,804
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,824
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 2421
; TYPE: PRT
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank NM 212475
; DATABASE ENTRY DATE: 2005-06-10
US-11-193-789-17

Query Match 3.0%; Score 118.5; DB 7; Length 2421;
Best Local Similarity 18.9%; Pred. No. 1.3;
Matches 171; Conservative 126; Mismatches 313; Indels 297; Gaps 46;

Qy 19 SVSTTSTPGTPTVVLGAS-----KTPASIPGSAASHLLILFTLNFTITNRYE----- 67
Db 698 TTTTSTPTVNTVTGETTFFPLVATSVTSVTEITASSFVSVWSASDVTSGFRVEVELS 757
Qy 68 -----ENMPGSRKFNTTTERVQLGLRLRFLKXNTSVGLYSGRLT 107
Db 758 BEGDEPOYLDLPSTATSVNIPDLLPGRKYIVNVQISEDEGEQSLILSTS----- 806
Qy 108 LLRPEKGEATGVDAICTHRPDTGPGCLDRQYLIELSLQTHSITELGPTLDRDSLY-- 165
Db 807 -----QTTAPDA---PPDPTVDQDDTSIVVRWSRPAQIT---GYRI---VYSP 847
Qy 166 -VNGFTHRSVPSTTCVWSEEPFTLNFTINNLRVYMDMCPGSLKFNITDNVW---KHL 221
Db 848 SVESSTELMLPETANSV-----TUSDL-----OPG-VQNIITIIYAVENQES 889
Qy 222 LSPFORSSLG-----ARYTGCRVIALRSVKGAE--RVDLLCTYLQPL 264
Db 890 TPVVIQOETTGTPRSDDTVPSPRDLQFVEVTDVKTIMWTPPEASAVTGYRVDVIPVNLPG 949
Qy 265 SGPLPT-KQVFHELQOQTHGIT---RLGYSLDKOSLYLNGYNEPGPDEP-----PT 313
Db 950 HGQRLPTSRNTFAEVTGLSPGVTYFYKFAVSHGRESKPLTAQQTTKLDAPTNLQFVNET 1009
Qy 314 TPXPATTFPLPSEATTAMGYHLKTLTNFTISNLOYSPDMGKGSATFNSTEGVLOHLLR 373
Db 1010 DSTVLVWTPPRAQIT---GYRL-TVGLTRGQPRQY-----NVGPSVSKYPLR 1054
Qy 374 PLFQKSGMGPYFLGCQLISLRPEKOG-AATGVDTTCTYHPDPVPGGLDIOOLYWELSQLT 432
Db 1055 NLQASE-----YTVSLVAIKGQESPKATGVFTT-----LQPGSSIPPYNTEVTETT 1102
Qy 433 HGVT-----OLGF-----YVL-----DR 445
Db 1103 IVITWTPAPRIGFKLGVRPSQGGAPREVTSDSGSIIVVSGLTGCVYVYTIQVLRDQGER 1162
Qy 446 DSLFINGYA-----PQNLISIRGEVQINFHIVNNLSNPDPTSSSEYITLLRDIQDKVTTLY 500
Db 1163 DAPIVNVKVTPLSPPTNLHLEANDPTGVLTVSWERSTTDPITGYRIT-----TTPT 1213
Qy 501 KGSO-----LHDTFRFCIVTNLT-----MDSVLVTVKALFSS 532
Db 1214 NGQGNLSLEEVHADQSSCTFDNLSPGLEYNVSVYTVKDKESVPISDTIPEV----- 1267
Qy 533 NLDPQLVEQVFLDKT-INASFWH--LGSTYQVLDIHTVEMESS-----VYQPTSSSSSTQHF 585
Db 1268 ---PQLTDLSEFVDITDSSIGLRWTPLNSS-TIIGYRITVVAAGGEGIFEDFVDSVGVY- 1322
Qy 586 YLNFITITNLPYSQDKAQPGTINYORKNRI-----EDALNOLFNRSSIKS-----YFSDQV 637
Db 1323 ---YTVTGL-----EPG-IDYDISVITLINGESAPTTLTQQTAVPPPTDLRFTNIGP 1371
Qy 638 STFRS--VPNRHHTGVDSLNCNFSPLARRVDRVAIYEEFLMRTRNGTOLQ-----FTLD 689
Db 1372 DTRVWTWAPPSIDLTVFLVRYSPVKNEED---VAELSISSDNNAVLTNLLPCTEYVVS 1428
Qy 690 RSSVLVDGYSPPNRNEPTTGNADIOHSGGRSSLEGPRFEQKLISEEDLNH-----T 741
Db 1429 VSSV---YEQHESSTPLRG-----RQKTGLDSTPTGIDFSD--ITANSFTVHWIAPRATIT 1477
Qy 742 GHHHHH 748
Db 1478 GYIRRH 1484

RESULT 18

US-11-193-806-17
; Sequence 17, Application US/11193806
; Publication No. US20060024724A1
; GENERAL INFORMATION:
; APPLICANT: Husse, Robert
; APPLICANT: Fisher-Colbrie, Mark

```

1214 NGQCGNSLEEVHADOSSCTFDNLSGLENNVSVTVKDDKESVPISDTLIEEV-----1267
Qy 533 NLDPSLVEQVFLDKT-LNASFWH--LGSTYQLVDIHVTEMESS-----VYOPTSSSSTQHP 585
1268 ---PQLTDLSFVDITDSSISGLRWTPLNSS-TIIGVRIITVVAAGEGIPEDFVDDSSVG- 1322
Qy 586 YLMFTITNLPSYQDKAQPGTWTAYQRNKRI-----EDALNQLFNSSIKS-----YFSDCQV 637
1323 ---YTVGL-----EPG-IDYDISVITLINGESAPTTLTQCTAVAPPTDLURFTNIGP 1371
Qy 638 STPRS--VPNRHHTGVDSLCNFSPLARRDVAIYEEFLMRTRNGTQLON-----FTLD 689
1372 DTMRVTAWPPPSIDLTNFLVRYSPVKNEED---VAELSI SPDNVAVLNLLPGTEVVVS. 1428
Qy 690 RSVLVGDGVSFNRNEPLTGNSSADIQHSGRSSLEGPRFEOKLISEEDLNWH-----T 741
1429 VSSV----YEQHESTPLRG-----ROKTLGDSPTGIDFSD--ITANSFTVHVIAPRATIT 1477
Qy 742 GHHHHHH 748
1478 GYRIHH 1484

```

```

; PUDICATION NO.: US20060024725A1
; GENERAL INFORMATION:
; APPLICANT: Hussa, Robert
; APPLICANT: Fisher-Colbrie, Mark
; APPLICANT: Hickok, Durlin
; APPLICANT: LaPointe, Jerome P.
; TITLE OF INVENTION: Oncofetal Fibronectin as Marker for Pregnancy-Related Infection
; FILE REFERENCE: 17101-026001/827
; CURRENT APPLICATION NUMBER: US/11/193,857
; CURRENT FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: 60/592,823
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,803
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,825
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,804
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,824
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 2421
; TYPE: PRN
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank NM 212475
; DATABASE ENTRY DATE: 2005-06-10
US-11-193-857-17

Query Match          3.0%; Score 118.5; DB 7; Length 2421;
Best Local Similarity 18.9%; Pred. No. 1.3;
Matches 171; Conservative 126; Mismatches 313; Indels 297; Gaps 46;

Qy      19 SVYSTSTGCTPTTVYLGAS-----KTPASIFGPASAASHLLILFTNTITNLRYE--- 67
Db      698 TTISTSTPVTNSVTTGTETPPSPFLVATSESVTEITASSPFVSWWSASDTVSGRFVEYELS 757
Qy      68 -----ENMWFGSRKFNTTTERVLQGLLRPLFKNTSVGPLYSGCRLT 107
Db      758 EEGDEBPQYLDLPSTATSNVPDLLPGKRYIVNVYQISEDGEQSILSTS----- 806
Qy      108 LLRPEKDGEATGVDAICTHRPPTPGPLDREGLYLELSQLTHSITELGPLYTLDRSLY-- 165
Db      907 -----QTAPDA-----PPDPETVDQVDDTSIVVRWRSRPQAPIT---GYRI---VVSP 847

```

```
QY 166 -VNGFTHRSVPSTSTGVSSEBFTLNFTINRLRYMADMGQSLKFNITDNVM---KHL 221
Db 848 SVESGSELNLPETANSV-----TLSDL-----QPG-VQNTIITYAEEQES 889
QY 222 LSLPFRSSSLG-----ARYGCRVIALRSVKNGAET--RVDLLCTYLQPL 264
Db 890 TPVVIQOETGTSPRSDTVPSPRDLQFVEVTDVKVIMWTPPEASVTCYRVDVIVPNLPG 949
QY 265 SGPLPT-KQVFHLSQOOTHGIT---RLGPSYLDKDSLYLNGYNEPQDEP-----PT 313
Db 950 HGQRLPISRNTFAEVTGLSPGVYTFKFAVSHGRESKPLTAQOQTKLDAPTNLQFVNET 1009
QY 314 TPKPATFLPLSEATAMGYHLKTLNFTINLQYSPDMGKSATFNSTEGVLQHLR 373
Db 1010 DSTVLVRWTPPRAQIT---GYRL-TVGLTRRGPRQY-----NVGPSYSKYPLR 1054
QY 374 PLFQKSMGPFYLGCOLISLRPEKDG-AATGVDVDTCTYHPDPVPGGLDIQOLYWELSQLT 432
Db 1055 NLQPAE-----YTVSLVAIKGQESPKATGVFTT-----LQPGSSIPPYNTEVETT 1102
QY 433 HGVT-----OLGF-----YVL-----DR 445
Db 1103 IVITWTPAPRIGFKLGVPRSQGGEAPREVTSDSGSIIVVSGLTGPEVYVYTIQVLRDQGR 1162
QY 446 DSLFINGYA-----PQNLISIRGEVQINFHIVNNLSNPDPTSSEYITLLRDIQDKVTTY 500
Db 1163 DAPIVNVKVTPLSPPTNLHLEANDPTGVLTVSWERSTTPTDITGYRIT---TTPT 1213
QY 501 KGSO-----LHDTFRCLVNLTL-----MDSVLVTVKALFSS 532
Db 1214 NGQGNLSLEEVHADQSSCTFDNLSPGLEYNVSVYTVKDKESVPISDTIPEV-----1267
QY 533 NLDPQLSVQVFLDKT-LNASFWH--LGSTYQVLDIHVTEMESS-----VYQPTSSSSTQHF 585
Db 1368 ---POLTDLFSVDITDSSIGLRWTPLNSS-TIIGYRITVVAAGSIGPIFEDFVDSVGY- 1322
QY 586 YLNFITINLPSQDKAQPGTNYQNRKNI-----EDALNQLFRNSSIKS-----YFSDCQV 637
Db 1323 ---YTVTGL-----BFG-IDYDISVITLNGESAPTTLTQQTAVPPPTDLRFTNIGP 1371
QY 638 STFRS--VPNRHHTGVDSLCNFSPLARRVDRVAIYEEFLMRNGTQLOK-----FTLD 689
Db 1372 DTRVWTPAPPSIDLTNLFYRSPVKNEED---VAELSISPSDNAVLTNLLRGTETVVS 1428
QY 690 RSSVLVDGYSNNRNEPLTGNASADIQHSGRSSLEGPRFEQKLISEEDLNMH-----T 741
Db 1429 VSSV---YEQHSTPLRG-----RQKTGLDPSPTGIDFSD--ITANSFTVHWIAPRATIT 1477
QY 742 GHHHHH 748
Db 1478 GYRIRHH 1484

RESULT 20
US-11-193-561-15
; Sequence 15, Application US/11193561
; Publication No. US20060024757A1
; GENERAL INFORMATION:
; APPLICANT: Husea, Robert
; TITLE OF INVENTION: Detection of Oncofetal Fibronectin for Selection of Concepti
; FILE REFERENCE: 17101-080001/831
; CURRENT APPLICATION NUMBER: US/11/193,561
; PRIOR FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: 60/592,823
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,803
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,825
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,804
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,824
```

```
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 2477
; TYPE: PRT
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank NM 212482
; DATABASE ENTRY DATE: 2005-06-10
; US-11-193-561-15

Query Match 3.0%; Score 118.5; DB 7; Length 2477;
Best Local Similarity 18.9%; Pred. No. 1.4;
Matches 171; Conservative 126; Mismatches 313; Indels 297; Gaps 46;

QY 19 SVSTSTPGPTTYVLGAS-----KTPASIFGSAASHLLILFTLNFTINLRYE---- 67
Db 698 TTTSTSTPVTNTVTGTTTTPFPLVATSESVTEITASSFVSVWSASDVTSGFRVEYELS 757
QY 68 -----ENMWPGSRKENTTTERVLQGLLRPLFKNTSVGLYSGCRLT 107
Db 758 EGDPEQYLDLPSTATSVNIPDLLPGRKYIVNVYQISEDEGEQSLILSTS----- 806
QY 108 LLRPEKDGATGVDAICTHRPDPTGCLDREQLYLELSQLTHSITELGPTTLDRDSLY-- 165
Db 807 -----QTTAPDA-----PPDPTVOVDVTSIVVWSRPOAPIT---GYRI---VYSP 847
QY 166 -VNGFTHRSVPSTSTGVSSEBFTLNFTINRLRYMADMGQSLKFNITDNVM---KHL 221
Db 848 SVESGSELNLPETANSV-----TLSDL-----QPG-VQNTIITYAEEQES 889
QY 222 LSLPFRSSSLG-----ARYGCRVIALRSVKNGAET--RVDLLCTYLQPL 264
Db 890 TPVVIQOETGTSPRSDTVPSPRDLQFVEVTDVKVIMWTPPEASVTCYRVDVIVPNLPG 949
QY 265 SGPLPT-KQVFHLSQOOTHGIT---RLGPSYLDKDSLYLNGYNEPQDEP-----PT 313
Db 950 HGQRLPISRNTFAEVTGLSPGVYTFKFAVSHGRESKPLTAQOQTKLDAPTNLQFVNET 1009
QY 314 TPKPATFLPLSEATAMGYHLKTLNFTINLQYSPDMGKSATFNSTEGVLQHLR 373
Db 1010 DSTVLVRWTPPRAQIT---GYRL-TVGLTRRGPRQY-----NVGPSYSKYPLR 1054
QY 374 PLFQKSMGPFYLGCOLISLRPEKDG-AATGVDVDTCTYHPDPVPGGLDIQOLYWELSQLT 432
Db 1055 NLQPAE-----YTVSLVAIKGQESPKATGVFTT-----LQPGSSIPPYNTEVETT 1102
QY 433 HGVT-----OLGF-----YVL-----DR 445
Db 1103 IVITWTPAPRIGFKLGVPRSQGGEAPREVTSDSGSIIVVSGLTGPEVYVYTIQVLRDQGR 1162
QY 446 DSLFINGYA-----PQNLISIRGEVQINFHIVNNLSNPDPTSSEYITLLRDIQDKVTTY 500
Db 1163 DAPIVNVKVTPLSPPTNLHLEANDPTGVLTVSWERSTTPTDITGYRIT---TTPT 1213
QY 501 KGSO-----LHDTFRCLVNLTL-----MDSVLVTVKALFSS 532
Db 1214 NGQGNLSLEEVHADQSSCTFDNLSPGLEYNVSVYTVKDKESVPISDTIPEV-----1267
QY 533 NLDPQLSVQVFLDKT-LNASFWH--LGSTYQVLDIHVTEMESS-----VYQPTSSSSTQHF 585
Db 1368 ---POLTDLFSVDITDSSIGLRWTPLNSS-TIIGYRITVVAAGSIGPIFEDFVDSVGY- 1322
QY 586 YLNFITINLPSQDKAQPGTNYQNRKNI-----EDALNQLFRNSSIKS-----YFSDCQV 637
Db 1323 ---YTVTGL-----BFG-IDYDISVITLNGESAPTTLTQQTAVPPPTDLRFTNIGP 1371
QY 638 STFRS--VPNRHHTGVDSLCNFSPLARRVDRVAIYEEFLMRNGTQLOK-----FTLD 689
Db 1372 DTRVWTPAPPSIDLTNLFYRSPVKNEED---VAELSISPSDNAVLTNLLRGTETVVS 1428
QY 690 RSSVLVDGYSNNRNEPLTGNASADIQHSGRSSLEGPRFEQKLISEEDLNMH-----T 741
```

Db	1429	VSSV----	YQHESTPLRG-----	RQKTGLDSTGIDFSD--	ITANSFTVHWIAPRATIT	1477
Qy	742	GHHHHH	748			
Db	1478	GYIRHH	1484			

Search completed: March 20, 2006, 07:32:41
Job time : 15.0158 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 20, 2006, 07:31:52 ; Search time 132.781 Seconds
(without alignments)
2353.772 Million cell updates/sec

Title: US-10-687-035-1

Perfect score: 3945

Sequence: 1 AAQARRARTKLFTTHRSV.....QKLSEEDLNMTHGHHHH 748

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Published Applications_AA_Main:*

- 1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep:*
- 3: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep:*
- 4: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 5: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3945	100.0	748	5	US-10-687-035-1
2	3904.5	99.0	809	5	US-10-687-035-2
3	3665	92.9	6995	5	US-10-983-340-4
4	3663	92.9	833	3	US-09-884-441-389
5	3663	92.9	833	3	US-09-907-969-389
6	3663	92.9	833	3	US-09-827-271-389
7	3663	92.9	833	4	US-10-198-053-389
8	3663	92.9	833	5	US-10-860-790-389
9	3663	92.9	914	3	US-09-778-320-206
10	3663	92.9	914	3	US-09-910-689-206
11	3663	92.9	914	3	US-09-884-441-312
12	3663	92.9	914	3	US-09-884-441-478
13	3663	92.9	914	3	US-09-907-969-312
14	3663	92.9	914	3	US-09-907-969-478
15	3663	92.9	914	3	US-09-827-271-312
16	3663	92.9	914	4	US-10-010-742-206
17	3663	92.9	914	4	US-10-198-053-312
18	3663	92.9	914	4	US-10-198-053-478
19	3663	92.9	914	4	US-10-714-389-206
20	3663	92.9	914	4	US-10-717-296-206
21	3663	92.9	914	5	US-10-860-790-312
22	3663	92.9	914	5	US-10-860-790-478
23	3658	92.7	1899	4	US-10-142-515-5
24	3658	92.7	1890	4	US-10-097-340-217
25	3658	92.7	1890	4	US-10-245-871-314
26	3658	92.7	1890	4	US-10-253-286-314
27	3658	92.7	1890	6	US-11-050-926-217

28	3651	92.5	3451	3	US-09-907-969-595	Sequence 595, App
29	3651	92.5	3451	4	US-10-198-053-595	Sequence 595, App
30	3651	92.5	3451	5	US-10-860-790-595	Sequence 595, App
31	3649	92.5	1148	3	US-09-965-738-48	Sequence 48, Appl
32	3649	92.5	2248	3	US-09-965-738-50	Sequence 50, Appl
33	3649	92.5	11721	3	US-09-965-738-162	Sequence 162, App
34	3649	92.5	22152	4	US-10-715-066-5	Sequence 5, Appl
35	3642	92.3	1148	3	US-09-884-441-458	Sequence 458, App
36	3642	92.3	1148	3	US-09-884-441-479	Sequence 479, App
37	3642	92.3	1148	3	US-09-907-969-458	Sequence 458, App
38	3642	92.3	1148	3	US-09-907-969-479	Sequence 479, App
39	3642	92.3	1148	3	US-09-827-271-458	Sequence 458, App
40	3642	92.3	1148	4	US-10-097-340-216	Sequence 216, App
41	3642	92.3	1148	4	US-10-198-053-458	Sequence 458, App
42	3642	92.3	1148	4	US-10-198-053-479	Sequence 479, App
43	3642	92.3	1148	4	US-10-257-021-56	Sequence 56, Appl
44	3642	92.3	1148	4	US-10-383-368-2	Sequence 2, Appl
45	3642	92.3	1148	4	US-10-734-564-131	Sequence 131, App
46	3642	92.3	1148	5	US-10-860-790-458	Sequence 458, App
47	3642	92.3	1148	5	US-10-860-790-479	Sequence 479, App
48	3642	92.3	1148	5	US-10-936-626-129	Sequence 129, App
49	3642	92.3	1148	5	US-10-938-061-129	Sequence 129, App
50	3642	92.3	1148	6	US-11-050-926-216	Sequence 216, App
51	3642	92.3	1156	3	US-09-884-441-459	Sequence 459, App
52	3642	92.3	1156	3	US-09-907-969-459	Sequence 459, App
53	3642	92.3	1156	3	US-09-827-271-459	Sequence 459, App
54	3642	92.3	1156	4	US-10-198-053-459	Sequence 459, App
55	3642	92.3	1156	5	US-10-860-790-459	Sequence 459, App
56	3616	91.7	1148	3	US-09-932-419-2	Sequence 2, Appl
57	3189	80.8	772	3	US-09-884-441-388	Sequence 388, App
58	3189	80.8	772	3	US-09-907-969-388	Sequence 388, App
59	3189	80.8	772	3	US-09-827-271-388	Sequence 388, App
60	3189	80.8	772	4	US-10-198-053-388	Sequence 388, App
61	3189	80.8	772	5	US-10-860-790-388	Sequence 388, App
62	3166.5	80.3	1783	4	US-10-097-340-214	Sequence 214, App
63	3166.5	80.3	1783	6	US-11-050-926-214	Sequence 214, App
64	2743	69.5	583	4	US-10-142-515-4	Sequence 4, Appl
65	2545	64.0	545	4	US-10-243-243A-4	Sequence 4, Appl
66	2484	63.0	9799	3	US-09-965-738-146	Sequence 146, App
67	2445	62.0	526	4	US-10-333-900-30	Sequence 30, Appl
68	2018	51.2	2234	4	US-10-612-090-20	Sequence 20, Appl
69	2000	50.7	439	3	US-09-965-738-148	Sequence 148, App
70	1996	50.6	438	3	US-09-884-441-483	Sequence 483, App
71	1996	50.6	438	3	US-09-907-969-483	Sequence 483, App
72	1996	50.6	438	4	US-10-198-053-483	Sequence 483, App
73	1996	50.6	438	5	US-10-860-790-483	Sequence 483, App
74	1990	50.4	438	3	US-09-884-441-390	Sequence 390, App
75	1990	50.4	438	3	US-09-907-969-390	Sequence 390, App
76	1990	50.4	438	3	US-09-827-271-390	Sequence 390, App
77	1990	50.4	438	4	US-10-198-053-390	Sequence 390, Appl
78	1990	50.4	438	4	US-10-333-900-19	Sequence 19, Appl
79	1990	50.4	438	5	US-10-860-790-390	Sequence 390, App
80	1980.5	50.2	456	5	US-10-858-412-226	Sequence 226, App
81	1931	48.9	367	4	US-10-333-900-27	Sequence 27, Appl
82	1830	46.4	396	5	US-10-858-412-225	Sequence 225, App
83	1615	40.9	5877	4	US-10-142-515-11	Sequence 11, Appl
84	1615	40.9	5935	4	US-10-243-243A-8	Sequence 8, Appl
85	1601.5	40.6	909	3	US-09-965-738-69	Sequence 69, Appl
86	1591	40.3	1366	3	US-09-965-738-47	Sequence 47, Appl
87	1558	39.5	1362	4	US-10-142-515-8	Sequence 8, Appl
88	1542	39.1	780	3	US-09-965-738-159	Sequence 159, App
89	1518	38.5	780	3	US-09-965-738-158	Sequence 158, App
90	1436	36.4	304	3	US-09-884-441-486	Sequence 486, App
91	1436	36.4	304	3	US-09-907-969-486	Sequence 486, App
92	1436	36.4	304	4	US-10-198-053-486	Sequence 486, App
93	1436	36.4	304	5	US-10-860-790-486	Sequence 486, App
94	1406	35.1	624	3	US-09-965-738-160	Sequence 160, App
95	1346.5	34.1	594	3	US-09-965-738-71	Sequence 71, Appl
96	1345	34.1	318	3	US-09-907-969-594	Sequence 594, App
97	1345	34.1	318	4	US-10-198-053-594	Sequence 594, App
98	1345	34.1	318	5	US-10-860-790-594	Sequence 594, App
99	1306	33.1	597	3	US-09-965-738-78	Sequence 78, Appl
100	1284.5	32.6	525	3	US-09-965-738-70	Sequence 70, Appl

ALIGNMENTS

RESULT 1

US-10-687-035-1
; Sequence 1, Application US/10687035
; Publication No. US20050064518A1
; GENERAL INFORMATION:
; APPLICANT: Albione, Earl F.
; APPLICANT: Soltis, Daniel A.
; TITLE OF INVENTION: ANTIBODIES THAT BIND CELL-ASSOCIATED
; TITLE OF INVENTION: CA 125/0772P AND METHODS OF USE THEREOF
; FILE REFERENCE: 6750-214-999
; CURRENT APPLICATION NUMBER: US/10/687,035
; CURRENT FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: 60/485,986
; PRIOR FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: 60/418,828
; PRIOR FILING DATE: 2003-10-12
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 748
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CA 125/0772P 3-repeat
US-10-687-035-1

Query Match 100.0%; Score 3945; DB 5; Length 748;
Best Local Similarity 100.0%; Pred. No. 3.1e-312; Indels 0; Gaps 0;
Matches 748; Conservative 0; Mismatches 0;
Qy 1 AAQPARARRTKLTHRSSVSTTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFT 60
Db 1 AAQPARARRTKLTHRSSVSTTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFT 60
Qy 61 ITNLRYEENWMPGSRKENTTERRVLOGLLRPLFKNTSVGPLYSGCRLTLRLPEKDGATGV 120
Db 61 ITNLRYEENWMPGSRKENTTERRVLOGLLRPLFKNTSVGPLYSGCRLTLRLPEKDGATGV 120
Qy 121 DAICTHRPDPGCLDREQLYLELSQI THSITELGPYTLDRDLSLVNGFTHRSSVPTTST 180
Db 121 DAICTHRPDPGCLDREQLYLELSQI THSITELGPYTLDRDLSLVNGFTHRSSVPTTST 180
Qy 181 GWSEEPFTLNFTINNLRYMADMGQPGSLKFNITDNVWKHLSPFLFORSSILGARYTGCRV 240
Db 181 GWSEEPFTLNFTINNLRYMADMGQPGSLKFNITDNVWKHLSPFLFORSSILGARYTGCRV 240
Qy 241 IALRSVKNGAETRVLLCTYLOPLSGPGLPIKQVFHLSQOQTHGITRLGYSLDKDSL 300
Db 241 IALRSVKNGAETRVLLCTYLOPLSGPGLPIKQVFHLSQOQTHGITRLGYSLDKDSL 300
Qy 301 NGYNEPGDEPPTPKATTPPLSEATTAMGVHKLTLNFTISNLQYSPDMGKGSAT 360
Db 301 NGYNEPGDEPPTPKATTPPLSEATTAMGVHKLTLNFTISNLQYSPDMGKGSAT 360
Qy 361 FNSTEGVLOHLRLPFLQKSSMGPPYLGCOLISLPEKDGATGVDVTTCTHYHPDPVGLD 420
Db 361 FNSTEGVLOHLRLPFLQKSSMGPPYLGCOLISLPEKDGATGVDVTTCTHYHPDPVGLD 420
Qy 421 IQQLYWELSQLTHGVTLQGFVLDRLDSLFINGYAPQNLISIRGEYQINPHI VNNWLSNPD 480
Db 421 IQQLYWELSQLTHGVTLQGFVLDRLDSLFINGYAPQNLISIRGEYQINPHI VNNWLSNPD 480
Qy 481 TSSEYITLLRDIQKVITLYKGSQIHLDTFRCLVNTLMDSVITVTKALFSSNLDPSLVE 540
Db 481 TSSEYITLLRDIQKVITLYKGSQIHLDTFRCLVNTLMDSVITVTKALFSSNLDPSLVE 540
Qy 541 QVFLDKTLNAGFWHLGTYQLVDIHVTEMSSVYQPTSSSTQHFYLNFTITNLPSYQDK 600
Db 541 QVFLDKTLNAGFWHLGTYQLVDIHVTEMSSVYQPTSSSTQHFYLNFTITNLPSYQDK 600

Db 541 QVFLDKTLNAGFWHLGTYQLVDIHVTEMSSVYQPTSSSTQHFYLNFTITNLPSYQDK 600
Qy 601 AOPGTNYORNKENIEDALNQLFRNSSIKSYFSDCOVSTFRSVNRRHHTGVDLSLCPSP 660
Db 601 AOPGTNYORNKENIEDALNQLFRNSSIKSYFSDCOVSTFRSVNRRHHTGVDLSLCPSP 660
Qy 661 ARVDRAVAYEEFLRMTRNGTQLQNFLLDRSSVLDGYSNNRNEPLTGNSSADIQHSGRS 720
Db 661 ARVDRAVAYEEFLRMTRNGTQLQNFLLDRSSVLDGYSNNRNEPLTGNSSADIQHSGRS 720
Qy 721 SLEGPPEQKLISEEDLNMTGHHHHH 748
Db 721 SLEGPPEQKLISEEDLNMTGHHHHH 748

RESULT 2

US-10-687-035-2
; Sequence 2, Application US/10687035
; Publication No. US20050064518A1
; GENERAL INFORMATION:
; APPLICANT: Albione, Earl F.
; APPLICANT: Soltis, Daniel A.
; TITLE OF INVENTION: ANTIBODIES THAT BIND CELL-ASSOCIATED
; TITLE OF INVENTION: CA 125/0772P AND METHODS OF USE THEREOF
; FILE REFERENCE: 6750-214-999
; CURRENT APPLICATION NUMBER: US/10/687,035
; CURRENT FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: 60/485,986
; PRIOR FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: 60/418,828
; PRIOR FILING DATE: 2003-10-12
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 809
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CA 125/0772P 3-repeat TM
US-10-687-035-2

Query Match 99.0%; Score 3904.5; DB 5; Length 809;
Best Local Similarity 92.5%; Pred. No. 7e-309;
Matches 748; Conservative 0; Mismatches 0; Indels 61; Gaps 1;

Qy 1 AAQPARARRTKLTHRSSVSTTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFT 60
Db 1 AAQPARARRTKLTHRSSVSTTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFT 60
Qy 61 ITNLRYEENWMPGSRKENTTERRVLOGLLRPLFKNTSVGPLYSGCRLTLRLPEKDGATGV 120
Db 61 ITNLRYEENWMPGSRKENTTERRVLOGLLRPLFKNTSVGPLYSGCRLTLRLPEKDGATGV 120
Qy 121 DAICTHRPDPGCLDREQLYLELSQI THSITELGPYTLDRDLSLVNGFTHRSSVPTTST 180
Db 121 DAICTHRPDPGCLDREQLYLELSQI THSITELGPYTLDRDLSLVNGFTHRSSVPTTST 180
Qy 181 GWSEEPFTLNFTINNLRYMADMGQPGSLKFNITDNVWKHLSPFLFORSSILGARYTGCRV 240
Db 181 GWSEEPFTLNFTINNLRYMADMGQPGSLKFNITDNVWKHLSPFLFORSSILGARYTGCRV 240
Qy 241 IALRSVKNGAETRVLLCTYLOPLSGPGLPIKQVFHLSQOQTHGITRLGYSLDKDSL 300
Db 241 IALRSVKNGAETRVLLCTYLOPLSGPGLPIKQVFHLSQOQTHGITRLGYSLDKDSL 300
Qy 301 NGYNEPGDEPPTPKATTPPLSEATTAMGVHKLTLNFTISNLQYSPDMGKGSAT 360
Db 301 NGYNEPGDEPPTPKATTPPLSEATTAMGVHKLTLNFTISNLQYSPDMGKGSAT 360
Qy 361 FNSTEGVLOHLRLPFLQKSSMGPPYLGCOLISLPEKDGATGVDVTTCTHYHPDPVGLD 420
Db 361 FNSTEGVLOHLRLPFLQKSSMGPPYLGCOLISLPEKDGATGVDVTTCTHYHPDPVGLD 420

QY 421 IQQLYHLSQTHGVTQGLGPFVLDRLSLFNGVAPQNLIRGEYQINFIHVNWNLNPD 480
Db 421 IQQLYHLSQTHGVTQGLGPFVLDRLSLFNGVAPQNLIRGEYQINFIHVNWNLNPD 480
QY 481 TSSEYITLLRDIDQKVTLLKGSQQLHDTFRCLVNTLMDSVLVTKALPSSNLDPSLVE 540
Db 481 TSSEYITLLRDIDQKVTLLKGSQQLHDTFRCLVNTLMDSVLVTKALPSSNLDPSLVE 540
QY 541 QVFLDKTLNASFWLGSYQLVDIHVTEMESSYVQPTSSSTQHFIYNTLTPYSQDK 600
Db 541 QVFLDKTLNASFWLGSYQLVDIHVTEMESSYVQPTSSSTQHFIYNTLTPYSQDK 600
QY 601 AQPCTTNYQNKNIEDALNQLFRNSIKSYFSDCQVSTFRSVPNRHHTGVDSLCNPSPL 660
Db 601 AQPCTTNYQNKNIEDALNQLFRNSIKSYFSDCQVSTFRSVPNRHHTGVDSLCNPSPL 660
QY 661 ARVDRAVAYEEFLMTRNGTQNLQNTLDRSSVLVDGYSNNRNEPLTG----- 708
Db 661 ARVDRAVAYEEFLMTRNGTQNLQNTLDRSSVLVDGYSNNRNEPLTG----- 708
QY 709 -----NSADIQHSGR 719
Db 721 GLAGLLGLITCLICGLVLTTRRRKGEYNNVQQCPGYQSHLDLQNSADIQHSGR 780
QY 720 SSLEGPRFEQKLISEEDLNWHTGHHHH 748
Db 781 SSLEGPRFEQKLISEEDLNWHTGHHHH 809

RESULT 3
US-10-983-340-4
; Sequence 4, Application US/10983340
; Publication No. US20050238649A1
; GENERAL INFORMATION:
; APPLICANT: Doronina, Svetlana O.
; APPLICANT: Toki, Brian E.
; APPLICANT: Senter, Peter D.
; APPLICANT: Ebens, Allen J.
; APPLICANT: Polakis, Paul
; APPLICANT: Sliwowski, Mark X.
; APPLICANT: Spencer, Susan D.
; APPLICANT: Kline, Toni Beth
; TITLE OF INVENTION: MONOMETHYLVALINE COMPOUNDS CAPABLE OF CONJUGATION TO LIGANDS
; FILE REFERENCE: 018991-001020US
; CURRENT APPLICATION NUMBER: US/10/983,340
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: US 60/598,899
; PRIOR FILING DATE: 2004-08-04
; PRIOR APPLICATION NUMBER: US 60/557,116
; PRIOR FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: US 60/518,534
; PRIOR FILING DATE: 2003-11-06
; NUMBER OF SEQ ID NOS: 35
; SEQ ID NO 4
; LENGTH: 6995
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-983-340-4

Query Match 92.9%; Score 3665; DB 5; Length 6995;
Best Local Similarity 99.9%; Pred. No. 6.8e-288;
Matches 696; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 14 FTHRSVSTSTPGTPTVYLGASKTPASIFGPSAASHLLILPTLNTITNLRYEENWPG 73
Db 6240 FTHRSVSTSTPGTPTVYLGASKTPASIFGPSAASHLLILPTLNTITNLRYEENWPG 6299
QY 74 SRKFNTTTERVQLGLRPLFKNTSVGLYSGCRITLLRPEKGEATGVDAICTHRPDP 133
Db 6300 SRKFNTTTERVQLGLRPLFKNTSVGLYSGCRITLLRPEKGEATGVDAICTHRPDP 6359
QY 134 GLDRSOLYLELSQTHSITELGPYTLDRSLYNGFTHRSSVPTTSTGVVSEBPPTLNFT 193

Db 6360 GLDRSOLYLELSQTHSITELGPYTLDRSLYNGFTHRSSVPTTSTGVVSEBPPTLNFT 6419
QY 194 INNLRVMDMGPGSLKFNITONVMKHLSPFORSSLGARYTGCRIALRSVKNAGETR 253
Db 6420 INNLRVMDMGPGSLKFNITONVMKHLSPFORSSLGARYTGCRIALRSVKNAGETR 6479
QY 254 VDLCTYLQPLSGPLPIKQVPHLSQOQTHGTRGLPYSLDKSLYNGNEPDPBPPT 313
Db 6480 VDLCTYLQPLSGPLPIKQVPHLSQOQTHGTRGLPYSLDKSLYNGNEPDPBPPT 6539
QY 314 TRKPATTFPLPSEATTANGYHLKTLTANFTISNLOYSMDMGKGSATFNSTEGVLQHLR 373
Db 6540 TRKPATTFPLPSEATTANGYHLKTLTANFTISNLOYSMDMGKGSATFNSTEGVLQHLR 6599
QY 374 PLFQKSSMGPFYLGCOLISLRPEKGAATGVDTTCTYHDPVPGGLDIQQLYHLSQTH 433
Db 6600 PLFQKSSMGPFYLGCOLISLRPEKGAATGVDTTCTYHDPVPGGLDIQQLYHLSQTH 6659
QY 434 GVTQLGPFYVLDRLSLFNGVAPQNLIRGEYQINFIHVNWNLNPDPTSSSEYITLLRDIQ 493
Db 6660 GVTQLGPFYVLDRLSLFNGVAPQNLIRGEYQINFIHVNWNLNPDPTSSSEYITLLRDIQ 6719
QY 494 DKVTTLKGSQQLHDTFRCLVNTLMDSVLVTKALPSSNLDPSLVEQVFLDKTLNASPH 553
Db 6720 DKVTTLKGSQQLHDTFRCLVNTLMDSVLVTKALPSSNLDPSLVEQVFLDKTLNASPH 6779
QY 554 WLGSYQLVDIHVTEMESSYVQPTSSSTQHFIYNTLTPYSQDKAQPCTTNYQNK 613
Db 6780 WLGSYQLVDIHVTEMESSYVQPTSSSTQHFIYNTLTPYSQDKAQPCTTNYQNK 6839
QY 614 NIEDALNQLFRNSIKSYFSDCQVSTFRSVPNRHHTGVDSLCNPSPLARRVDRVAIYEEF 673
Db 6840 NIEDALNQLFRNSIKSYFSDCQVSTFRSVPNRHHTGVDSLCNPSPLARRVDRVAIYEEF 6899
QY 674 LRMTRNGTQNLQNTLDRSSVLVDGYSNNRNEPLTGNS 710
Db 6900 LRMTRNGTQNLQNTLDRSSVLVDGYSNNRNEPLTGNS 6936

RESULT 4
US-09-884-441-389
; Sequence 389, Application US/09884441
; Patent No. US20020119158A1
; GENERAL INFORMATION:
; APPLICANT: Algate, Paul A.
; APPLICANT: Carter, Darrick
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C7
; CURRENT APPLICATION NUMBER: US/09/884,441
; CURRENT FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 389
; LENGTH: 833
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-884-441-389

Query Match 92.9%; Score 3663; DB 3; Length 833;
Best Local Similarity 99.9%; Pred. No. 3.6e-289;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 FTHRSVSTSTPGTPTVYLGASKTPASIFGPSAASHLLILPTLNTITNLRYEENWPG 73
Db 78 FTHRSVSTSTPGTPTVYLGASKTPASIFGPSAASHLLILPTLNTITNLRYEENWPG 137
QY 74 SRKFNTTTERVQLGLRPLFKNTSVGLYSGCRITLLRPEKGEATGVDAICTHRPDP 133
Db 138 SRKFNTTTERVQLGLRPLFKNTSVGLYSGCRITLLRPEKGEATGVDAICTHRPDP 197
QY 134 GLDRSOLYLELSQTHSITELGPYTLDRSLYNGFTHRSSVPTTSTGVVSEBPPTLNFT 193

Db 198 GLDREQLYLELSQTHSITELGPTVTLDRSLYNGFTHRSSVPTTSTGVVSEBPTTLNFT 257
Qy 194 INNLRYMADMGQPSGLKFNTDNVMKHLSPFORSSLGARYTGCRRVIALRSVKNAGETR 253
Db 258 INNLRYMADMGQPSGLKFNTDNVMKHLSPFORSSLGARYTGCRRVIALRSVKNAGETR 317
Qy 254 VDLCTVQLPSGPGPLIKQVFHELSSQTHGIRLGPYSLDKDSLGLYNGYNEPDEPPT 313
Db 318 VDLCTVQLPSGPGPLIKQVFHELSSQTHGIRLGPYSLDKDSLGLYNGYNEPDEPPT 377
Qy 314 TPXPATTFPLPPLSEATTAMGYHLKTLTNFTISNLOYSPDMGKGSATFNSSTEGVLOHLR 373
Db 378 TPXPATTFPLPPLSEATTAMGYHLKTLTNFTISNLOYSPDMGKGSATFNSSTEGVLOHLR 437
Qy 374 PLFQKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVPGGLDIOQLYWELSQLTH 433
Db 438 PLFQKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVPGGLDIOQLYWELSQLTH 497
Qy 434 GVTOLGFFVLDRLSLFNGVAPQNLISIRGEYQINFIHVNWNLNPDPTSSSEYITLLRDIO 493
Db 498 GVTOLGFFVLDRLSLFNGVAPQNLISIRGEYQINFIHVNWNLNPDPTSSSEYITLLRDIO 557
Qy 494 DKVTTLKGSQQLHDTFRFCLVTLNLTWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFH 553
Db 558 DKVTTLKGSQQLHDTFRFCLVTLNLTWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFH 617
Qy 554 WLGSSTYQLVDIHVTEMESSYVQPTSSSTQHFYLNFTITNLPYSQDKAQPGTTNYQRNKR 613
Db 618 WLGSSTYQLVDIHVTEMESSYVQPTSSSTQHFYLNFTITNLPYSQDKAQPGTTNYQRNKR 677
Qy 614 NIEDALNQLFRNSSIKSYFSDCQVSTFRSPNRHHTGVDLSLNCNFSPLARRVDRVAIYEEF 673
Db 678 NIEDALNQLFRNSSIKSYFSDCQVSTFRSPNRHHTGVDLSLNCNFSPLARRVDRVAIYEEF 737
Qy 674 LRMRNGTQLQNFITLDRSSVLVDGYSNRPNEPLTGN 710
Db 738 LRMRNGTQLQNFITLDRSSVLVDGYSNRPNEPLTGN 774

RESULT 5

US-09-907-969-389

; Sequence 389, Application US/09907969

; Publication No. US20030091580A1

; GENERAL INFORMATION:

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: King, Gordon E.

; APPLICANT: Algate, Paul A.

; APPLICANT: Fling, Steven P.

; APPLICANT: Retter, Marc W.

; APPLICANT: Fanger, Gary Richard

; APPLICANT: Reed, Steven G.

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Carter, Darriack

; APPLICANT: Hill, Paul

; APPLICANT: Albone, Earl

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER

; FILE REFERENCE: 210121.462C8

; CURRENT APPLICATION NUMBER: US/09/907,969

; CURRENT FILING DATE: 2001-07-17

; NUMBER OF SEQ ID NOS: 596

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 389

; LENGTH: 833

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-907-969-389

Query Match 92.9%; Score 3663; DB 3; Length 833;

Best Local Similarity 99.9%; Pred. No. 3.6e-289;

Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 78 FTHRSSVSTTSTPGTPTVYLGASKTPASIFGSAASHLLILFTLNTITNLRBYENMWPG 137
Qy 74 SRKFNTTERTVQLGLRPLFKNTSVGPLYSGCRLLTLARPEKDGATGVDALCTHRPDDTGP 133
Db 138 SRKFNTTERTVQLGLRPLFKNTSVGPLYSGCRLLTLARPEKDGATGVDALCTHRPDDTGP 197
Qy 134 GLDREQLYLELSQTHSITELGPTVTLDRSLYNGFTHRSSVPTTSTGVVSEBPTTLNFT 193
Db 198 GLDREQLYLELSQTHSITELGPTVTLDRSLYNGFTHRSSVPTTSTGVVSEBPTTLNFT 257
Qy 194 INNLRYMADMGQPSGLKFNTDNVMKHLSPFORSSLGARYTGCRRVIALRSVKNAGETR 253
Db 258 INNLRYMADMGQPSGLKFNTDNVMKHLSPFORSSLGARYTGCRRVIALRSVKNAGETR 317
Qy 254 VDLCTVQLPSGPGPLIKQVFHELSSQTHGIRLGPYSLDKDSLGLYNGYNEPDEPPT 313
Db 318 VDLCTVQLPSGPGPLIKQVFHELSSQTHGIRLGPYSLDKDSLGLYNGYNEPDEPPT 377
Qy 314 TPXPATTFPLPPLSEATTAMGYHLKTLTNFTISNLOYSPDMGKGSATFNSSTEGVLOHLR 373
Db 378 TPXPATTFPLPPLSEATTAMGYHLKTLTNFTISNLOYSPDMGKGSATFNSSTEGVLOHLR 437
Qy 374 PLFQKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVPGGLDIOQLYWELSQLTH 433
Db 438 PLFQKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVPGGLDIOQLYWELSQLTH 497
Qy 434 GVTOLGFFVLDRLSLFNGVAPQNLISIRGEYQINFIHVNWNLNPDPTSSSEYITLLRDIO 493
Db 498 GVTOLGFFVLDRLSLFNGVAPQNLISIRGEYQINFIHVNWNLNPDPTSSSEYITLLRDIO 557
Qy 494 DKVTTLKGSQQLHDTFRFCLVTLNLTWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFH 553
Db 558 DKVTTLKGSQQLHDTFRFCLVTLNLTWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFH 617
Qy 554 WLGSSTYQLVDIHVTEMESSYVQPTSSSTQHFYLNFTITNLPYSQDKAQPGTTNYQRNKR 613
Db 618 WLGSSTYQLVDIHVTEMESSYVQPTSSSTQHFYLNFTITNLPYSQDKAQPGTTNYQRNKR 677
Qy 614 NIEDALNQLFRNSSIKSYFSDCQVSTFRSPNRHHTGVDLSLNCNFSPLARRVDRVAIYEEF 673
Db 678 NIEDALNQLFRNSSIKSYFSDCQVSTFRSPNRHHTGVDLSLNCNFSPLARRVDRVAIYEEF 737
Qy 674 LRMRNGTQLQNFITLDRSSVLVDGYSNRPNEPLTGN 710
Db 738 LRMRNGTQLQNFITLDRSSVLVDGYSNRPNEPLTGN 774

RESULT 6

US-09-827-271-389

; Sequence 389, Application US/09827271

; Publication No. US20030165504A1

; GENERAL INFORMATION:

; APPLICANT: Retter, Marc W.

; APPLICANT: Fanger, Gary R.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER

; FILE REFERENCE: 210121.462C6

; CURRENT APPLICATION NUMBER: US/09/827,271

; CURRENT FILING DATE: 2001-04-04

; NUMBER OF SEQ ID NOS: 461

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 389

; LENGTH: 833

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-827-271-389

Query Match 92.9%; Score 3663; DB 3; Length 833;

Best Local Similarity 99.9%; Pred. No. 3.6e-289;

Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 14 FTHRSSVSTTSTPGTPTVYLGASKTPASIFGSAASHLLILFTLNTITNLRBYENMWPG 73

Db 78 FTHRSSVTTSTPGTPTVYLKASCTPASIFGSAASHLLILFTLNFTITNLRYEENWPG 137
 Qy 74 SRKFNTERVLOGLRLRPLFKNTSVGPLYSGCRLTLRPEKDGATGVDALCTHRPDPGP 133
 Db 138 SRKFNTERVLOGLRLRPLFKNTSVGPLYSGCRLTLRPEKDGATGVDALCTHRPDPGP 197
 Qy 134 GLDREQLYLELSQTHSITELGPTTLDROSLYNGFTHRSSVPTTSTGVVSEBPTLNFT 193
 Db 198 GLDREQLYLELSQTHSITELGPTTLDROSLYNGFTHRSSVPTTSTGVVSEBPTLNFT 257
 Qy 194 INNLRYMADMGQPSGLKFNITDNVMKHLSPFORSSLGARYTGCRRVIALRSVKNAGETR 253
 Db 258 INNLRYMADMGQPSGLKFNITDNVMKHLSPFORSSLGARYTGCRRVIALRSVKNAGETR 317
 Qy 254 VDLCTYLOLPSGGLPIKQVPHLSQTHGIRLGPYSLDKOSLYLNGVNEBPDPPPT 313
 Db 318 VDLCTYLOLPSGGLPIKQVPHLSQTHGIRLGPYSLDKOSLYLNGVNEBPDPPPT 377
 Qy 314 TPKPATTPLPPLSEATTAMGYHLKTLTTLNFTISNLOYSPDMGKGSATFNSSTEGVLQHLR 373
 Db 378 TPKPATTPLPPLSEATTAMGYHLKTLTTLNFTISNLOYSPDMGKGSATFNSSTEGVLQHLR 437
 Qy 374 PLQKSSMGPFYLGCOLISLRPEKDGATGVDCTTCTHYDPVPGGLDIOQLYWELSQLTH 433
 Db 438 PLQKSSMGPFYLGCOLISLRPEKDGATGVDCTTCTHYDPVPGGLDIOQLYWELSQLTH 497
 Qy 434 GVTOLGFVLDROSLFINGVAPONLSIRGEYQINFIHVNWNLNPNPDTSEYITLLRDIO 493
 Db 498 GVTOLGFVLDROSLFINGVAPONLSIRGEYQINFIHVNWNLNPNPDTSEYITLLRDIO 557
 Qy 494 DKVTLLYKGSQLDHTRFCLVNTLWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFH 553
 Db 558 DKVTLLYKGSQLDHTRFCLVNTLWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFH 617
 Qy 554 WLGSSTYQLVDIHVTMESSYQPTSSSTQHFYLNFTITNLPYSQDKAOPGTTNYQRNKR 613
 Db 618 WLGSSTYQLVDIHVTMESSYQPTSSSTQHFYLNFTITNLPYSQDKAOPGTTNYQRNKR 677
 Qy 614 NIEDALNQLFRNSIKSYFSDCOVSTFRSPNRRHTGVDSLCNFSPPLARRVDRVAIYEEF 673
 Db 678 NIEDALNQLFRNSIKSYFSDCOVSTFRSPNRRHTGVDSLCNFSPPLARRVDRVAIYEEF 737
 Qy 674 LRMRNGTQLOQNFTRDRSSVLVDGYSNRPNEPLTGN 710
 Db 738 LRMRNGTQLOQNFTRDRSSVLVDGYSNRPNEPLTGN 774

RESULT 7

US-10-198-053-389
 ; Sequence 389, Application US/10198053
 ; Publication No. US20030124140A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bangur, Chaitanya S.
 ; APPLICANT: Retter, Marc W.
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Hill, Paul
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
 ; FILE REFERENCE: 210121.462C9
 ; CURRENT APPLICATION NUMBER: US/10/198,053
 ; CURRENT FILING DATE: 2002-07-17
 ; NUMBER OF SEQ ID NOS: 624
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 389
 ; LENGTH: 833
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-198-053-389

Query Match 92.9%; Score 3663; DB 4; Length 833;
 Best Local Similarity 99.9%; Pred. No. 3.6e-289;
 Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 14 FTHRSSVTTSTPGTPTVYLKASCTPASIFGSAASHLLILFTLNFTITNLRYEENWPG 73
 Db 78 FTHRSSVTTSTPGTPTVYLKASCTPASIFGSAASHLLILFTLNFTITNLRYEENWPG 137
 Qy 74 SRKFNTERVLOGLRLRPLFKNTSVGPLYSGCRLTLRPEKDGATGVDALCTHRPDPGP 133
 Db 138 SRKFNTERVLOGLRLRPLFKNTSVGPLYSGCRLTLRPEKDGATGVDALCTHRPDPGP 197
 Qy 134 GLDREQLYLELSQTHSITELGPTTLDROSLYNGFTHRSSVPTTSTGVVSEBPTLNFT 193
 Db 198 GLDREQLYLELSQTHSITELGPTTLDROSLYNGFTHRSSVPTTSTGVVSEBPTLNFT 257
 Qy 194 INNLRYMADMGQPSGLKFNITDNVMKHLSPFORSSLGARYTGCRRVIALRSVKNAGETR 253
 Db 258 INNLRYMADMGQPSGLKFNITDNVMKHLSPFORSSLGARYTGCRRVIALRSVKNAGETR 317
 Qy 254 VDLCTYLOLPSGGLPIKQVPHLSQTHGIRLGPYSLDKOSLYLNGVNEBPDPPPT 313
 Db 318 VDLCTYLOLPSGGLPIKQVPHLSQTHGIRLGPYSLDKOSLYLNGVNEBPDPPPT 377
 Qy 314 TPKPATTPLPPLSEATTAMGYHLKTLTTLNFTISNLOYSPDMGKGSATFNSSTEGVLQHLR 373
 Db 378 TPKPATTPLPPLSEATTAMGYHLKTLTTLNFTISNLOYSPDMGKGSATFNSSTEGVLQHLR 437
 Qy 374 PLQKSSMGPFYLGCOLISLRPEKDGATGVDCTTCTHYDPVPGGLDIOQLYWELSQLTH 433
 Db 438 PLQKSSMGPFYLGCOLISLRPEKDGATGVDCTTCTHYDPVPGGLDIOQLYWELSQLTH 497
 Qy 434 GVTOLGFVLDROSLFINGVAPONLSIRGEYQINFIHVNWNLNPNPDTSEYITLLRDIO 493
 Db 498 GVTOLGFVLDROSLFINGVAPONLSIRGEYQINFIHVNWNLNPNPDTSEYITLLRDIO 557
 Qy 494 DKVTLLYKGSQLDHTRFCLVNTLWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFH 553
 Db 558 DKVTLLYKGSQLDHTRFCLVNTLWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFH 617
 Qy 554 WLGSSTYQLVDIHVTMESSYQPTSSSTQHFYLNFTITNLPYSQDKAOPGTTNYQRNKR 613
 Db 618 WLGSSTYQLVDIHVTMESSYQPTSSSTQHFYLNFTITNLPYSQDKAOPGTTNYQRNKR 677
 Qy 614 NIEDALNQLFRNSIKSYFSDCOVSTFRSPNRRHTGVDSLCNFSPPLARRVDRVAIYEEF 673
 Db 678 NIEDALNQLFRNSIKSYFSDCOVSTFRSPNRRHTGVDSLCNFSPPLARRVDRVAIYEEF 737
 Qy 674 LRMRNGTQLOQNFTRDRSSVLVDGYSNRPNEPLTGN 710
 Db 738 LRMRNGTQLOQNFTRDRSSVLVDGYSNRPNEPLTGN 774

RESULT 8

US-10-860-790-389
 ; Sequence 389, Application US/10860790
 ; Publication No. US20050031634A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bangur, Chaitanya S.
 ; APPLICANT: Retter, Marc W.
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Hill, Paul
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
 ; FILE REFERENCE: 210121.462C11
 ; CURRENT APPLICATION NUMBER: US/10/860,790
 ; CURRENT FILING DATE: 2004-06-02
 ; NUMBER OF SEQ ID NOS: 624
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 389
 ; LENGTH: 833
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-860-790-389

Query Match 92.9%; Score 3663; DB 5; Length 833;

Best Local Similarity 99.9%; Pred. No. 3.6e-289; Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 14 FTHRSSVSTSTGCTPTVYLGASKTPASIFGSAASHLLILFTLNFTITNLRVEENWPG 73
Db 78 FTHRSSVSTSTGCTPTVYLGASKTPASIFGSAASHLLILFTLNFTITNLRVEENWPG 137
Qy 74 SRKFNTERVLOGLLRPLFKNTSVGLYSGCRLLTLLRPEKDGATGDAICTHRPDPTGP 133
Db 138 SRKFNTERVLOGLLRPLFKNTSVGLYSGCRLLTLLRPEKDGATGDAICTHRPDPTGP 197
Qy 134 GLDREQLYLELSQTHSITELGPTTLDRLSYNGFTHRSSVPTTSTGVVSEEPFTLNFT 193
Db 198 GLDREQLYLELSQTHSITELGPTTLDRLSYNGFTHRSSVPTTSTGVVSEEPFTLNFT 257
Qy 194 INNLRYMADMGQPSGLKFNITDNVMKHLSPFORSLGARYTGCRIALRSVKNAGETR 253
Db 258 INNLRYMADMGQPSGLKFNITDNVMKHLSPFORSLGARYTGCRIALRSVKNAGETR 317
Qy 254 VDLICTYLOPLSGPLPIKQVFHELSSQTHGITRLGYSLDKDSLYLNGYNEPDEPPT 313
Db 318 VDLICTYLOPLSGPLPIKQVFHELSSQTHGITRLGYSLDKDSLYLNGYNEPDEPPT 377
Qy 314 TPKEPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLOHLLR 373
Db 378 TPKEPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLOHLLR 437
Qy 374 PLFQKSSMGPFYLGCOLISLRPEKDGATGVDTTCTTHPDPVPGGLDIQQLYWELSQLTH 433
Db 438 PLFQKSSMGPFYLGCOLISLRPEKDGATGVDTTCTTHPDPVPGGLDIQQLYWELSQLTH 497
Qy 434 GVTOLGFVLDRLSLFINGYAPQNLISIRGEYQINFIHVNWNLSPDPTSESSEYITLLRDIQ 493
Db 498 GVTOLGFVLDRLSLFINGYAPQNLISIRGEYQINFIHVNWNLSPDPTSESSEYITLLRDIQ 557
Qy 494 DKVTTLKGSQQLHDTFRFCLVTNLTMDSVLVTKALFSSNLDPSLVQVFLDKTLNASFH 553
Db 558 DKVTTLKGSQQLHDTFRFCLVTNLTMDSVLVTKALFSSNLDPSLVQVFLDKTLNASFH 617
Qy 554 WLGSTYQLVDIHVTEMESVYQPTSSSTQHFYLNFTITNLPYSQDKAQPGTTNYQRNKR 613
Db 618 WLGSTYQLVDIHVTEMESVYQPTSSSTQHFYLNFTITNLPYSQDKAQPGTTNYQRNKR 677
Qy 614 NIEDALNQLFRNSSIKSYFSDCQVSTFRSPVNRHHTGVDLSLGNFPLARRVDRVAIYEEF 673
Db 678 NIEDALNQLFRNSSIKSYFSDCQVSTFRSPVNRHHTGVDLSLGNFPLARRVDRVAIYEEF 737
Qy 674 LRMTNRGTQLQNFTLDRSSVLVDGYFPNREPLTGN 710
Db 738 LRMTNRGTQLQNFTLDRSSVLVDGYFPNREPLTGN 774

RESULT 9
US-09-778-320-206
; Sequence 206, Application US/09778320
; Patent No. US20010034052A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Day, Craig H.
; APPLICANT: Jiang, Yugu
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Wang, Tongtong
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.491C5
; CURRENT APPLICATION NUMBER: US/09/778,320
; CURRENT FILING DATE: 2001-02-06
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 206
; LENGTH: 914

; TYPE: PRT
; ORGANISM: Homo sapien
US-09-778-320-206

Query Match 92.9%; Score 3663; DB 3; Length 914;
Best Local Similarity 99.9%; Pred. No. 4.2e-289;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 14 FTHRSSVSTSTGCTPTVYLGASKTPASIFGSAASHLLILFTLNFTITNLRVEENWPG 73
Db 159 FTHRSSVSTSTGCTPTVYLGASKTPASIFGSAASHLLILFTLNFTITNLRVEENWPG 218
Qy 74 SRKFNTERVLOGLLRPLFKNTSVGLYSGCRLLTLLRPEKDGATGDAICTHRPDPTGP 133
Db 219 SRKFNTERVLOGLLRPLFKNTSVGLYSGCRLLTLLRPEKDGATGDAICTHRPDPTGP 278
Qy 134 GLDREQLYLELSQTHSITELGPTTLDRLSYNGFTHRSSVPTTSTGVVSEEPFTLNFT 193
Db 279 GLDREQLYLELSQTHSITELGPTTLDRLSYNGFTHRSSVPTTSTGVVSEEPFTLNFT 338
Qy 194 INNLRYMADMGQPSGLKFNITDNVMKHLSPFORSLGARYTGCRIALRSVKNAGETR 253
Db 339 INNLRYMADMGQPSGLKFNITDNVMKHLSPFORSLGARYTGCRIALRSVKNAGETR 398
Qy 254 VDLICTYLOPLSGPLPIKQVFHELSSQTHGITRLGYSLDKDSLYLNGYNEPDEPPT 313
Db 399 VDLICTYLOPLSGPLPIKQVFHELSSQTHGITRLGYSLDKDSLYLNGYNEPDEPPT 458
Qy 314 TPKEPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLOHLLR 373
Db 459 TPKEPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLOHLLR 518
Qy 374 PLFQKSSMGPFYLGCOLISLRPEKDGATGVDTTCTTHPDPVPGGLDIQQLYWELSQLTH 433
Db 519 PLFQKSSMGPFYLGCOLISLRPEKDGATGVDTTCTTHPDPVPGGLDIQQLYWELSQLTH 578
Qy 434 GVTOLGFVLDRLSLFINGYAPQNLISIRGEYQINFIHVNWNLSPDPTSESSEYITLLRDIQ 493
Db 579 GVTOLGFVLDRLSLFINGYAPQNLISIRGEYQINFIHVNWNLSPDPTSESSEYITLLRDIQ 638
Qy 494 DKVTTLKGSQQLHDTFRFCLVTNLTMDSVLVTKALFSSNLDPSLVQVFLDKTLNASFH 553
Db 639 DKVTTLKGSQQLHDTFRFCLVTNLTMDSVLVTKALFSSNLDPSLVQVFLDKTLNASFH 698
Qy 554 WLGSTYQLVDIHVTEMESVYQPTSSSTQHFYLNFTITNLPYSQDKAQPGTTNYQRNKR 613
Db 699 WLGSTYQLVDIHVTEMESVYQPTSSSTQHFYLNFTITNLPYSQDKAQPGTTNYQRNKR 758
Qy 614 NIEDALNQLFRNSSIKSYFSDCQVSTFRSPVNRHHTGVDLSLGNFPLARRVDRVAIYEEF 673
Db 759 NIEDALNQLFRNSSIKSYFSDCQVSTFRSPVNRHHTGVDLSLGNFPLARRVDRVAIYEEF 818
Qy 674 LRMTNRGTQLQNFTLDRSSVLVDGYFPNREPLTGN 710
Db 819 LRMTNRGTQLQNFTLDRSSVLVDGYFPNREPLTGN 855

RESULT 10
US-09-910-689-206
; Sequence 206, Application US/09910689
; Patent No. US20020081609A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Day, Craig H.
; APPLICANT: Jiang, Yugu
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Wang, Tongtong
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.491C6

; CURRENT APPLICATION NUMBER: US/09/910,689
; CURRENT FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 307
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 206
; LENGTH: 914
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-910-689-206

Query Match 92.9%; Score 3663; DB 3; Length 914;
Best Local Similarity 99.9%; Pred. No. 4.2e-289;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	14	FTHRSSVSTTSGTPTVYLGASKTPASIFGSAASHLLILFTLNFTITNLRYYENWMPG	73
DB	159	FTHRSSVSTTSGTPTVYLGASKTPASIFGSAASHLLILFTLNFTITNLRYYENWMPG	218
QY	74	SRKFNTERVLOGLLRPLFKNTSVGLYSGCRLLTLRPEKDGATGVDAICTHRPDPGTP	133
DB	219	SRKFNTERVLOGLLRPLFKNTSVGLYSGCRLLTLRPEKDGATGVDAICTHRPDPGTP	278
QY	134	GLDREQLYLELSQTHSITELGPTTLDRDSLYVNGFTHRSSVPTTSTGVVSEBEPFTLNFT	193
DB	279	GLDREQLYLELSQTHSITELGPTTLDRDSLYVNGFTHRSSVPTTSTGVVSEBEPFTLNFT	338
QY	194	INNLRVMDMGQPSLKFNTIDNMKHLSPLFQSSLGARYTGCRIALRSVKNAGETR	253
DB	339	INNLRVMDMGQPSLKFNTIDNMKHLSPLFQSSLGARYTGCRIALRSVKNAGETR	398
QY	254	VDLLCTYQLPSGGLPIKQVFHELSQOHTGITRLGPYSLDKDSLNGYNEBEPDEPPT	313
DB	399	VDLLCTYQLPSGGLPIKQVFHELSQOHTGITRLGPYSLDKDSLNGYNEBEPDEPPT	458
QY	314	TPKPATTFPLPSEATTAMGYHLKTLTLNFTISNLOYSMDMGKGSATFSTEGVLOHLLR	373
DB	459	TPKPATTFPLPSEATTAMGYHLKTLTLNFTISNLOYSMDMGKGSATFSTEGVLOHLLR	518
QY	374	PLFQKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVGPGLDIOQLYWELSQLTH	433
DB	519	PLFQKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVGPGLDIOQLYWELSQLTH	578
QY	434	GVTLQGFYVLDRLDSLPINGYAPQNLISIRGEYQINFIHVNMLSNPDPSTSEYITLLRDIQ	493
DB	579	GVTLQGFYVLDRLDSLPINGYAPQNLISIRGEYQINFIHVNMLSNPDPSTSEYITLLRDIQ	638
QY	494	DKVTTLKGSQSLDHTFRFCLVTLNLTWDSVLVTVKALFSSNLDPSLYEQVFLDKTLNASFH	553
DB	639	DKVTTLKGSQSLDHTFRFCLVTLNLTWDSVLVTVKALFSSNLDPSLYEQVFLDKTLNASFH	698
QY	554	WLGSTYQLVDIHVTMESSVYQPTSSSTQHFYLNFTITNLPYSQDKAOPGTINYORNR	613
DB	699	WLGSTYQLVDIHVTMESSVYQPTSSSTQHFYLNFTITNLPYSQDKAOPGTINYORNR	758
QY	614	NIEDALNQLFRNSSIKSYFSDCQVSTFRSPVNRHHTGVDSLNCNFSPLARRVDRVAIYEEF	673
DB	759	NIEDALNQLFRNSSIKSYFSDCQVSTFRSPVNRHHTGVDSLNCNFSPLARRVDRVAIYEEF	818
QY	674	LRMTRNGTOLQNFTRDSSVLVDGYSPNRNEPLTGNS	710
DB	819	LRMTRNGTOLQNFTRDSSVLVDGYSPNRNEPLTGNS	855

RESULT 11
US-09-884-441-312
; Sequence 312, Application US/09884441
; Patent No. US20020119158A1
; GENERAL INFORMATION:
; APPLICANT: Algate, Paul A.
; APPLICANT: Carter, Darrick
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C7

; CURRENT APPLICATION NUMBER: US/09/884,441.
; CURRENT FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 312
; LENGTH: 914
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-884-441-312

Query Match 92.9%; Score 3663; DB 3; Length 914;
Best Local Similarity 99.9%; Pred. No. 4.2e-289;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	14	FTHRSSVSTTSGTPTVYLGASKTPASIFGSAASHLLILFTLNFTITNLRYYENWMPG	73
DB	159	FTHRSSVSTTSGTPTVYLGASKTPASIFGSAASHLLILFTLNFTITNLRYYENWMPG	218
QY	74	SRKFNTERVLOGLLRPLFKNTSVGLYSGCRLLTLRPEKDGATGVDAICTHRPDPGTP	133
DB	219	SRKFNTERVLOGLLRPLFKNTSVGLYSGCRLLTLRPEKDGATGVDAICTHRPDPGTP	278
QY	134	GLDREQLYLELSQTHSITELGPTTLDRDSLYVNGFTHRSSVPTTSTGVVSEBEPFTLNFT	193
DB	279	GLDREQLYLELSQTHSITELGPTTLDRDSLYVNGFTHRSSVPTTSTGVVSEBEPFTLNFT	338
QY	194	INNLRVMDMGQPSLKFNTIDNMKHLSPLFQSSLGARYTGCRIALRSVKNAGETR	253
DB	339	INNLRVMDMGQPSLKFNTIDNMKHLSPLFQSSLGARYTGCRIALRSVKNAGETR	398
QY	254	VDLLCTYQLPSGGLPIKQVFHELSQOHTGITRLGPYSLDKDSLNGYNEBEPDEPPT	313
DB	399	VDLLCTYQLPSGGLPIKQVFHELSQOHTGITRLGPYSLDKDSLNGYNEBEPDEPPT	458
QY	314	TPKPATTFPLPSEATTAMGYHLKTLTLNFTISNLOYSMDMGKGSATFSTEGVLOHLLR	373
DB	459	TPKPATTFPLPSEATTAMGYHLKTLTLNFTISNLOYSMDMGKGSATFSTEGVLOHLLR	518
QY	374	PLFQKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVGPGLDIOQLYWELSQLTH	433
DB	519	PLFQKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVGPGLDIOQLYWELSQLTH	578
QY	434	GVTLQGFYVLDRLDSLPINGYAPQNLISIRGEYQINFIHVNMLSNPDPSTSEYITLLRDIQ	493
DB	579	GVTLQGFYVLDRLDSLPINGYAPQNLISIRGEYQINFIHVNMLSNPDPSTSEYITLLRDIQ	638
QY	494	DKVTTLKGSQSLDHTFRFCLVTLNLTWDSVLVTVKALFSSNLDPSLYEQVFLDKTLNASFH	553
DB	639	DKVTTLKGSQSLDHTFRFCLVTLNLTWDSVLVTVKALFSSNLDPSLYEQVFLDKTLNASFH	698
QY	554	WLGSTYQLVDIHVTMESSVYQPTSSSTQHFYLNFTITNLPYSQDKAOPGTINYORNR	613
DB	699	WLGSTYQLVDIHVTMESSVYQPTSSSTQHFYLNFTITNLPYSQDKAOPGTINYORNR	758
QY	614	NIEDALNQLFRNSSIKSYFSDCQVSTFRSPVNRHHTGVDSLNCNFSPLARRVDRVAIYEEF	673
DB	759	NIEDALNQLFRNSSIKSYFSDCQVSTFRSPVNRHHTGVDSLNCNFSPLARRVDRVAIYEEF	818
QY	674	LRMTRNGTOLQNFTRDSSVLVDGYSPNRNEPLTGNS	710
DB	819	LRMTRNGTOLQNFTRDSSVLVDGYSPNRNEPLTGNS	855

RESULT 12
US-09-884-441-478
; Sequence 478, Application US/09884441
; Patent No. US20020119158A1
; GENERAL INFORMATION:
; APPLICANT: Algate, Paul A.
; APPLICANT: Carter, Darrick
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C7

; CURRENT APPLICATION NUMBER: US/09/884,441
; CURRENT FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 478
; LENGTH: 914
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-884-441-478

Query Match 92.9%; Score 3663; DB 3; Length 914;
Best Local Similarity 99.9%; Pred. No. 4.2e-289;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
QY 14 FTHRSSVSTTSTGCTPTVYLGASKTPASIFGPSAASHLLILFTLFTITNLRYEENWMPG 73
DB 159 FTHRSSVSTTSTGCTPTVYLGASKTPASIFGPSAASHLLILFTLFTITNLRYEENWMPG 218

QY 74 SRKFNTERVLOGLLRPLFKNTSVGLYSGCRLTLRPEKDGATGVDAICTHRPDPDTPG 133
DB 219 SRKFNTERVLOGLLRPLFKNTSVGLYSGCRLTLRPEKDGATGVDAICTHRPDPDTPG 278

QY 134 GLDREQLYLELSQTHSITELGPTVTLDRDSLRYNGFTHRSSVPTTSTGVVSEEPFTLNFT 193
DB 279 GLDREQLYLELSQTHSITELGPTVTLDRDSLRYNGFTHRSSVPTTSTGVVSEEPFTLNFT 338

QY 194 INNLRYMADMGQPSLAKFNITDNVMKHLSPFORSSIGARYTCRVIARSVKNAGETR 253
DB 339 INNLRYMADMGQPSLAKFNITDNVMKHLSPFORSSIGARYTCRVIARSVKNAGETR 398

QY 254 VDLICTVLOPLSGPLPIKOVFHELQOOTHGIFRLGYSKDLKSLYNGYNEPDPDPPT 313
DB 399 VDLICTVLOPLSGPLPIKOVFHELQOOTHGIFRLGYSKDLKSLYNGYNEPDPDPPT 458

QY 314 TPKPATTFLLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLOHLR 373
DB 459 TPKPATTFLLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLOHLR 518

QY 374 PLFOKSSMGPFYLGCOLISLRPEKDGATGVDTTCTTHPDVPGGLDIQOLYWELSQTH 433
DB 519 PLFOKSSMGPFYLGCOLISLRPEKDGATGVDTTCTTHPDVPGGLDIQOLYWELSQTH 578

QY 434 GVTOLGPFVLDRLDSLFIINGAPQNLSIRGEYQINFIHVNWNLNPNPDTSESSEYITLLRDIO 493
DB 579 GVTOLGPFVLDRLDSLFIINGAPQNLSIRGEYQINFIHVNWNLNPNPDTSESSEYITLLRDIO 638

QY 494 DKVTTLKGSQQLHDTFRCLVTNLTMDSVLVTKALFSSNLDPSLVQVFLDKTINASFH 553
DB 639 DKVTTLKGSQQLHDTFRCLVTNLTMDSVLVTKALFSSNLDPSLVQVFLDKTINASFH 698

QY 554 WLGSYQLVDIHVTEMESSEYVQPTSSSTQHFYLNFTITNLPSQDKAQPGTTNYQRNKR 613
DB 699 WLGSYQLVDIHVTEMESSEYVQPTSSSTQHFYLNFTITNLPSQDKAQPGTTNYQRNKR 758

QY 614 NIEDALNQLFRNSIKSYFSDCVSTFRSPVNRHHTGVDSLNCNFSPLARRVDRVAIYEEF 673
DB 759 NIEDALNQLFRNSIKSYFSDCVSTFRSPVNRHHTGVDSLNCNFSPLARRVDRVAIYEEF 818

QY 674 LRMTNRGTQLQNFTLDRSSVLVDGYSNPNRNEPLTGN 710
DB 819 LRMTNRGTQLQNFTLDRSSVLVDGYSNPNRNEPLTGN 855
```

RESULT 13

US-09-907-969-312
; Sequence 312, Application US/09907969
; Publication No. US20030091580A1
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; APPLICANT: Retter, Marc W.

; APPLICANT: Fanger, Gary Richard
; APPLICANT: Reed, Steven G.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Hill, Paul
; APPLICANT: Albone, Earl
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.462C8
; CURRENT APPLICATION NUMBER: US/09/907,969
; CURRENT FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 596
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 312
; LENGTH: 914
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-907-969-312

Query Match 92.9%; Score 3663; DB 3; Length 914;
Best Local Similarity 99.9%; Pred. No. 4.2e-289;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
QY 14 FTHRSSVSTTSTGCTPTVYLGASKTPASIFGPSAASHLLILFTLFTITNLRYEENWMPG 73
DB 159 FTHRSSVSTTSTGCTPTVYLGASKTPASIFGPSAASHLLILFTLFTITNLRYEENWMPG 218

QY 74 SRKFNTERVLOGLLRPLFKNTSVGLYSGCRLTLRPEKDGATGVDAICTHRPDPDTPG 133
DB 219 SRKFNTERVLOGLLRPLFKNTSVGLYSGCRLTLRPEKDGATGVDAICTHRPDPDTPG 278

QY 134 GLDREQLYLELSQTHSITELGPTVTLDRDSLRYNGFTHRSSVPTTSTGVVSEEPFTLNFT 193
DB 279 GLDREQLYLELSQTHSITELGPTVTLDRDSLRYNGFTHRSSVPTTSTGVVSEEPFTLNFT 338

QY 194 INNLRYMADMGQPSLAKFNITDNVMKHLSPFORSSIGARYTCRVIARSVKNAGETR 253
DB 339 INNLRYMADMGQPSLAKFNITDNVMKHLSPFORSSIGARYTCRVIARSVKNAGETR 398

QY 254 VDLICTVLOPLSGPLPIKOVFHELQOOTHGIFRLGYSKDLKSLYNGYNEPDPDPPT 313
DB 399 VDLICTVLOPLSGPLPIKOVFHELQOOTHGIFRLGYSKDLKSLYNGYNEPDPDPPT 458

QY 314 TPKPATTFLLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLOHLR 373
DB 459 TPKPATTFLLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLOHLR 518

QY 374 PLFOKSSMGPFYLGCOLISLRPEKDGATGVDTTCTTHPDVPGGLDIQOLYWELSQTH 433
DB 519 PLFOKSSMGPFYLGCOLISLRPEKDGATGVDTTCTTHPDVPGGLDIQOLYWELSQTH 578

QY 434 GVTOLGPFVLDRLDSLFIINGAPQNLSIRGEYQINFIHVNWNLNPNPDTSESSEYITLLRDIO 493
DB 579 GVTOLGPFVLDRLDSLFIINGAPQNLSIRGEYQINFIHVNWNLNPNPDTSESSEYITLLRDIO 638

QY 494 DKVTTLKGSQQLHDTFRCLVTNLTMDSVLVTKALFSSNLDPSLVQVFLDKTINASFH 553
DB 639 DKVTTLKGSQQLHDTFRCLVTNLTMDSVLVTKALFSSNLDPSLVQVFLDKTINASFH 698

QY 554 WLGSYQLVDIHVTEMESSEYVQPTSSSTQHFYLNFTITNLPSQDKAQPGTTNYQRNKR 613
DB 699 WLGSYQLVDIHVTEMESSEYVQPTSSSTQHFYLNFTITNLPSQDKAQPGTTNYQRNKR 758

QY 614 NIEDALNQLFRNSIKSYFSDCVSTFRSPVNRHHTGVDSLNCNFSPLARRVDRVAIYEEF 673
DB 759 NIEDALNQLFRNSIKSYFSDCVSTFRSPVNRHHTGVDSLNCNFSPLARRVDRVAIYEEF 818

QY 674 LRMTNRGTQLQNFTLDRSSVLVDGYSNPNRNEPLTGN 710
DB 819 LRMTNRGTQLQNFTLDRSSVLVDGYSNPNRNEPLTGN 855
```

RESULT 14

US-09-907-969-478
; Sequence 478, Application US/09907969
; Publication No. US20030091580A1
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary Richard
; APPLICANT: Reed, Steven G.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Hill, Paul
; APPLICANT: Albane, Earl
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C8
; CURRENT APPLICATION NUMBER: US/09/907,969
; CURRENT FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 596
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 478
; LENGTH: 914
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-907-969-478

Query Match 92.9%; Score 3663; DB 3; Length 914;
Best Local Similarity 99.9%; Pred. No. 4.2e-289;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	14	FTHRSSVSTTSGTPTVYLGSKTPTASIFGSAASHLLILFTLNFTITNLRYEENWPG	73
DB	159	FTHRSSVSTTSGTPTVYLGSKTPTASIFGSAASHLLILFTLNFTITNLRYEENWPG	218
QY	74	SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRITLLRPEKDGATGVDAICTHRPDPTGP	133
DB	219	SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRITLLRPEKDGATGVDAICTHRPDPTGP	278
QY	134	GLDREQLYLELSQTHSITELGPTVTLDRDSLYNGFTHRSSVPTTSTGVVSEBPTLNFT	193
DB	279	GLDREQLYLELSQTHSITELGPTVTLDRDSLYNGFTHRSSVPTTSTGVVSEBPTLNFT	338
QY	194	INNLRVMADMGQSGSLKFNTIDNMVHLLSPLFORSSLGARYTGCRIALRSVKNGAETR	253
DB	339	INNLRVMADMGQSGSLKFNTIDNMVHLLSPLFORSSLGARYTGCRIALRSVKNGAETR	398
QY	254	VDLLCTYLQPLSGPLPIKQVFHELSSQTHGITRLGYSLDKDSLYLNGYNEBGPDEPPT	313
DB	399	VDLLCTYLQPLSGPLPIKQVFHELSSQTHGITRLGYSLDKDSLYLNGYNEBGPDEPPT	458
QY	314	TPKPATTFPLPPLSEATTAMGYHLKTLTNFTISNLOQSPDMGKSATFNSTEGVLOHLR	373
DB	459	TPKPATTFPLPPLSEATTAMGYHLKTLTNFTISNLOQSPDMGKSATFNSTEGVLOHLR	518
QY	374	PLFQKSMGPFYLGCOLISLRPEKOGAATGVDTTCTTHPDVPVPGGLDIOQLYWELSQLTH	433
DB	519	PLFQKSMGPFYLGCOLISLRPEKOGAATGVDTTCTTHPDVPVPGGLDIOQLYWELSQLTH	578
QY	434	GVTLQGFYVLDRLDPLFNGVAPQNLISIRGEYQINFIHNVNWLNSNPDPSTSEYITLLRDIQ	493
DB	579	GVTLQGFYVLDRLDPLFNGVAPQNLISIRGEYQINFIHNVNWLNSNPDPSTSEYITLLRDIQ	638
QY	494	DKVTTLKGSQLDHTRFCLVTLNMTDMSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFH	553
DB	639	DKVTTLKGSQLDHTRFCLVTLNMTDMSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFH	698
QY	554	WLGSTYQLVDIHVTENESSVYQPTSSSTQHFLYFNFTITNLRYSQDKAQPGTTNYQRNKR	613
DB	699	WLGSTYQLVDIHVTENESSVYQPTSSSTQHFLYFNFTITNLRYSQDKAQPGTTNYQRNKR	758
QY	614	NIEDALNQLFRNSSIKSYFSDCQVSTFRSVPNRHTGTVDLSLNCNFSPLARRVDRVAIYEEF	673

Db 759 NIEDALNQLFRNSSIKSYFSDCQVSTFRSVPNRHTGTVDLSLNCNFSPLARRVDRVAIYEEF 818
QY 674 LRMRNGTQLOQNTFLDRSSVLDGYSPPNNEPLTGN 710
Db 819 LRMRNGTQLOQNTFLDRSSVLDGYSPPNNEPLTGN 855

RESULT 15
US-09-827-271-312
; Sequence 312, Application US/09827271
; Publication No. US20030165504A1
; GENERAL INFORMATION:
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.462C6
; CURRENT APPLICATION NUMBER: US/09/827,271
; CURRENT FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 312
; LENGTH: 914
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-827-271-312

Query Match 92.9%; Score 3663; DB 3; Length 914;
Best Local Similarity 99.9%; Pred. No. 4.2e-289;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	14	FTHRSSVSTTSGTPTVYLGSKTPTASIFGSAASHLLILFTLNFTITNLRYEENWPG	73
DB	159	FTHRSSVSTTSGTPTVYLGSKTPTASIFGSAASHLLILFTLNFTITNLRYEENWPG	218
QY	74	SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRITLLRPEKDGATGVDAICTHRPDPTGP	133
DB	219	SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRITLLRPEKDGATGVDAICTHRPDPTGP	278
QY	134	GLDREQLYLELSQTHSITELGPTVTLDRDSLYNGFTHRSSVPTTSTGVVSEBPTLNFT	193
DB	279	GLDREQLYLELSQTHSITELGPTVTLDRDSLYNGFTHRSSVPTTSTGVVSEBPTLNFT	338
QY	194	INNLRVMADMGQSGSLKFNTIDNMVHLLSPLFORSSLGARYTGCRIALRSVKNGAETR	253
DB	339	INNLRVMADMGQSGSLKFNTIDNMVHLLSPLFORSSLGARYTGCRIALRSVKNGAETR	398
QY	254	VDLLCTYLQPLSGPLPIKQVFHELSSQTHGITRLGYSLDKDSLYLNGYNEBGPDEPPT	313
DB	399	VDLLCTYLQPLSGPLPIKQVFHELSSQTHGITRLGYSLDKDSLYLNGYNEBGPDEPPT	458
QY	314	TPKPATTFPLPPLSEATTAMGYHLKTLTNFTISNLOQSPDMGKSATFNSTEGVLOHLR	373
DB	459	TPKPATTFPLPPLSEATTAMGYHLKTLTNFTISNLOQSPDMGKSATFNSTEGVLOHLR	518
QY	374	PLFQKSMGPFYLGCOLISLRPEKOGAATGVDTTCTTHPDVPVPGGLDIOQLYWELSQLTH	433
DB	519	PLFQKSMGPFYLGCOLISLRPEKOGAATGVDTTCTTHPDVPVPGGLDIOQLYWELSQLTH	578
QY	434	GVTLQGFYVLDRLDPLFNGVAPQNLISIRGEYQINFIHNVNWLNSNPDPSTSEYITLLRDIQ	493
DB	579	GVTLQGFYVLDRLDPLFNGVAPQNLISIRGEYQINFIHNVNWLNSNPDPSTSEYITLLRDIQ	638
QY	494	DKVTTLKGSQLDHTRFCLVTLNMTDMSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFH	553
DB	639	DKVTTLKGSQLDHTRFCLVTLNMTDMSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFH	698
QY	554	WLGSTYQLVDIHVTENESSVYQPTSSSTQHFLYFNFTITNLRYSQDKAQPGTTNYQRNKR	613
DB	699	WLGSTYQLVDIHVTENESSVYQPTSSSTQHFLYFNFTITNLRYSQDKAQPGTTNYQRNKR	758
QY	614	NIEDALNQLFRNSSIKSYFSDCQVSTFRSVPNRHTGTVDLSLNCNFSPLARRVDRVAIYEEF	673

```

|||||
759 NIEDALNQLFRNSSIKSYFSDCQVSIFRSVPNRHHTGVDSLNCNFSPLARVDRVAIYEEF 818
Db

674 LRMRNGTQLONFTRDRSSVLVDGYSNRPNEPLTGN 710
Qy

819 LRMRNGTQLONFTRDRSSVLVDGYSNRPNEPLTGN 855
Db

RESULT 16
US-10-010-742-206
; Sequence 206, Application US/10010742
; Publication No. US20020146727A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Day, Craig H.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Wang, Tongtong
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Bennington, Angela Ann
; APPLICANT: Zehentner, Barbara
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.491C7
; CURRENT APPLICATION NUMBER: US/10/010,742
; CURRENT FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 307
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 206
; LENGTH: 914
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-010-742-206

Query Match 92.9%; Score 3663; DB 4; Length 914;
Best Local Similarity 99.9%; Pred. No. 4.2e-289;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 14 FTHRSSVSTSTGCTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 73
Db 159 FTHRSSVSTSTGCTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 218
Qy 74 SRKFNTTERTVLQGLLRPLFKNTSVGPLYSGCRLLTLLRPEKDGATGVDAICTHRPDPTGP 133
Db 219 SRKFNTTERTVLQGLLRPLFKNTSVGPLYSGCRLLTLLRPEKDGATGVDAICTHRPDPTGP 278
Qy 134 GLDREQLYLELSQLTHTSITELGPTTLDRLDSLYNGFTHRSSVPTTSTGVVSEEPFTLNFT 193
Db 279 GLDREQLYLELSQLTHTSITELGPTTLDRLDSLYNGFTHRSSVPTTSTGVVSEEPFTLNFT 338
Qy 194 INNLRYMADMGQPSGLKFNITDNMKHLLSPLFORSSIGARYTCRCVIALRSVKNGAETR 253
Db 339 INNLRYMADMGQPSGLKFNITDNMKHLLSPLFORSSIGARYTCRCVIALRSVKNGAETR 398
Qy 254 VDLICTYQLPSGPGPLIKQVFHLSQQTHTGIRLGPYSLDKOSLYLNGYNPEGPDEPPT 313
Db 399 VDLICTYQLPSGPGPLIKQVFHLSQQTHTGIRLGPYSLDKOSLYLNGYNPEGPDEPPT 458
Qy 314 TPKPATTFPLPSLSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATFNSTEGVLOHLR 373
Db 459 TPKPATTFPLPSLSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATFNSTEGVLOHLR 518
Qy 374 PLFKSSMGPPYLGCOLISLRPEKDGATGVDTTCTVHPDPVGPGLDIQQLYWELSQTH 433
Db 519 PLFKSSMGPPYLGCOLISLRPEKDGATGVDTTCTVHPDPVGPGLDIQQLYWELSQTH 578
Qy 434 GVTQLGFVLDRLDSLFINGYAPQNLSIRGEQINFIHVNWNLNPNPDTSSSEYITLLRDIQ 493
Db 579 GVTQLGFVLDRLDSLFINGYAPQNLSIRGEQINFIHVNWNLNPNPDTSSSEYITLLRDIQ 638

```

```

Qy 494 DKVTTLVKGSQLHDTFRFCLVTNLTMDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASPH 553
Db 639 DKVTTLVKGSQLHDTFRFCLVTNLTMDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASPH 698
Qy 554 WLGSTYQLVDIHVTEMESSYQPTSSSTQHFYLNFTITNLPSYQDKAQPGTTNYQNRK 613
Db 699 WLGSTYQLVDIHVTEMESSYQPTSSSTQHFYLNFTITNLPSYQDKAQPGTTNYQNRK 758
Qy 614 NIEDALNQLFRNSSIKSYFSDCQVSIFRSVPNRHHTGVDSLNCNFSPLARVDRVAIYEEF 673
Db 759 NIEDALNQLFRNSSIKSYFSDCQVSIFRSVPNRHHTGVDSLNCNFSPLARVDRVAIYEEF 818
Qy 674 LRMRNGTQLONFTRDRSSVLVDGYSNRPNEPLTGN 710
Db 819 LRMRNGTQLONFTRDRSSVLVDGYSNRPNEPLTGN 855

RESULT 17
US-10-198-053-312
; Sequence 312, Application US/10198053
; Publication No. US20030124140A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hill, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C9
; CURRENT APPLICATION NUMBER: US/10/198,053
; CURRENT FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 624
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 312
; LENGTH: 914
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-198-053-312

Query Match 92.9%; Score 3663; DB 4; Length 914;
Best Local Similarity 99.9%; Pred. No. 4.2e-289;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 14 FTHRSSVSTSTGCTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 73
Db 159 FTHRSSVSTSTGCTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 218
Qy 74 SRKFNTTERTVLQGLLRPLFKNTSVGPLYSGCRLLTLLRPEKDGATGVDAICTHRPDPTGP 133
Db 219 SRKFNTTERTVLQGLLRPLFKNTSVGPLYSGCRLLTLLRPEKDGATGVDAICTHRPDPTGP 278
Qy 134 GLDREQLYLELSQLTHTSITELGPTTLDRLDSLYNGFTHRSSVPTTSTGVVSEEPFTLNFT 193
Db 279 GLDREQLYLELSQLTHTSITELGPTTLDRLDSLYNGFTHRSSVPTTSTGVVSEEPFTLNFT 338
Qy 194 INNLRYMADMGQPSGLKFNITDNMKHLLSPLFORSSIGARYTCRCVIALRSVKNGAETR 253
Db 339 INNLRYMADMGQPSGLKFNITDNMKHLLSPLFORSSIGARYTCRCVIALRSVKNGAETR 398
Qy 254 VDLICTYQLPSGPGPLIKQVFHLSQQTHTGIRLGPYSLDKOSLYLNGYNPEGPDEPPT 313
Db 399 VDLICTYQLPSGPGPLIKQVFHLSQQTHTGIRLGPYSLDKOSLYLNGYNPEGPDEPPT 458
Qy 314 TPKPATTFPLPSLSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATFNSTEGVLOHLR 373
Db 459 TPKPATTFPLPSLSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATFNSTEGVLOHLR 518
Qy 374 PLFKSSMGPPYLGCOLISLRPEKDGATGVDTTCTVHPDPVGPGLDIQQLYWELSQTH 433
Db 519 PLFKSSMGPPYLGCOLISLRPEKDGATGVDTTCTVHPDPVGPGLDIQQLYWELSQTH 578
Qy 434 GVTQLGFVLDRLDSLFINGYAPQNLSIRGEQINFIHVNWNLNPNPDTSSSEYITLLRDIQ 493

```

Db 579 GVTQLGFYVLDRLSLFINGAPQNLISIRGEYQINFIHVNWNLNPNPDPTSSSEYITLLRDIQ 638
QY 494 DKVTTLTKGSQLHDTFRFCLVNTLMDSVLTVTKALFSSNLDPSLVEQVFLDKTLNASPH 553
Db 639 DKVTTLTKGSQLHDTFRFCLVNTLMDSVLTVTKALFSSNLDPSLVEQVFLDKTLNASPH 698
QY 554 WLGSTVQLVDIHVTEMESSEYQPTSSSTQHFLNFTIITNLPSQDKAQPGTTNYQRNKR 613
Db 699 WLGSTVQLVDIHVTEMESSEYQPTSSSTQHFLNFTIITNLPSQDKAQPGTTNYQRNKR 758
QY 614 NIEDALNQLFRNSSIKSYFSDCOVSTFRSPVNRHHTGVDSLNCNFSPLARRVDRVAIYEEF 673
Db 759 NIEDALNQLFRNSSIKSYFSDCOVSTFRSPVNRHHTGVDSLNCNFSPLARRVDRVAIYEEF 818
QY 674 LWMTRNGTQLQNFITLDRSSVLVDGYSPNNEPLTGN 710
Db 819 LWMTRNGTQLQNFITLDRSSVLVDGYSPNNEPLTGN 855

RESULT 18

US-10-198-053-478
; Sequence 478, Application US/10198053
; Publication No. US20030124140A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hill, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.462C9
; CURRENT APPLICATION NUMBER: US/10/198,053
; CURRENT FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 624
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 478
; LENGTH: 914
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-198-053-478

Query Match 92.9%; Score 3663; DB 4; Length 914;
Best Local Similarity 99.9%; Pred. No. 4.2e-289;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 FTHRSSVSTTSTPGTPTVYLKASCTPASIFGPSAASHLLILFTLNFTITNLRYENMMWPG 73
Db 159 FTHRSSVSTTSTPGTPTVYLKASCTPASIFGPSAASHLLILFTLNFTITNLRYENMMWPG 218
QY 74 SRKENTTERTVLQGLRLPLKNTSVGPLYSGCRLTLRLPEKDGATGVDAICTHRPDPGTP 133
Db 219 SRKENTTERTVLQGLRLPLKNTSVGPLYSGCRLTLRLPEKDGATGVDAICTHRPDPGTP 278
QY 134 GLDREQLYLELSQTHSITELGPYTLDRDSLTVNGFTHRSSVPTTSTGVWSEEPFTLNFT 193
Db 279 GLDREQLYLELSQTHSITELGPYTLDRDSLTVNGFTHRSSVPTTSTGVWSEEPFTLNFT 338
QY 194 INNLRYMADMCGQPSGLKFNITDNVMKHLSPFORSSIGARYTCGRVIALSVKNGAETR 253
Db 339 INNLRYMADMCGQPSGLKFNITDNVMKHLSPFORSSIGARYTCGRVIALSVKNGAETR 398
QY 254 VDLCTYLOPLSGPLPIKQVFHLSQTHGITRLGYSLDKDSLYLNGYNEPGDPPT 313
Db 399 VDLCTYLOPLSGPLPIKQVFHLSQTHGITRLGYSLDKDSLYLNGYNEPGDPPT 458
QY 314 TPXPATTFPLPSAATTAMGYHLKTLITNLFTISNLQYSPDMGKGSATFNSTEGVLOHLR 373
Db 459 TPXPATTFPLPSAATTAMGYHLKTLITNLFTISNLQYSPDMGKGSATFNSTEGVLOHLR 518
QY 374 PLFOKSMGPPYLGCOLISLRPEKDGATGVDTTCTVHPDPVPGCLDIQQLYWELSQLTH 433
Db 519 PLFOKSMGPPYLGCOLISLRPEKDGATGVDTTCTVHPDPVPGCLDIQQLYWELSQLTH 578

QY 434 GVTQLGFYVLDRLSLFINGAPQNLISIRGEYQINFIHVNWNLNPNPDPTSSSEYITLLRDIQ 493
Db 579 GVTQLGFYVLDRLSLFINGAPQNLISIRGEYQINFIHVNWNLNPNPDPTSSSEYITLLRDIQ 638
QY 494 DKVTTLTKGSQLHDTFRFCLVNTLMDSVLTVTKALFSSNLDPSLVEQVFLDKTLNASPH 553
Db 639 DKVTTLTKGSQLHDTFRFCLVNTLMDSVLTVTKALFSSNLDPSLVEQVFLDKTLNASPH 698
QY 554 WLGSTVQLVDIHVTEMESSEYQPTSSSTQHFLNFTIITNLPSQDKAQPGTTNYQRNKR 613
Db 699 WLGSTVQLVDIHVTEMESSEYQPTSSSTQHFLNFTIITNLPSQDKAQPGTTNYQRNKR 758
QY 614 NIEDALNQLFRNSSIKSYFSDCOVSTFRSPVNRHHTGVDSLNCNFSPLARRVDRVAIYEEF 673
Db 759 NIEDALNQLFRNSSIKSYFSDCOVSTFRSPVNRHHTGVDSLNCNFSPLARRVDRVAIYEEF 818
QY 674 LWMTRNGTQLQNFITLDRSSVLVDGYSPNNEPLTGN 710
Db 819 LWMTRNGTQLQNFITLDRSSVLVDGYSPNNEPLTGN 855

RESULT 19

US-10-714-389-206
; Sequence 206, Application US/10714389
; Publication No. US20040101899A1
; GENERAL INFORMATION:
; APPLICANT: Dallon, Davin C.
; APPLICANT: Day, Craig H.
; APPLICANT: Jiang, Yugu
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Wang, TongTong
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.491D1
; CURRENT APPLICATION NUMBER: US/10/714,389;
; CURRENT FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 206
; LENGTH: 914
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-714-389-206

Query Match 92.9%; Score 3663; DB 4; Length 914;
Best Local Similarity 99.9%; Pred. No. 4.2e-289;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 FTHRSSVSTTSTPGTPTVYLKASCTPASIFGPSAASHLLILFTLNFTITNLRYENMMWPG 73
Db 159 FTHRSSVSTTSTPGTPTVYLKASCTPASIFGPSAASHLLILFTLNFTITNLRYENMMWPG 218
QY 74 SRKENTTERTVLQGLRLPLKNTSVGPLYSGCRLTLRLPEKDGATGVDAICTHRPDPGTP 133
Db 219 SRKENTTERTVLQGLRLPLKNTSVGPLYSGCRLTLRLPEKDGATGVDAICTHRPDPGTP 278
QY 134 GLDREQLYLELSQTHSITELGPYTLDRDSLTVNGFTHRSSVPTTSTGVWSEEPFTLNFT 193
Db 279 GLDREQLYLELSQTHSITELGPYTLDRDSLTVNGFTHRSSVPTTSTGVWSEEPFTLNFT 338
QY 194 INNLRYMADMCGQPSGLKFNITDNVMKHLSPFORSSIGARYTCGRVIALSVKNGAETR 253
Db 339 INNLRYMADMCGQPSGLKFNITDNVMKHLSPFORSSIGARYTCGRVIALSVKNGAETR 398
QY 254 VDLCTYLOPLSGPLPIKQVFHLSQTHGITRLGYSLDKDSLYLNGYNEPGDPPT 313
Db 399 VDLCTYLOPLSGPLPIKQVFHLSQTHGITRLGYSLDKDSLYLNGYNEPGDPPT 458
QY 314 TPXPATTFPLPSAATTAMGYHLKTLITNLFTISNLQYSPDMGKGSATFNSTEGVLOHLR 373

Mon Mar 20 08:49:44 2006

459 TPKPATTFPLPSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLOHLR 518
374 PLFOKSSMGPFYLGCGQLISLRPEKDGAAATGVDTTCTTHPDPVPGGLDIQQLYWELSOLTH 433
519 PLFOKSSMGPFYLGCGQLISLRPEKDGAAATGVDTTCTTHPDPVPGGLDIQQLYWELSOLTH 578
434 GVTOLGFFVLDRLDSLFINGYAPQNLISIRGEYQINFIHVNWNLSPDPPTSSEYIITLLRDIQ 493
579 GVTOLGFFVLDRLDSLFINGYAPQNLISIRGEYQINFIHVNWNLSPDPPTSSEYIITLLRDIQ 638
494 DKVTTLKGSQSLHDTFRCLVTNLTMDSVLTVKALFSSNLDPSLVEQVFLDKTLNASFH 553
639 DKVTTLKGSQSLHDTFRCLVTNLTMDSVLTVKALFSSNLDPSLVEQVFLDKTLNASFH 698
554 WLGSTYQLVDIHVTMESSVYQPTSSSTQHFYLNFTITNLPYSQDKAQPQGTNNYQNRKR 613
699 WLGSTYQLVDIHVTMESSVYQPTSSSTQHFYLNFTITNLPYSQDKAQPQGTNNYQNRKR 758
614 NIEDALNQLFRNSSIKSYFSDCQVSTFRSPVNRHHTGVDLSLGNFSPPLARRVDRVAIYEEF 673
759 NIEDALNQLFRNSSIKSYFSDCQVSTFRSPVNRHHTGVDLSLGNFSPPLARRVDRVAIYEEF 818
674 LMRTRNGTQLOQNFLLDRSSVLVDGYPPNNEPLTGNS 710
819 LMRTRNGTQLOQNFLLDRSSVLVDGYPPNNEPLTGNS 855

Search completed: March 20, 2006, 07:35:08
Job time : 137.781 secs

459 TPKPATTFPLPSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLOHLR 518
374 PLFOKSSMGPFYLGCGQLISLRPEKDGAAATGVDTTCTTHPDPVPGGLDIQQLYWELSOLTH 433
519 PLFOKSSMGPFYLGCGQLISLRPEKDGAAATGVDTTCTTHPDPVPGGLDIQQLYWELSOLTH 578
434 GVTOLGFFVLDRLDSLFINGYAPQNLISIRGEYQINFIHVNWNLSPDPPTSSEYIITLLRDIQ 493
579 GVTOLGFFVLDRLDSLFINGYAPQNLISIRGEYQINFIHVNWNLSPDPPTSSEYIITLLRDIQ 638
494 DKVTTLKGSQSLHDTFRCLVTNLTMDSVLTVKALFSSNLDPSLVEQVFLDKTLNASFH 553
639 DKVTTLKGSQSLHDTFRCLVTNLTMDSVLTVKALFSSNLDPSLVEQVFLDKTLNASFH 698
554 WLGSTYQLVDIHVTMESSVYQPTSSSTQHFYLNFTITNLPYSQDKAQPQGTNNYQNRKR 613
699 WLGSTYQLVDIHVTMESSVYQPTSSSTQHFYLNFTITNLPYSQDKAQPQGTNNYQNRKR 758
614 NIEDALNQLFRNSSIKSYFSDCQVSTFRSPVNRHHTGVDLSLGNFSPPLARRVDRVAIYEEF 673
759 NIEDALNQLFRNSSIKSYFSDCQVSTFRSPVNRHHTGVDLSLGNFSPPLARRVDRVAIYEEF 818
674 LMRTRNGTQLOQNFLLDRSSVLVDGYPPNNEPLTGNS 710
819 LMRTRNGTQLOQNFLLDRSSVLVDGYPPNNEPLTGNS 855

RESULT 20
US-10-717-296-206
; Sequence 206, Application US/10717296
; Publication No. US20040142361A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Jiang, Yuqiu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.491C8
; CURRENT APPLICATION NUMBER: US/10717,296
; NUMBER OF SEQ ID NOS: 313
; CURRENT FILING DATE: 2003-11-19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 206
; LENGTH: 914
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-717-296-206

Query Match 92.9%; Score 3663; DB 4; Length 914;
Best Local Similarity 99.9%; Pred. NO. 4.2e-289;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 FTHRSSVSTTTPGTPTYLGASKTPASIFGSPASASHLLILFTLNFTITNLRYEENMWP 73
DB 159 FTHRSSVSTTTPGTPTYLGASKTPASIFGSPASASHLLILFTLNFTITNLRYEENMWP 218
QY 74 SRKFNTTERRVLOGLRLPKNTSVGLYSGCRLLLRPEKDGAAATGVDICTHRRDPDTPG 133
DB 219 SRKFNTTERRVLOGLRLPKNTSVGLYSGCRLLLRPEKDGAAATGVDICTHRRDPDTPG 278
QY 134 GLDREQLYLELSQLTHSITELGPTLDRDSLTVNGFTHRSSVPTTSTGVVSEEPFTLNFT 193
DB 279 GLDREQLYLELSQLTHSITELGPTLDRDSLTVNGFTHRSSVPTTSTGVVSEEPFTLNFT 338
QY 194 INNLRYMADMGQSGSLKFNITDVMKHLISPLFORSLGARYTCRVIALRSVKNGAETR 253
DB 339 INNLRYMADMGQSGSLKFNITDVMKHLISPLFORSLGARYTCRVIALRSVKNGAETR 398
QY 254 VDLICTYLOPLSGGLPIKOVFHELSSQTHGITRLGPYSLDKDSLTVNGFTHRSSVPTTSTGVVSEEPFTLNFT 313
DB 399 VDLICTYLOPLSGGLPIKOVFHELSSQTHGITRLGPYSLDKDSLTVNGFTHRSSVPTTSTGVVSEEPFTLNFT 458
QY 314 TPKPATTFPLPSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLOHLR 373

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 20, 2006, 07:28:38 ; Search time 26.0454 Seconds
(without alignments)

3765.293 Million cell updates/sec

Title: US-10-687-035-34

Perfect score: 758

Sequence: 1 MGWSWIFLLSCTAGVHSE.....FGSGYFDYWGQGTTLTVSS 139

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	601.5	79.4	472	2	Q6PJA7_MOUSE
2	596.5	78.7	483	2	Q4VAB6_MOUSE
3	585.5	77.2	470	2	Q7TKM1_MOUSE
4	579	76.4	117	1	HV14_MOUSE
5	575.5	75.9	477	2	Q58E56_MOUSE
6	564	74.4	481	2	Q8VCV5_MOUSE
7	555	73.2	488	2	Q91WR1_MOUSE
8	533.5	70.4	481	2	Q91WT1_MOUSE
9	532.5	70.3	140	1	HV02_MOUSE
10	531	70.1	465	2	Q6PJ82_MOUSE
11	525.5	69.3	488	2	Q569H9_MOUSE
12	522	68.9	139	1	HV07_MOUSE
13	514.5	67.9	136	1	HV15_MOUSE
14	512	67.5	485	2	Q58E61_MOUSE
15	512	67.5	590	2	Q4V9V8_MOUSE
16	508.5	67.1	480	2	Q8K0Z4_MOUSE
17	502.5	66.3	473	2	Q9D8L4_MOUSE
18	501.5	66.2	438	2	Q5BUZ2_RAT
19	499	65.8	137	1	HV11_MOUSE
20	499	65.8	613	2	Q8VCX7_MOUSE
21	498.5	65.8	614	2	Q7TWT6_MOUSE
22	497.5	65.6	475	2	Q5FVP3_RAT
23	495	65.3	118	2	Q5R3X0_MOUSE
24	493	65.0	463	2	Q991C4_MOUSE
25	492.5	65.0	117	2	Q9QXF0_MOUSE
26	490.5	64.7	464	2	Q6PF95_MOUSE
27	489	64.5	598	2	Q568Y0_RAT
28	488.5	64.4	188	2	Q8VDC9_MOUSE
29	486.5	64.2	489	2	Q8VCX4_MOUSE
30	485	64.0	591	2	Q4QQW0_RAT
31	484	63.9	617	2	Q4KML5_MOUSE

32	480	63.3	487	2	Q65ZL2_MOUSE
33	479.5	63.3	134	2	Q65ZR6_MOUSE
34	479	63.2	482	2	Q8K172_MOUSE
35	476	62.8	117	1	HV52_MOUSE
36	475	62.7	486	2	Q5HZV6_MOUSE
37	471	62.1	118	1	HV51_MOUSE
38	470.5	62.1	117	1	HV12_MOUSE
39	470.5	62.1	616	2	Q504M7_MOUSE
40	470	62.0	488	2	Q8K0F2_MOUSE
41	469.5	61.9	117	1	HV13_MOUSE
42	469.5	61.9	117	1	Q9QX59_MOUSE
43	469.5	61.9	138	1	HV48_MOUSE
44	460	60.7	145	2	Q924Q7_MOUSE
45	458.5	60.5	170	2	Q925S2_MOUSE
46	458.5	60.5	458	2	Q5BK05_RAT
47	457.5	60.4	146	2	Q924R8_MOUSE
48	456.5	60.2	483	2	Q52L51_MOUSE
49	455.5	60.1	120	1	HV03_MOUSE
50	449.5	59.3	120	2	Q920E8_MOUSE
51	445	58.7	145	2	Q924R1_MOUSE
52	444	58.6	143	2	Q924R0_MOUSE
53	443.5	58.5	123	2	Q8VIJ1_MOUSE
54	441	58.2	145	2	Q924R4_MOUSE
55	438	57.8	137	2	Q924R6_MOUSE
56	437.5	57.7	140	2	Q924P8_MOUSE
57	437	57.7	117	1	HV09_MOUSE
58	436.5	57.6	481	2	Q91WT3_MOUSE
59	435.5	57.5	474	2	Q8R3H6_MOUSE
60	435	57.4	145	2	Q924R3_MOUSE
61	434.5	57.3	146	2	Q924Q3_MOUSE
62	434	57.3	117	1	HV04_MOUSE
63	434	57.3	143	2	Q924Q0_MOUSE
64	434	57.3	145	2	Q924P7_MOUSE
65	433.5	57.2	142	2	Q924Q1_MOUSE
66	431	56.9	117	1	HV06_MOUSE
67	431	56.8	145	2	Q924Q6_MOUSE
68	430.5	56.8	144	2	Q924P5_MOUSE
69	430.5	56.8	468	2	Q505N9_MOUSE
70	428	56.5	120	1	HV50_MOUSE
71	428	56.5	141	2	Q924Q4_MOUSE
72	428	56.5	145	2	Q924Q9_MOUSE
73	426	56.2	117	1	HV05_MOUSE
74	424	55.9	117	1	HV49_MOUSE
75	424	55.9	143	2	Q924Q5_MOUSE
76	423	55.8	243	2	Q7TQM2_MOUSE
77	422.5	55.7	147	2	Q925S3_MOUSE
78	422	55.7	143	2	Q924P9_MOUSE
79	421	55.5	109	2	Q9JL75_MOUSE
80	420.5	55.5	140	2	Q924R2_MOUSE
81	420.5	55.5	480	2	Q6P089_HUMAN
82	420.5	55.5	500	2	Q6N091_HUMAN
83	416.5	54.9	146	2	Q924Q8_MOUSE
84	416.5	54.9	208	2	Q62P87_HUMAN
85	416	54.9	136	2	Q7TPE3_MOUSE
86	416	54.9	143	2	Q924R7_MOUSE
87	415	54.7	117	1	HV10_MOUSE
88	413.5	54.6	121	1	HV01_MOUSE
89	411	54.2	143	2	Q91V67_MOUSE
90	411	54.2	143	2	Q91VA2_MOUSE
91	410.5	54.2	142	2	Q924Q2_MOUSE
92	408.5	53.9	120	2	Q5F211_MOUSE
93	408	53.8	118	2	Q921C4_MOUSE
94	407	53.7	143	2	Q924P6_MOUSE
95	406	53.6	518	2	Q6N030_HUMAN
96	404.5	53.4	497	2	Q8WJ24_HUMAN
97	404	53.3	114	2	Q9JL81_MOUSE
98	403	53.2	498	2	Q6N041_HUMAN
99	402	53.0	147	1	HV1C_HUMAN
100	400.5	52.8	476	2	Q569X1_MOUSE

ALIGNMENTS

Qy 1 MGWSWTFPLFLSGTAGVHSEVQLQOOSGPPELVKPGASVKLSCKASGVTFTFDYDNIHWVKQSH 60

ph 1 MGWSWTFPLFLI.SGTAGVTSVQLQOOSGPPELVKPGASVKLSCKASGVTFTFDYDNIHWVKQSH 60


```
Best Local Similarity 75.5%; Pred. No. 5.1e-45;
Matches 105; Conservative 13; Mismatches 19; Indels 2; Gaps 1;

QY 1 MGWSWIFLLSGLTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFDTYNIHWKQSH 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MGWSWIFLLSGLTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFDTYNIHWKQSH 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 GKLEWIGYTPYNGVSDYNQNFKSKATLVDNSSNTAYMELSLTSEDSAVYYCARWDF 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 GKLEWIGYTPYNGVSDYNQNFKSKATLVDNSSNTAYMELSLTSEDSAVYYCARWDF 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 GSGYFEDYNGQGTTLTVSS 139
    |||||:|||||:|||||:|||||:|||||:|||||:
Db 121 GA--WFAFWGQGTTLTVSSA 137
    |||||:|||||:|||||:|||||:|||||:|||||:

RESULT 7
Q91WRI_MOUSE
ID Q91WRI_MOUSE PRELIMINARY; PRT; 488 AA.
AC Q91WRI;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Igh-VJ558 protein.
GN Name=Igh-VJ558;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Bosak S.A., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013539; AAH13539.1; -; mRNA.
DR HSSP; P01751; 1A6W.
DR Ensembl; ENSMUSG000000021155; Mus musculus.
DR MGI; MGI:96486; Igh-VJ558.
DR GO; GO:0003823; P:antigen binding; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Immunoglobulin domain.

SQ SEQUENCE 488 AA; 52965 MW; F12068460B400B9D CRC64;
Query Match 73.2%; Score 555; DB 2; Length 488;
Best Local Similarity 72.6%; Pred. No. 3.7e-44;
Matches 106; Conservative 13; Mismatches 17; Indels 10; Gaps 2;

QY 1 MGWSWIFLLSGLTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFDTYNIHWKQSH 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MGWSWIFLLSGLTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFDTYNIHWKQSH 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 GKLEWIGYTPYNGVSDYNQNFKSKATLVDNSSNTAYMELSLTSEDSAVYYCARWDF 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 GKLEWIGYTPYNGVSDYNQNFKSKATLVDNSSNTAYMELSLTSEDSAVYYCARWDF 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 GSGYFEDYNGQGTTLTVSS 139
    |||||:|||||:|||||:|||||:|||||:|||||:
Db 118 GPVYYSFSDYRCDYWGQGTTLTVSSA 143
    |||||:|||||:|||||:|||||:|||||:|||||:

RESULT 8
Q91WTL_MOUSE
ID Q91WTL_MOUSE PRELIMINARY; PRT; 481 AA.
AC Q91WTL;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Igh-VJ558 protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Bosak S.A., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Colon;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013490; AAH13490.1; -; mRNA.
DR HSSP; P01751; 1A6W.
DR Ensembl; ENSMUSG000000021155; Mus musculus.
DR GO; GO:0003823; P:antigen binding; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
```

```
KW Immunoglobulin domain.
SQ SEQUENCE 481 AA; 52105 MW; 97DF68D159463F65 CRC64;

Query Match 70.4%; Score 533.5; DB 2; Length 481;
Best Local Similarity 74.1%; Pred. No. 4e-42;
Matches 103; Conservative 9; Mismatches 24; Indels 3; Gaps 1;

Qy 1 MGNSWIFLLSGTAGVHSEVLOQSGPELVKPGASVKISCKASGYTFTDYNHWVKQSH 60
Db 1 MGMRWIFLLSGTAGVHSEVLOQSGPELVKPGASVKISCKASGYTFTSYIHVVKQRP 60
Qy 61 GKLEWIGIYIPYNGVSDYNQNFKSKATLIVDNSENNTAYMELRSLTSDSAVYFCARWDF 120
Db 61 GQGLVWIGIYIPYNGVSDYNQNFKSKATLIVDNSENNTAYMELRSLTSDSAVYFCARWDF 120
Qy 121 GSGYFYFDYWGQGTTLTVSS 139
Db 118 GGGWAFDYWGQGTTLTVSS 136

RESULT 9
HV02 MOUSE STANDARD; PRT; 140 AA.
ID HV02 MOUSE
AC P01746;
DC 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 10-MAY-2005 (Rel. 47, Last annotation update)
DE IG heavy chain V region 93G7 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Murioidea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=A/J;
RC MEDLINE=82152818; PubMed=6801765;
RX Sims J.; Rabbits T.H., Essex P., Slaughter C., Tucker P.W.,
RA Capra J.D.;
RT "Somatic mutation in genes for the variable portion of the
RL immunoglobulin heavy chain."
CC Science 216:309-311(1982).
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; J00493; AAA38128.1; -; mRNA.
DR HSSP; P01747; 1JFQ.
DR SMR; P01746; 20-140.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Hybridoma; Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1
FT CHAIN 19
FT DCHAIN 20 140 Ig heavy chain V region 93G7.
FT NON_TER 20 139 Ig-like.
FT NON_TER 140 140
SQ SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DA5CE8 CRC64;

Query Match 70.3%; Score 532.5; DB 1; Length 140;
Best Local Similarity 74.3%; Pred. No. 1.3e-42;
Matches 104; Conservative 12; Mismatches 23; Indels 1; Gaps 1;

Qy 1 MGNSWIFLLSGTAGVHSEVLOQSGPELVKPGASVKISCKASGYTFTDYNHWVKQSH 60
Db 1 MGMRWIFLLSGTAGVHSEVLOQSGPELVKPGASVKISCKASGYTFTSYIHVVKQRP 60
Qy 61 GKLEWIGIYIPYNGVSDYNQNFKSKATLIVDNSENNTAYMELRSLTSDSAVYFCARWDF 120
Db 61 GQGLVWIGIYIPYNGVSDYNQNFKSKATLIVDNSENNTAYMELRSLTSDSAVYFCARWDF 120
Qy 121 GSGYFYFDYWGQGTTLTVSS 139
Db 118 GGGWAFDYWGQGTTLTVSS 136

RESULT 10
Q6PJB2 MOUSE PRELIMINARY; PRT; 465 AA.
ID Q6PJB2 MOUSE
AC Q6PJB2;
DC 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN Name=Igh-la;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Murioidea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Czech II;
RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.
RC Expression driven by an MMTV-LTR enhancer.;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udgin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences."
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Czech II;
RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.
RC Expression driven by an MMTV-LTR enhancer.;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018280; AAHL8280.1; -; mRNA.
DR HSSP; P01865; 1KB5.
DR SMR; Q6PJB2; 20-461.
DR MGI; MGI:96443; Igh-la.
DR GO; GO:0003823; F:antigen binding; IEA.
DR InterPro; IPR003599; Ig-like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51329 MW; 394F43C4E8DB3E21 CRC64;
```

Query Match 70.1%; Score 531; DB 2; Length 465;
 Best Local Similarity 72.9%; Pred. No. 6.7e-42;
 Matches 102; Conservative 11; Mismatches 21; Indels 6; Gaps 2;

QY 1 MGWSWIFLLSSTAGVHSEVQLOQSGPELVKPCASVKISKASGYTFTDYNHWWKQSH 60
 DB 1 MGWSWIFLLSSTAGVHSEVQLOQSGPELVKPCASVKISKASGYTFTDYNHWWKQSH 60
 QY 61 GKILEWIGYIYPYNGVDYQNFKSKATLIVDSSNTAYMELSLTSDSAVYCARWDF 120
 DB 61 GKILEWIGYIYPYNGVDYQNFKSKATLIVDSSNTAYMELSLTSDSAVYCARWDF 120
 QY 121 GSGYI-FDYWGQGTTLTVSS 139
 DB 118 -GYVFDYWGQGTTLTVSS 135

RESULT 11
 Q569W9 MOUSE PRELIMINARY; PRT; 468 AA.
 AC Q569W9;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Hypothetical protein.
 GN Names=Igh-1a;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=CZECH II;
 RC TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;
 RX MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haie F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
 RA Brownstein M.J., Udutin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Faney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences."
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=CZECH II;
 RC TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;
 RG NTH MGC Project;
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC092271; AAH92271.1; -; mRNA.
 DR SRR: Q569W9; 20-464.
 DR MGI: MGI:96443; Igh-1a.
 DR GO: GO:0003823; F:antigen binding; IEA.
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003597; Ig cl.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF07654; Cl-set; 3.

DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGcl; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 468 AA; 51666 MW; 5BF6527329F8461 CRC64;

Query Match 69.3%; Score 525.5; DB 2; Length 468;
 Best Local Similarity 72.3%; Pred. No. 2.3e-41;
 Matches 102; Conservative 15; Mismatches 19; Indels 5; Gaps 2;

QY 1 MGWSWIFLLSSTAGVHSEVQLOQSGPELVKPCASVKISKASGYTFTDYNHWWKQSH 60
 DB 1 MGWSWIFLLSSTAGVHSEVQLOQSGPELVKPCASVKISKASGYTFTDYNHWWKQSH 60
 QY 61 GKILEWIGYIYPYNGVDYQNFKSKATLIVDSSNTAYMELSLTSDSAVYCARWDF 120
 DB 61 GKILEWIGYIYPYNGVDYQNFKSKATLIVDSSNTAYMELSLTSDSAVYCARWDF 120
 QY 121 GSGYI-FDYWGQGTTLTVSS 139
 DB 118 TGGYDGYVGYWGQGTTLTVSS 138

RESULT 12
 HV07 MOUSE STANDARD; PRT; 139 AA.
 AC P01751; P01752;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Ig heavy chain V region B1-8/186-2 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6;
 RX MEDLINE=81234548; PubMed=6788376; DOI=10.1016/0092-8674(81)90089-1;
 RA Bothwell A.L.M., Faskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
 RA Baltimore D.;
 RT "Heavy chain variable region contribution to the NPB family of
 antibodies: somatic mutation evident in a gamma 2a variable region."
 Cell 24:625-637(1981).
 CC -1- MISCELLANEOUS: The B1-8 mu chain mRNA was cloned from a hybridoma
 making antibodies to the hapten (4-hydroxy-3-nitrophenyl)acetyl
 (NPB antibodies).
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not
 removed.
 CC EMBL: J00529; AAA38170.1; -; mRNA.
 DR FIR; A90809; MEMS18.
 DR PDB: 1AG0; X-ray; H=20-139.
 DR PDB: 1AGV; X-ray; H/I/J=20-139.
 DR PDB: 1AGW; X-ray; H=20-139.
 DR PDB: 1NGP; X-ray; H=20-139.
 DR PDB: 1NGQ; X-ray; H=20-139.
 DR PDB: 1NQB; X-ray; A/C=20-139.
 DR Ensembl: ENSMUSG0000063737; Mus musculus.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003596; Ig_v.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 KW 3D-structure; Immunoglobulin domain; Immunoglobulin V region; Signal.
 FT SIGNAL 1 19 Ig heavy chain V region B1-8/186-2.
 FT CHAIN 20 139


```

FT REGION 20 49 Framework-1.
FT REGION 50 54 Complementarity-determining-1.
FT REGION 55 68 Framework-2.
FT REGION 69 85 Complementarity-determining-2.
FT REGION 86 117 Framework-3.
FT REGION 118 124 D segment.
FT REGION 125 139 JH2 segment.
FT DISULFID 41 115 By similarity.
FT NON_TER 139 139
FT STRAND 22 24
FT STRAND 28 31
FT TURN 33 34
FT TURN 37 38
FT STRAND 48 50
FT HELIX 52 58
FT TURN 60 61
FT STRAND 64 70
FT TURN 72 74
FT STRAND 77 79
FT HELIX 81 83
FT TURN 84 86
FT STRAND 87 92
FT TURN 93 96
FT STRAND 97 102
FT HELIX 107 109
FT STRAND 111 118
FT TURN 120 123
FT STRAND 129 129
FT STRAND 133 137
SQ SEQUENCE 139 AA; 15419 MW; 1B57DD4FD0C9F465 CRC64;

Query Match 68.9%; Score 522; DB 1; Length 139;
Best Local Similarity 71.9%; Pred. No. 1.2e-41;
Matches 100; Conservative 12; Mismatches 27; Indels 0; Gaps 0;

Qy 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFDYNIHVKQSH 60
Db 1 MGWSCIMFLAATATGATGHSVQLQSGPELVKPGASVKISCKASGYTFDYNIHVKQSH 60

Qy 61 GKILEWIGIYYPYNGVSDYNQNFKSKATLIVDSSNTAYMELRLTSDSNAVYTCARWDF 120
Db 61 GRGLEWIGRIDPNSGTYKNEKFSKATLIVDSSNTAYMELRLTSDSNAVYTCARWDF 120

Qy 121 GSGYFDYWGQGTTLTVSS 139
Db 121 YGSSYFDYWGQGTTLTVSS 139

RESULT 13
HV15_MOUSE STANDARD; PRT; 136 AA.
AC P01759;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Igh heavy chain V region BC1 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=8222262; PubMed=6806821;
RA Knapp M.R., Liu C.-P., Newell N., Ward R.B., Tucker P.W., Strober S.,
RA Blattner P.R.;
RT "Simultaneous expression of immunoglobulin mu and delta heavy chains
RT by a cloned B-cell lymphoma: a single copy of the VH gene is shared by
RT two adjacent CH genes."
RL Proc. Natl. Acad. Sci. U.S.A. 79:2996-3000(1982).
RC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration

```

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

CC -----
 CC EMBL; J00494; AAA38130.1; -; Genomic_DNA.

CC PIR; A02042; HVMSB1.

CC HSP; P01751; INQB.

CC SMR; P01759; 20-136.

CC Ensembl; ENSMUSG000000063048; Mus musculus.

CC InterPro; IPR007110; Ig-like.

CC InterPro; IPR003596; Ig_v.

CC SMART; SM00406; IGV; 1.

CC PROSITE; PS50835; IG_LIKE; 1.

KW immunoglobulin domain; Immunoglobulin V region; Signal.

FT SIGNAL 1 19

FT CHAIN 20 136 Ig heavy chain V region BC1.

FT DOMAIN 20 135 Ig-like.

FT NON_TER 136 136

SQ SEQUENCE 136 AA; 15078 MW; 6827CFBC6DB3F35E CRC64;

Query Match 67.9%; Score 514.5; DB 1; Length 136;

Best Local Similarity 70.5%; Pred. No. 6.2e-41;

Matches 98; Conservative 11; Mismatches 27; Indels 3; Gaps 1;

Qy 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFDYNIHVKQSH 60

Db 1 MGWSCIIFFLVATATGATGHSVQLQSGPELVKPGASVKISCKASGYTFDYNIHVKQSH 60

Qy 61 GKILEWIGIYYPYNGVSDYNQNFKSKATLIVDSSNTAYMELRLTSDSNAVYTCARWDF 120

Db 61 AKSLEWIGVISTYNGNTSYNQKPKGKATMTVDKSSSTVHMLARLTSDSNAVYTCARWDF 118

Qy 121 GSGYFDYWGQGTTLTVSS 139

Db 119 -YGNFYDWGQGTTLTVSS 136

RESULT 14

Q5861_MOUSE

ID Q5861_MOUSE PRELIMINARY; PRT; 485 AA.

AC Q5861;

DT 10-MAY-2005 (TrEMBLrel. 30, Created)

DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)

DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)

DE Igh-VJ558 protein.

GN Name=Igh-VJ558;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=Czech II;

RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.

RC Expression driven by an MMTV-LTR enhancer.

RX MEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,

RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A.C., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RN
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Mammary gland;
 RG NIH MGC Project;
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC096667; AAH96667.1; -, mRNA.
 DR MGI; MGI:196448; Igh-6.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig.C1.
 DR InterPro; IPR003006; Ig.MHC.
 DR InterPro; IPR003596; Ig.V.
 DR Pfam; PF07654; C1-set; 4.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGc1; 4.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 5.
 DR PROSITE; PS00290; IG MHC; UNKNOWN_3.
 KW Hypothetical protein.
 SQ SEQUENCE 590 AA; 64892 MW; D425318P9A198B14 CRC64;

 Query Match 67.5%; Score 512; DB 2; Length 590;
 Best Local Similarity 70.5%; Pred. No. 5.6e-40;
 Matches 98; Conservative 16; Mismatches 21; Indels 4; Gaps

 Qy 1 MGWSWIFLPLLSGTAGVHSEVOLOQSGPELYKPGASVKISKASYTFTDYNHHVWKQSH
 Db 1 MGWSWIFFLLSLGTAGVHCQVQLKQSGAELRPGASVKLSCKASYTFTDYYINWVKQRP

 Qy 61 GKILEWTGYIYPNGVSDYNQNFKSKATLIIVDNSNTAYMELRSITSDSAVYYCARWDF
 Db 61 GQGLEWARIYPGSGNTYYNEKFGKATLTAEKSSSTAYMQLSITSDSAVYFCAR---

 Qy 121 GSGYFYDYGQGTTLTVSS 139
 Db 118 -TGTDMDYWGQGTSTVTVSS 135

 RESULT 16
 Q8KOZ4 MOUSE
 ID Q8KOZ4 MOUSE PRELIMINARY; PRT; 480 AA.
 AC Q8KOZ4;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE LOC238447 protein.
 GN Name=LOC238447;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Mix FVB/N;
 RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
 RX MEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datschenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ugin T.B., Toshivuki S., Carninci P., Pance C.,
 RA


```

DR PIR; PH1165; PH1165.
DR PIR; S19966; S19966.
DR PIR; S26746; S26746.
DR HSP; P01864; 1B0G.
DR SRR; Q9D814; 20-469.
DR Ensembl; ENSMUSG00000054328; Mus musculus.
DR MGI; MGI:96443; Igh-1a.
DR GO; GO:0042571; C:immunoglobulin complex, circulating; IDA.
DR GO; GO:0005771; C:multivesicular body; IDA.
DR GO; GO:0003823; P:antigen binding; IDA.
DR GO; GO:0001788; P:antibody-dependent cellular cytotoxicity; IDA.
DR GO; GO:0030333; P:antigen processing; IDA.
DR GO; GO:0006938; P:complement activation; IDA.
DR GO; GO:0045022; P:early endosome to late endosome transport; IDA.
DR GO; GO:0008333; P:endosome to lysosome transport; IDA.
DR GO; GO:0006911; P:phagocytosis, engulfment; IDA.
DR GO; GO:0006910; P:phagocytosis, recognition; IDA.
DR GO; GO:0050871; P:positive regulation of B cell activation; IDA.
DR GO; GO:0050778; P:positive regulation of immune response; IDA.
DR GO; GO:0050766; P:positive regulation of phagocytosis; IDA.
DR GO; GO:0001812; P:positive regulation of type I hypersensitivity; IDA.
DR GO; GO:0001798; P:positive regulation of type II hypersensitivity; IDA.
DR GO; GO:0030162; P:regulation of proteolysis and peptidolysis; IDA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR Immunoglobulin domain.
KW SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;

Query Match 66.3%; Score 502.5; DB 2; Length 473;
Best Local Similarity 70.4%; Pred. No. 3.5e-39;
Matches 100; Conservative 14; Mismatches 21; Indels 7; Gaps 2;

QY 1 MGWSWFLFLSAGVHSEVQLQSGPVLKPGASVKISCKASGYTFTDYNHWKQSH 60
DB 1 MWSWFLFLSAGVHSEVQLQSGPVLKPGASVKISCKASGYTFTDYNHWKQSH 60
QY 61 GKLEWIGYIYPNGVSDYNQNFKSKATLVDNNSNTAYMELSLTSEDSAVYCARWDF 120
DB 61 GQLEWIGKIGPGSGSYNNEKFGKATLTADKSSSTAYMQLSLSLTSSEDSAVYFCAR--- 117
QY 121 GSGY---YFDYWGQGTTLTVSS 139
DB 118 -SGYDWDYFAYWGQGTTLTVSSA 138

RESULT 18
QSBZ22_RAT PRELIMINARY; PRT; 458 AA.
AC QSBZ22;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE LOC367586 protein.
GN Name=LOC367586;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Thymus;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner C.M., Shenmen C.H., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.S., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Thymus;
RG NIH MGC Project;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Beta-2-microglobulin is the beta-chain of major
CC histocompatibility complex class I molecules (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC EMBL; BC091272; AAH91272.1; -; mRNA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; Repeat.
KW Immunoglobulin domain; Repeat.
SQ SEQUENCE 458 AA; 50161 MW; A0A61DCDD2CA433E CRC64;

Query Match 66.2%; Score 501.5; DB 2; Length 458;
Best Local Similarity 69.8%; Pred. No. 4.2e-39;
Matches 97; Conservative 14; Mismatches 25; Indels 3; Gaps 2;

QY 1 MGWSWFLFLSAGVHSEVQLQSGPVLKPGASVKISCKASGYTFTDYNHWKQSH 60
DB 1 MGWSWFLFLSAGVHSEVQLQSGPVLKPGASVKISCKASGYTFTDYNHWKQSH 60
QY 61 GKLEWIGYIYPNGVSDYNQNFKSKATLVDNNSNTAYMELSLTSEDSAVYCARWDF 120
DB 61 GNGLEWIGYIYPNGVSDYNQNFKSKATLVDNNSNTAYMELSLTSEDSAVYCARWDF 119
QY 121 GSGYFDYWGQGTTLTVSS 139
DB 120 FDGY--DYWGQGVMTVSS 136

RESULT 19
HVL1_MOUSE STANDARD; PRT; 137 AA.
ID HVL1_MOUSE
AC P01755;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V region S43 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Thymus;
RA Botwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;

```

RT "Heavy chain variable region contribution to the NPb family of
 RT antibodies: somatic mutation evident in a gamma 2a variable region.";
 RL Cell 24:625-637(1981).
 CC -1- MTSCELLANEUS: The gamma-2a chain mRNA was cloned from a hybridoma
 CC making antibodies to the haptens (4-hydroxy-3-nitrophenyl)acetyl
 CC (NPB antibodies).
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----

DR ENBL; J00539; AAA38172.1; -; mRNA.
 DR STRAIN: FVB/N; TISSUE: Salivary gland;
 DR HSP; P01751; IAGW.
 DR SMR; P01755; 20-137.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR Immunoglobulin domain; Immunoglobulin V region; Signal.

FT SIGNAL 1 19
 FT CHAIN 20 137 Ig heavy chain V region S43.
 FT REGION 20 49 Framework-1.
 FT REGION 20 54 Complementarity-determining-1.
 FT REGION 50 54 Framework-2.
 FT REGION 55 68 Complementarity-determining-2.
 FT REGION 65 85 Complementarity-determining-3.
 FT REGION 86 117 Framework-3.
 FT REGION 118 122 D segment.
 FT REGION 123 137 JH2 segment.
 FT DISULFID 41 115 By similarity.
 FT NON TER 137 137
 SQ SEQUENCE 137 AA; 15200 MW; ADD5881BP44B8EC9 CRC64;

Query Match 65.8%; Score 499; DB 1; Length 137;
 Best Local Similarity 69.1%; Pred. No. 1.9e-39;
 Matches 96; Conservative 14; Mismatches 27; Indels 2; Gaps 1;
 Oy 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISKASGYTFTDNIHNVKQSH 60
 Db 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISKASGYTFTDNIHNVKQSH 60
 Oy 61 GKILEWIGYIPYNGVSDYNQNFKSKATLIVDNSNTAYMELRLSLTSDSAVYVCARWDF 120
 Db 61 GRGLEWIGRIDPNSGGTYNEHFRSKATLTIDKPSSTAYMQLSLTSDSAVYVCARYL 120
 Oy 121 GSGYFYDWGGTTLTVSS 139
 Db 121 GR--YFDYWGQGTTLTVSS 137

RESULT 20
 Q8VCX7_MOUSE PRELIMINARY; PRT; 613 AA.
 AC Q8VCX7;
 DT 01-MAR-2002 (TRENBLrel. 20, Created)
 DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Igh-6 protein.
 GN Name=Igh-6;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN: FVB/N; TISSUE: Salivary gland;
 RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heiehl F.,
 RA Diatchenko L., Marusina K., Farmer A.F., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
 [2]

NUCLEOTIDE SEQUENCE.
 STRAIN: FVB/N; TISSUE: Salivary gland;
 RC Strausberg R.; Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 RL [3]

NUCLEOTIDE SEQUENCE.
 PubMed=2464031;
 RA Sikder S.K., Borden P., Gruzo F., Akolkar P.N., Bhattacharya S.B.,
 RA Morrison S.L., Kabat E.A.,
 RT "Amino acid substitutions in VH CDR2 change the idiotype but not the
 RT antigen-binding of monoclonal antibodies to alpha(1----6)dextran.";
 RL J. Immunol. 142:888-893(1989).
 DR ENBL; BC018315; AAH18315.1; -; mRNA.
 DR PIR; C30562; C30562.
 DR HSP; P01751; IAGW.
 DR Ensembl; ENSMUSG0000054328; Mus musculus.
 DR MGI; MGI:96448; Igh-6.
 DR GO; GO:0019815; C:B cell receptor complex; IDA.
 DR GO; GO:0009897; C:external side of plasma membrane; IDA.
 DR GO; GO:0042571; C:immunoglobulin complex, circulating; IDA.
 DR GO; GO:0048471; C:perinuclear region; IDA.
 DR GO; GO:0038233; F:antigen binding; IDA.
 DR GO; GO:0005515; F:protein binding; IPI.
 DR GO; GO:0004888; F:transmembrane receptor activity; IDA.
 DR GO; GO:0001037; P:activation of MAPK activity; IDA.
 DR GO; GO:0030333; P:antigen processing; IDA.
 DR GO; GO:0050853; P:B cell receptor signaling pathway; IDA.
 DR GO; GO:0016064; P:early endosome to late endosome transport; IDA.
 DR GO; GO:0030890; P:positive regulation of B cell proliferation; IDA.
 DR GO; GO:0045807; P:positive regulation of endocytosis; IDA.
 DR GO; GO:0050731; P:positive regulation of peptidyl-tyrosine ph. .; IDA.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF07654; C1-set; 4.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 5.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
 KW Immunoglobulin domain.
 SQ SEQUENCE 613 AA; 67855 MW; 41A9384DD4C22862 CRC64;

Query Match 65.8%; Score 499; DB 2; Length 613;
 Best Local Similarity 68.5%; Pred. No. 1e-38;
 Matches 98; Conservative 12; Mismatches 23; Indels 10; Gaps 2;

Oy 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISKASGYTFTDNIHNVKQSH 60
 Db 1 MEWTWVFLSLTAGVHSEVQLQSGPELVKPGASVKISKATGYTFTDNIHNVKQSH 60
 Oy 61 GKILEWIGYIPYNGVSDYNQNFKSKATLIVDNSNTAYMELRLSLTSDSAVYVCARWDF 116
 Db 61 GRGLEWIGRIDPNSGGTYNEHFRSKATLTIDKPSSTAYMQLSLTSDSAVYVCARYL 120

Qy 117 RWDFSGYFDYWGCGTTLTVSS 139
||
121 RW-----YFDVWGAGTTTVSS 137

Search completed: March 20, 2006, 07:32:04
Job time : 26.0454 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 20, 2006, 07:29:34 ; Search time 5.07199 Seconds
(without alignments)
2636.859 Million cell updates/sec

Title: US-10-687-035-34

Perfect score: 758

Sequence: 1 MGMSWIFLLSCTAGVHSE.....FGSGYYFDYWGQTTLTVSS 139

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

PIR_80:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	597	78.8	139	2 A27609	Ig heavy chain pre
2	585	77.2	137	2 H32513	Ig heavy chain pre
3	579	76.4	117	1 HVMS8A	Ig heavy chain pre
4	566.5	74.7	151	2 PL0011	Ig heavy chain pre
5	565.5	74.6	140	2 T01407	Ig heavy chain (my
6	559	73.7	469	2 S37483	Ig gamma-2a chain
7	548.5	72.4	138	2 PH0105	anti-digoxin trans
8	547.5	72.2	140	2 PH1482	Ig heavy chain v r
9	547	72.2	135	2 PS0057	Ig heavy chain pre
10	544	71.8	150	2 PN0444	Ig heavy chain v r
11	535.5	70.6	138	2 S45249	Ig heavy chain pre
12	532.5	70.3	140	1 HVMSG7	Ig heavy chain pre
13	531.5	70.1	140	2 PH1489	Ig heavy chain v r
14	530.5	70.0	166	2 PL0012	Ig heavy chain pre
15	525.5	69.3	140	2 PH1484	Ig heavy chain v r
16	522	68.9	139	1 MHMS18	Ig heavy chain pre
17	521.5	68.8	135	2 PH1493	Ig heavy chain v r
18	520.5	68.7	140	2 PH1498	Ig heavy chain v r
19	520.5	68.7	140	2 PH1483	Ig heavy chain v r
20	520.5	68.7	140	2 PH1488	Ig heavy chain v r
21	520	68.6	474	1 G2MS11	Ig gamma-2b chain
22	517.5	68.3	138	2 S21810	Ig heavy chain v r
23	514.5	67.9	136	1 HVMSB1	Ig heavy chain pre
24	512.5	67.6	140	2 PH1486	Ig heavy chain v r
25	506.5	66.8	140	2 A36194	Ig heavy chain v r
26	505.5	66.7	135	2 PH1492	Ig heavy chain v r
27	503	66.4	139	2 PS0024	Ig heavy chain pre
28	502.5	66.3	136	2 PL0208	Ig heavy chain pre
29	499	65.8	128	2 I37267	Ig heavy chain v r

30	499	65.8	137	1 G2MS43	Ig heavy chain pre
31	497.5	65.6	135	2 PH1494	Ig heavy chain v r
32	494	65.2	128	2 C37267	Ig heavy chain v r
33	491	64.8	133	2 PC1155	Ig heavy chain pre
34	489.5	64.6	138	2 E32513	Ig heavy chain pre
35	489	64.5	120	2 A49982	Ig heavy chain v r
36	489	64.5	141	2 JL0076	Ig heavy chain pre
37	487.5	64.3	140	2 PH1499	Ig heavy chain v r
38	483	63.7	119	2 F30502	Ig heavy chain v r
39	483	63.7	141	2 A39276	Ig heavy chain pre
40	482	63.6	135	2 A30577	Ig heavy chain pre
41	480.5	63.4	117	2 S03305	Ig heavy chain v r
42	479.5	63.3	136	2 B47159	Ig heavy chain v r
43	479	63.2	128	2 A37267	Ig heavy chain v r
44	477.5	63.0	131	2 A27472	Ig heavy chain pre
45	476.5	62.9	117	2 S09961	Ig heavy chain V-D
46	476.5	62.9	140	2 S04575	Ig heavy chain pre
47	476	62.8	117	1 HVMSA1	Ig heavy chain pre
48	474	62.5	122	2 PH0887	Ig heavy chain v r
49	473	62.4	140	2 S09216	Ig heavy chain pre
50	471	62.1	118	1 MHMS38	Ig heavy chain v r
51	471	62.1	118	2 S38717	Ig heavy chain v r
52	470.5	62.1	117	1 MHMS4E	Ig heavy chain v r
53	470.5	62.1	121	2 F37266	Ig heavy chain v r
54	470	62.0	137	2 E29380	Ig heavy chain pre
55	469.5	61.9	117	1 HVMSJ5	Ig heavy chain v r
56	469.5	61.9	138	1 HVMSJ7	Ig heavy chain pre
57	466	61.5	475	2 S01321	Ig gamma-2b chain
58	464	61.2	137	2 PH1227	Ig heavy chain pre
59	460	60.7	120	2 B27669	Ig heavy chain v r
60	460	60.7	137	2 E29380	Ig heavy chain pre
61	460	60.7	287	4 PC4402	pelB leader/Ig hea
62	458.5	60.5	246	2 S38950	Ig gamma chain - m
63	458.5	60.5	446	2 S40295	Ig gamma-2a chain
64	458	60.4	112	2 S09957	Ig heavy chain V-D
65	458	60.4	136	2 JL0077	Ig heavy chain pre
66	457.5	60.4	118	2 S38565	Ig heavy chain v r
67	457	60.3	117	2 S25176	Ig heavy chain v r
68	455.5	60.1	119	2 B53285	Ig heavy chain v a
69	454.5	60.0	119	2 PH1520	Ig heavy chain v r
70	454.5	60.0	121	2 H37266	Ig heavy chain v r
71	454	59.9	102	2 S42176	Ig gamma chain v r
72	453.5	59.8	113	2 PH0974	Ig heavy chain v r
73	452.5	59.7	119	2 PH1502	Ig heavy chain v r
74	452.5	59.7	119	2 S20640	Ig heavy chain v r
75	451.5	59.6	119	2 PH1521	Ig heavy chain v r
76	451	59.5	122	2 E37267	Ig heavy chain v r
77	450	59.4	113	2 S55535	Ig heavy chain v r
78	450	59.4	113	2 S55534	Ig heavy chain v r
79	450	59.4	120	2 E45722	anti-glycoprotein
80	449.5	59.3	119	2 S45714	Ig heavy chain v r
81	448.5	59.2	119	2 PH1518	Ig heavy chain v r
82	448.5	59.2	119	2 PH0099	Ig heavy chain v r
83	448.5	59.2	119	2 PH1504	Ig heavy chain v r
84	448.5	59.2	119	2 PH1512	Ig heavy chain v r
85	448	59.1	115	2 A54378	Ig heavy chain v r
86	447.5	59.0	123	2 S20646	Ig heavy chain v r
87	447	59.0	114	2 S26319	Ig heavy chain v r
88	445.5	58.8	119	2 PH1500	Ig heavy chain v r
89	445	58.7	108	2 PH0975	Ig heavy chain v r
90	444.5	58.6	119	2 PH1503	Ig heavy chain v r
91	444	58.6	113	2 S55533	Ig heavy chain pre
92	444	58.6	119	2 A24672	Ig heavy chain v r
93	443.5	58.5	121	2 A26405	Ig heavy chain v r
94	443	58.4	113	2 S55528	Ig heavy chain v r
95	442.5	58.4	117	2 S01822	Ig heavy chain V-D
96	442	58.3	117	2 S03289	Ig heavy chain pre
97	441.5	58.2	118	2 PL0200	anti-DNA autoantib
98	441.5	58.2	121	2 A30551	Ig heavy chain v r
99	441.5	58.2	125	2 PH0100	Ig heavy chain v r
100	441	58.2	113	2 S55532	Ig heavy chain v r

ALIGNMENTS

```
RESULT 1
A27609
Ig heavy chain precursor V region (I29) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Dec-1998 #sequence_revision 30-Jun-1991 #text_change 23-Jul-1999
C;Accession: A27609
R;Klein, D.; Nietupski, J.; Sirlin, S.; Stavnezer, J.
J. Immunol. 140, 1676-1684, 1988
A;Title: I.29 lymphoma cells express a nonmutated V-H gene before and after H chain switch
A;Reference number: A27609; MUID:88154467; PMID:3126234
A;Accession: A27609
A;Molecule type: DNA
A;Residues: 1-139 <KLE>
A;Cross-references: UNIPARC:UPI0000114D5D; EMBL:M19401; NID:g195441; PIDN:AAA38303.1; PT
C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/DNA: signal sequence #status predicted <SIG>
F;20-139/Product: Ig heavy chain V region I29 #status predicted <VAR>
F;34-117/DNA: immunoglobulin homology <IMV>

Query Match 78.8%; Score 597; DB 2; Length 139;
Best Local Similarity 80.6%; Pred. No. 4.3e-44;
Matches 112; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

Qy 1 MGWSWIFLLSLGAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHVKQSH 60
Db 1 MGWSWIFLLSLGAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHVKQSH 60

Qy 61 GKLEWIGIYYPNGVDYNGNFKSKATLIVDNSSNTAYMELSLTSDSAVYCARWDF 120
Db 61 GKLEWIGIYYPNGVDYNGNFKSKATLIVDNSSNTAYMELSLTSDSAVYCARWDF 120

Qy 121 GSGYFDYWGQGTTLTVSS 139
Db 121 YSYAMDYWGQGTSTVTVSS 139

RESULT 2
H32513
Ig heavy chain precursor V region (BXW16) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000
C;Accession: H32513
R;Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.;
J. Clin. Invest. 82, 852-860, 1988
A;Title: Immunoglobulin kappa light chain variable region gene complex organization and
A;Reference number: A94689; MUID:88331394; PMID:3138286
A;Accession: H32513
A;Molecule type: DNA
A;Residues: 1-137 <KOF>
A;Cross-references: UNIPARC:UPI0000114D9A; GB:M20831; NID:g196949; PIDN:AAA38848.1; PID:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/DNA: immunoglobulin homology <IMV>

Query Match 77.2%; Score 585; DB 2; Length 137;
Best Local Similarity 80.6%; Pred. No. 4.4e-43;
Matches 112; Conservative 9; Mismatches 16; Indels 2; Gaps 1;

Qy 1 MGWSWIFLLSLGAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHVKQSH 60
Db 1 MGWSWIFLLSLGAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHVKQSH 60

Qy 61 GKLEWIGIYYPNGVDYNGNFKSKATLIVDNSSNTAYMELSLTSDSAVYCARWDF 120
Db 61 GKLEWIGIYYPNGVDYNGNFKSKATLIVDNSSNTAYMELSLTSDSAVYCARWDF 120

Qy 121 GSGYFDYWGQGTTLTVSS 139
```

```
Db 121 GSS--FDYWGQGTTLTVSS 137
```

RESULT 3

```
HVMS8A
Ig heavy chain precursor V region (108A) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Dec-1981 #sequence_revision 18-Dec-1981 #text_change 09-Jul-2004
C;Accession: A02041
R;Givol, D.; Zakut, R.; Effron, K.; Rechavi, G.; Ram, D.; Cohen, J.B.
Nature 292, 426-430, 1981
A;Title: Diversity of germ-line immunoglobulin V-H genes.
A;Reference number: A02041; MUID:81245215; PMID:6789211
A;Accession: A02041
A;Molecule type: DNA
A;Residues: 1-117 <GIV>
A;Cross-references: UNIPROT:P01758; UNIPARC:UPI00000270F3
A;Note: the sequence was determined from the germline gene
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/DNA: signal sequence #status predicted <SIG>
F;20-117/Product: Ig heavy chain V region (108A) #status predicted <MAT>
F;34-117/DNA: immunoglobulin homology <IMV>

Query Match 76.4%; Score 579; DB 1; Length 117;
Best Local Similarity 92.3%; Pred. No. 1.2e-42;
Matches 108; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MGWSWIFLLSLGAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHVKQSH 60
Db 1 MGWSWIFLLSLGAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHVKQSH 60

Qy 61 GKLEWIGIYYPNGVDYNGNFKSKATLIVDNSSNTAYMELSLTSDSAVYCAR 117
Db 61 GKLEWIGIYYPNGVDYNGNFKSKATLIVDNSSNTAYMELSLTSDSAVYCAR 117

RESULT 4
PL0011
Ig heavy chain precursor V region (4C11) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C;Accession: PL0011
R;Cheng, H.I.; Sood, A.K.; Ward, R.E.; Kieber-Emmons, T.; Kohler, H.
Mol. Immunol. 25, 33-40, 1988
A;Title: Structural basis of stimulatory anti-idiotypic antibodies.
A;Reference number: PL0011; MUID:88142863; PMID:3125424
A;Accession: PL0011
A;Molecule type: mRNA
A;Residues: 1-151 <CHE>
A;Cross-references: UNIPARC:UPI00000176D36
A;Experimental source: cell line 4C11
C;Comment: This protein is an anti-idiotypic antibody that induces an anti-phosphorylcholine
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/DNA: signal sequence #status predicted <SIG>
F;20-136/Product: Ig heavy chain V region 4C11 #status predicted <MAT>
F;34-117/DNA: immunoglobulin homology <IMV>
F;50-54/Region: complementarity-determining 1
F;69-85/Region: complementarity-determining 2
F;118-125/Region: complementarity-determining 3
F;137-151/DNA: C region (fragment) #status predicted <COR>

Query Match 74.7%; Score 566.5; DB 2; Length 151;
Best Local Similarity 78.4%; Pred. No. 1.9e-41;
Matches 109; Conservative 9; Mismatches 18; Indels 3; Gaps 1;

Qy 1 MGWSWIFLLSLGAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHVKQSH 60
Db 1 MGWSWIFLLSLGAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHVKQSH 60

Qy 61 GKLEWIGIYYPNGVDYNGNFKSKATLIVDNSSNTAYMELSLTSDSAVYCARWDF 120
```

```
Db 61 GKSLEWIGGDPNDYFNKFKKATLTVDKSSSTAYMELSLTSEDSAVYCASDY 120
Qy 121 GSGYFDYDYGQGTTLTVSS 139
Db 121 GA---LDYWGQGTSTVTVSS 136

RESULT 5
T01407
Ig heavy chain (myeloma M104E) - mouse (fragment)
C:Species: Mus sp. (mouse)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Jun-2000
C:Accession: T01407
R;Takahashi, S.; Matsura, Y.; Taniguchi, T.; Tamura, H.; Bito, S.; Onishi, S.; Yamamoto
Microbiol. Immunol. 36, 855-863, 1992
A:Title: Molecular analysis of immunoglobulin heavy chain genes coding for idiotypic and
A:Reference number: Z14317; MUID:93116638; PMID:1474935
A:Accession: T01407
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-140 <TAK>
A:Cross-references: UNIPARC:UPI000011B298; EMBL:S51851; NID:g262657
C:Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 74.6%; Score 565.5; DB 2; Length 140;
Best Local Similarity 79.9%; Pred. No. 2.1e-41;
Matches 111; Conservative 8; Mismatches 17; Indels 3; Gaps 2;

Qy 1 MGWSWIFLLSCTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHWKQSH 60
Db 1 MGWSWIFLLSCTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHWKQSH 60
Qy 61 GKILEWIGIYPYNGVDYQNFQKSKATLIVDSSNTAYMELSLTSEDSAVYCARWDF 120
Db 61 GKILEWIGIYPYNGVDYQNFQKSKATLIVDSSNTAYMELSLTSEDSAVYCARWDF 120
Qy 61 GKSLEWIGDINPNNGGTSYQKPKGKATLTVDKSSSTAYMQLSLTSEDSAVYCAR-DY 119
Db 61 GKSLEWIGDINPNNGGTSYQKPKGKATLTVDKSSSTAYMQLSLTSEDSAVYCAR-DY 119
Qy 121 GSGYFDYDYGQGTTLTVSS 139
Db 120 --DWYFDVWGAGTTVTVSS 136

RESULT 6
S37483
Ig gamma-2a chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37483
R;Ducancel, F.F.D.
Submitted to the EMBL Data Library, February 1993
A:Reference number: S37483
A:Accession: S37483
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-469 <DUC>
A:Cross-references: UNIPARC:UPI000002FB47; EMBL:X70423; NID:g406252; PIDN:CAA49868.1; P
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:276-345/Domain: immunoglobulin homology <IMM>

Query Match 73.7%; Score 559; DB 2; Length 469;
Best Local Similarity 75.5%; Pred. No. 2.8e-40;
Matches 105; Conservative 14; Mismatches 20; Indels 0; Gaps 0;

Qy 1 MGWSWIFLLSCTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHWKQSH 60
Db 1 MGWSWIFLLSCTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHWKQSH 60
Qy 61 GKILEWIGIYPYNGVDYQNFQKSKATLIVDSSNTAYMELSLTSEDSAVYCARWDF 120
Db 61 GQGLKIGWIPYASGTYKYNFKGKATLTVDTSSTAYMQLSLTSEDSAVYFCARWG 120
Qy 121 GSGYFDYDYGQGTTLTVSS 139
```

```
Db 121 ATATLLDYWGQGTTLTVSS 139

RESULT 7
PH0105
anti-digoxin transfectoma antibody light chain V region precursor - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C:Accession: PH0105
R;Near, R.I.; Ng, S.C.; Mudgett-Hunter, M.; Hudson, N.W.; Margolies, M.N.; Seidman, J.G.
Mol. Immunol. 27, 901-909, 1990
A:Title: Heavy and light chain contributions to antigen binding in an anti-digoxin chain
A:Reference number: PH0105; MUID:91015092; PMID:2120577
A:Accession: PH0105
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-138 <NEA>
A:Cross-references: UNIPARC:UPI0000115EC4; GB:X56622; GB:S44836; NID:g49875; PIDN:CAA399
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 72.4%; Score 548.5; DB 2; Length 138;
Best Local Similarity 74.8%; Pred. No. 5.8e-40;
Matches 104; Conservative 16; Mismatches 18; Indels 1; Gaps 1;

Qy 1 MGWSWIFLLSCTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHWKQSH 60
Db 1 MGWSWIFLLSCTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHWKQSH 60
Qy 61 GKILEWIGIYPYNGVDYQNFQKSKATLIVDSSNTAYMELSLTSEDSAVYCARWDF 120
Db 61 GKSLDYGIVTSPYSGVTGYNQKPKGKATLTVDKSSSTAYMELSLTSEDSAVYCA-GSS 119
Qy 121 GSGYFDYDYGQGTTLTVSS 139
Db 120 GNKWMADYWGAGTTVTVSS 138

RESULT 8
PH1482
Ig heavy chain V region (clones 36-35 [TG] and X7-TG) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C:Accession: PH1482; PH1495
R;Giusti, A.M.; Manser, T.
J. Exp. Med. 177, 797-809, 1993
A:Title: Hypermutation is observed only in antibody H chain V region transgenes that have
d for somatic mutation.
A:Reference number: PH1482; MUID:93171820; PMID:8436910
A:Accession: PH1482
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-140 <GIU>
A:Cross-references: UNIPARC:UPI0000176BA2
A:Experimental source: hybridoma cell
C:Genetics:
A:Introns: 16/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 72.2%; Score 547.5; DB 2; Length 140;
Best Local Similarity 75.7%; Pred. No. 7.2e-40;
Matches 106; Conservative 12; Mismatches 21; Indels 1; Gaps 1;

Qy 1 MGWSWIFLLSCTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHWKQSH 60
Db 1 MGWSWIFLLSCTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHWKQSH 60
Qy 61 GKILEWIGIYPYNGVDYQNFQKSKATLIVDSSNTAYMELSLTSEDSAVYCARWDF 119
Db 61 GQGLKIGWIPYASGTYKYNFKGKATLTVDKSSSTAYMQLSLTSEDSAVYFCARSVY 120
```

```
Qy 120 FGSYYFDYWGQGTTLTVSS 139
Db 121 YGGSYYFDYWGQGTTLTVSS 140

RESULT 9
PS0057
Ig heavy chain precursor V region (PAR) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 20-Jun-2000
C;Accession: PS0057
R;Yasuda, Y.; Takahashi, M.; Azuma, C.; Kanai, Y.; Honjo, T.
J. Biochem. 104, 337-343, 1988
A;Title: Biased expression of variable region gene families of the immunoglobulin heavy
A;Reference number: PS0057; MUID:89197817; PMID:2467902
A;Accession: PS0057
A;Molecule type: DNA
A;Residues: 1-135 <YAO>
A;Cross-references: UNIPARC:UPI000011B257; GB:D00307; NID:G220448; PIDN:BAA00213.1; PID:
A;Note: The authors translated the codon AAG for residue 32 as Asn and GAC for 92 as Gly
C;Comment: The gene encoding this protein was isolated from a hybridoma that produces an
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-135/Product: Ig heavy chain V region PAR #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 72.2%; Score 547; DB 2; Length 135;
Best Local Similarity 77.0%; Pred. No. 7.7e-40;
Matches 107; Conservative 10; Mismatches 18; Indels 4; Gaps 1;

Qy 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNIHVKQSH 60
Db 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYSTGYFNMWVKQSH 60

Qy 61 GKLEWIGYIYPNGVDYNGNQNFKSKATLVDNSNTAYMELRSLTSEDSAVYYCARWDF 120
Db 61 GKLEWIGIRINPYNGDFTPNQKFGKATLVDKSSSTAHELRSLTSEDSAVYYCARLNY 120

Qy 121 GSGYYFDYWGQGTTLTVSS 139
Db 121 RGA-----YWGQGTTLTVSA 135

RESULT 10
PN0444
Ig heavy chain V region precursor - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PN0444
R;Kaluza, B.; Betzel, G.; Shao, H.; Diamantstein, T.; Weidle, U.H.
Gene 122, 321-328, 1992
A;Title: A general method for chimerization of monoclonal antibodies by inverse polymers
A;Reference number: PN0444; MUID:93138402; PMID:1339379
A;Accession: PN0444
A;Molecule type: mRNA
A;Residues: 1-150 <KAL>
A;Cross-references: UNIPARC:UPI0000176A08; GB:L02346
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-150/Product: Ig heavy chain V region #status predicted <MAT>
F;20-117/Domain: variable region <VRG>
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 71.8%; Score 544; DB 2; Length 150;
Best Local Similarity 78.4%; Pred. No. 1.5e-39;
Matches 109; Conservative 4; Mismatches 29; Indels 2; Gaps 1;

Qy 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNIHVKQSH 60
Db 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYIFTDYNMDWVKQSH 60
```

```
Qy 61 GKLEWIGYIYPNGVDYNGNQNFKSKATLVDNSNTAYMELRSLTSEDSAVYYCARWDF 120
Db 61 GKLEWIGIDIDPNFSSSSNQKFGKATLVDKSSNTAYMELRSLTSEDSAVYYCARGGF 120

Qy 121 GSGYYFDYWGQGTTLTVSS 139
Db 121 --PYGMDYWGQGTSTVTVSS 137

RESULT 11
S45249
Ig heavy chain precursor V region (Mab 1G3) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 07-May-1998 #sequence_revision 15-May-1998 #text_change 21-Jan-2000
C;Accession: S45249; S41429
R;Sassano, M.; Repetto, M.; Cassani, G.; Corti, A.
Nucleic Acids Res. 22, 1768-1769, 1994
A;Title: PCR amplification of antibody variable regions using primers that anneal to conserved
A;Reference number: S45249; MUID:94261453; PMID:8202386
A;Accession: S45249
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-138 <SAS>
A;Cross-references: UNIPARC:UPI00001161D5; EMBL:X77230; NID:G452273; PIDN:CAAS4447.1; PID:
A;Note: The nucleotide sequence was submitted to the EMBL Data Library, January 1994
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 70.6%; Score 535.5; DB 2; Length 138;
Best Local Similarity 72.4%; Pred. No. 7.5e-39;
Matches 105; Conservative 10; Mismatches 17; Indels 13; Gaps 2;

Qy 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNIHVKQSH 60
Db 1 MGWSWIFLLSGTAGVLSAVQLQSGPELVKPGASVKISCKASGDSFTGNDLHWVRQSH 60

Qy 61 GKLEWIGYIYPNGVDYNGNQNFKSKATLVDNSNTAYMELRSLTSEDSAVYYCAR--- 117
Db 61 VRSLWIGIRISPYNGVTSYKKNFKDKATLVDSSSTAYMELHSLTSEDSAVYYCTPTTT 120

Qy 118 ---WDFGSGYYFDYWGQGTTLTVSS 139
Db 121 VDTW-----FPYWGQGTTLTVSA 138

RESULT 12
HVMSG7
Ig heavy chain precursor V region (93G7, 36-65) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 09-Jul-2004
C;Accession: A94264; A91261; A02028
R;Slims, J.; Rabbitts, T.H.; Estess, P.; Slaughter, C.; Tucker, P.W.; Capra, J.D.
Science 216, 309-311, 1982
A;Title: Somatic mutation in genes for the variable portion of the immunoglobulin heavy
A;Reference number: A94264; MUID:82152818; PMID:6801765
A;Accession: A94264
A;Molecule type: mRNA
A;Residues: 1-140 <SIM>
A;Cross-references: UNIPROT:P01746; UNIPARC:UPI00000270DA; GB:J00493; NID:G195006; PIDN:
A;Experimental source: strain A/J, hybridoma 93G7
R;Stekevit, M.; Geifert, M.L.; Brodeur, P.; Riblet, R.; Marshak-Rothstein, A.
Eur. J. Immunol. 12, 1023-1032, 1982
A;Title: The genetic basis of antibody production: the dominant anti-arsenate idiotype
A;Reference number: A91261; MUID:83131846; PMID:6186498
A;Accession: A91261
A;Molecule type: DNA
A;Residues: 20-76, 'TK', 79-118, 'V', 120-125, 'Y', 127-134, 'T', 136-140 <SIE>
A;Cross-references: UNIPARC:UPI0000114D5B; GB:M19292; NID:G196201; PIDN:AAA38625.1; PID:
A;Experimental source: strain A/J, hybridoma 36-65
A;Note: the sequence was determined from the differentiated gene
A;Note: from analysis of the sizes of several other differentiated genes that hybridize
```

C;Genetics: 16/1
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; hybridoma; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-140/Product: Ig heavy chain V region (93G7) #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>
F;41-115/Disulfide bonds: #status predicted

Query Match 70.1%; Score 532.5; DB 1; Length 140;
Best Local Similarity 74.3%; Pred. No. 1.7e-38;
Matches 104; Conservative 12; Mismatches 23; Indels 1; Gaps 1;

Qy 1 MGWSWIFLLSGTAGVHSEVQLQQSGPELVKPGASVKISKASGYFTFDYNIHWKQSH 60
Db 1 MGWSWIFLLSVTAGVHSEVQLQQSGAELVRAGSSVYKMSCKASGYFTTSGINWVKQRP 60

Qy 61 GKILEWIGIYIPYNGVSDYNQNPFSKATLIVDNSSNTAYMELSLTSEDSAVYCARWD- 119
Db 61 GQGLEWIGIYIPNGVSDYNQNPFSKATLIVDNSSNTAYMELSLTSEDSAVYCARWD- 119

Qy 120 FGSYYFDYWGQGTTLTVSS 139
Db 121 YGGSYYFDYWGQGTTLTVSS 140

RESULT 13
PH1489
Ig heavy chain V region (clone X41-2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C;Accession: PH1489
R;Giusti, A.M.; Manser, T.
J. Exp. Med. 177, 797-809, 1993
A;Title: Hypermutation is observed only in antibody H chain V region transgenes that have d for somatic mutation.
A;Reference number: PH1482; MUID:93171820; PMID:8436910
A;Accession: PH1489
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-140 <GIU>
A;Cross-references: UNIPARC:UPI0000176BA8
A;Experimental source: hybridoma cell
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 70.1%; Score 531.5; DB 2; Length 140;
Best Local Similarity 73.6%; Pred. No. 1.7e-38;
Matches 103; Conservative 13; Mismatches 23; Indels 1; Gaps 1;

Qy 1 MGWSWIFLLSGTAGVHSEVQLQQSGPELVKPGASVKISKASGYFTFDYNIHWKQSH 60
Db 1 MGWSWIFLLSVTAGVHSEVQLQQSGAELVRAGSSVYKMSCKASGYFTTSGINWVKQRP 60

Qy 61 GKILEWIGIYIPYNGVSDYNQNPFSKATLIVDNSSNTAYMELSLTSEDSAVYCAR-WD 119
Db 61 GQGLEWIGIYIPNGVSDYNQNPFSKATLIVDNSSNTAYMELSLTSEDSAVYCAR-WD 119

Qy 120 FGSYYFDYWGQGTTLTVSS 139
Db 121 YGGSYYFDYWGQGTTLTVSS 140

RESULT 14
PL0012
Ig heavy chain precursor V region (F6-3) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C;Accession: PL0012
R;Cheng, H.L.; Sood, A.K.; Ward, R.E.; Kieber-Emmons, T.; Kohler, H.
Mol. Immunol. 25, 33-40, 1988
A;Title: Structural basis of stimulatory anti-idiotypic antibodies.

A;Reference number: PL0011; MUID:88142863; PMID:3125424
A;Accession: PL0012
A;Molecule type: mRNA
A;Residues: 1-166 <CHE>
A;Cross-references: UNIPARC:UPI0000176D3C
A;Experimental source: cell line F6-3
C;Comment: This protein is an anti-idiotypic antibody which induces an anti-phosphorylcholine
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-32/Domain: signal sequence #status predicted <SIG>
F;33-151/Product: Ig heavy chain V region 4C11 #status predicted <MAT>
F;47-130/Domain: immunoglobulin homology <IMM>
F;63-67/Region: complementarity-determining 1
F;82-98/Region: complementarity-determining 2
F;131-140/Region: complementarity-determining 3
F;152-166/Domain: C region(fragment) #status predicted <COR>

Query Match 70.0%; Score 530.5; DB 2; Length 166;
Best Local Similarity 72.7%; Pred. No. 2.4e-38;
Matches 101; Conservative 14; Mismatches 23; Indels 1; Gaps 1;

Qy 1 MGWSWIFLLSGTAGVHSEVQLQQSGPELVKPGASVKISKASGYFTFDYNIHWKQSH 60
Db 14 MGWSWIFLLSGTAGVLSQVQLQQSGPELVKPGASVKISKASGYFTFDYNIHWKQSH 73

Qy 61 GKILEWIGIYIPYNGVSDYNQNPFSKATLIVDNSSNTAYMELSLTSEDSAVYCARWDF 120
Db 74 GKLEWIGIYIPYDITNYKENPKGRATVVDKSSSTVYVQLNSLTSEDSAVYCAR-EG 132

Qy 121 GSGYYFDYWGQGTTLTVSS 139
Db 133 GFGNSLDYWGQGTSTVNVSS 151

RESULT 15
PH1484
Ig heavy chain V region (clones X7-3C5 and X7-3C5H) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C;Accession: PH1484; PH1497
R;Giusti, A.M.; Manser, T.
J. Exp. Med. 177, 797-809, 1993
A;Title: Hypermutation is observed only in antibody H chain V region transgenes that have d for somatic mutation.
A;Reference number: PH1482; MUID:93171820; PMID:8436910
A;Accession: PH1484
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-140 <GIU>
A;Cross-references: UNIPARC:UPI0000176BA4
A;Experimental source: hybridoma cell
C;Genetics: 16/1
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 69.3%; Score 525.5; DB 2; Length 140;
Best Local Similarity 73.6%; Pred. No. 5.4e-38;
Matches 103; Conservative 13; Mismatches 23; Indels 1; Gaps 1;

Qy 1 MGWSWIFLLSGTAGVHSEVQLQQSGPELVKPGASVKISKASGYFTFDYNIHWKQSH 60
Db 1 MGWSWIFLLSVTAGVHSEVQLQQSGAELVRAGSSVYKMSCKASGYFTTNGINWVKQRP 60

Qy 61 GKILEWIGIYIPYNGVSDYNQNPFSKATLIVDNSSNTAYMELSLTSEDSAVYCAR-WD 119
Db 61 GQGLEWIGIYIPNGVSDYNQNPFSKATLIVDNSSNTAYMELSLTSEDSAVYCAR-WD 119

Qy 120 FGSYYFDYWGQGTTLTVSS 139
Db 121 YGGSYYFDYWGQGTTLTVSS 140

RESULT 16
MHWS18
IG heavy chain precursor V region (B1-8) - mouse
N;Contains: IG heavy chain precursor V region 186-2
C;Species: Mus musculus (house mouse)
C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 09-Jul-2004
C;Accession: A90809; B90809; A22769; A02034; A02036
R;Bothwell, A.L.M.; Paskind, M.; Reth, M.; Imanishi-Kari, T.; Rajewsky, K.; Baltimore, I.
Cell 24, 625-637, 1981
A;Title: Heavy chain variable region contribution to the NP(b) family of antibodies: som
A;Reference number: A90809; MUID:81234548; PMID:6788376
A;Accession: A90809
A;Molecule type: DNA
A;Residues: 1-139 <B18>
A;Cross-references: UNIPROT:P01751; UNIPARC:UPI00000270EB; GB:J00529; NID:ig195114; PIDN:
A;Accession: B90809
A;Molecule type: DNA
A;Residues: 1-117 <1862>
A;Cross-references: UNIPARC:UPI000017372F
A;Note: the B1-8 mu chain mRNA was cloned from a hybridoma making antibodies to the hapt
A;Note: the 186-2 germline gene was cloned from a library of C57BL/6 DNA
R;Dildrop, R.; Bruggemann, M.; Radbruch, A.; Rajewsky, K.; Beyreuther, K.
EMBO J. 1, 635-640, 1982
A;Title: Immunoglobulin V region variants in hybridoma cells. II. Recombination between
A;Reference number: A90971; MUID:84236026; PMID:7188353
A;Accession: A22769
A;Molecule type: protein
A;Residues: 20-139 <DIL>
A;Cross-references: UNIPARC:UPI000002BD97
A;Note: the V region of the B1-8 delta chain, derived as a spontaneous class switch vari
of the mu chain
C;Genetics: 16/
A;Introns: 16/
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-139/Product: IG kappa chain V region (B1-8) #status experimental <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>
F;118-124/Region: D segment
F;125-139/Region: J segment (JH2)

	Query Match	68.9%;	Score 522;	DB 1;	Length 139;
	Best Local Similarity	71.9%;	Pred. No. 1.1e-37;		
	Matches 100;	Conservative 12;	Mismatches 27;	Indels 0;	Gaps 0;
Qy	1	MGMSWIEFLLSGCTAGVHSEVOLQOSGPELVKPCASVKISKASGYTFTDYNTHWVKOSH	60		
		: : : : : : : : :			
Db	1	MGMSCIIMFLAATATGTVHSGVQVQOGAEVLKPCASVKLSKASGYTFTSYNHWVKQRP	60		
		: : : : : : : : :			
Qy	61	GKILEWIGXYTPYNGVSDYNNQNFKSKATLIVDNSNTAYMELSLTSEDNAVYYCARWDF	120		
		: : : : : : : : :			
Db	61	GRGLEWIGRIDPNSGGTKYNEKFKSKATLIVDKPSSTAYMQLSLTSEDNAVYYCARYDY	120		
		: : : : : : : : :			
Qy	121	GSYYFDYWGQGTTLTVSS	139		
		: : : : : : : : :			
Db	121	YGSSYFDYWGQGTTLTVSS	139		
		: : : : : : : : :			

RESULT 17
PH1493
IG heavy chain V region (clone PR14-3) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C/Accession: PH1493
E/Giusti, A. M.; Manser, T.
J. Exp. Med. 177, 797-809, 1993
A/Title: Hypermutation is observed only in antibody H chain V region transgenes that have
d for somatic mutation.
A/Reference number: PH1482; MUID:93171820; PMID:8436910
A/Accession: PH1493
A/Status: translation not shown
A/Molecule type: mRNA

```

A:Residues: 1-135 <GU>
A:Cross-references: UNIPARC:UPI0000176BA9
A:Experimental source: hybridoma cell
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match      68.8%; Score 521.5; DB 2; Length 135;
Best Local Similarity 74.1%; Pred. No. 1.2e-37;
Matches 100; Conservative 13; Mismatches 21; Indels 1; Gaps 1;

Qy      1  MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFDTYNIHWVKQSH 60
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      1  MGWSFIFLLSVTAGVHSEVQLQSGAEVLVAGSSVKMSCKASGYTFDTYGINWVKRP 60
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy      61  GKILEWIGTYTPYNGVSDYNQNFKSKATLIIVDNSNTAYMELRSITSDSAVYCAR-WD 119
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      61  GGQLEWIGYINPGNGFTKYNEKFGETTLITVDKSSITAYMLQRLSITSDSAVYFCARSVY 120
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy      120  FGSGYYFDYWGQGT 134
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      121  YGSGYYFDYWGQGT 135
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

RESULT 18

PH1498
Ig heavy chain V region (clone X7-4G7H) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C:Accession: PH1498
R:Giusti, A.M.; Manser, T.
J. Exp. Med. 177, 797-809, 1993
A:Title: Hypermutation is observed only in antibody H chain V region transgenes that have
d for somatic mutation.
A:Reference number: PH1482; MUID:93171820; PMID:8436910
A:Accession: PH1498
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-140 <GIU>
A:Cross-references: UNIPARC:UPI0000176BAB
A:Experimental source: hybridoma cell
C:Genetics:
A:Introns: 16/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
P:34-117/Domain: immunoglobulin homology <IMM>

Query Match	68.7%	Score	520.5	DB 2	Length	140			
Best Local Similarity	72.9%	Pred. No.	1.5e-37						
Matches	102	Conservative	11	Mismatches	26	Indels	1	Gaps	1
Qy	1	MGNSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNIHVWKQSH	60						
Db	1	MGNSFIFLLSVTAGVHSEVQLQSGAELVRAGSSVKMSCKASGYTFTSNGINHWKQRP	60						
Qy	61	GKILEWTGYTPYNGVDYDNQNFKSKATLIVDNSNTAYMELRLTSDSAVYYCA-RWD	119						
Db	61	GQGLEWGYINPGNGYINYNNAKFKGKTLTLLADKSSSTAYMQLRGLTSDSAVYFCAGSVY	120						
Qy	120	FGSGYYFDYWGQGTTLTVSS	139						
Db	121	YGGSYFDYWGQGTTLTVSS	140						

RESULT 19

IG heavy chain V region (clones X7-5D3 and X7-5D3H) - mouse (fragment)
 PH1483
 C:Species: Mus musculus (house mouse)
 C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
 C:Accession: PH1483; PH1496
 R:Giusti, A.M.; Manser, T.
 J. Exp. Med. 177, 797-809, 1993
 A:Title: Hypermutation is observed only in antibody H chain V region transgenes that have

d for somatic mutation.
A;Reference number: PH1482; MUID:93171820; PMID:8436910
A;Accession: PH1483
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-140 <GIU>
A;Cross-references: UNIPARC:UPI0000176BA3
A;Experimental source: hybridoma cell
C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 68.7%; Score 520.5; DB 2; Length 140;
Best Local Similarity 72.9%; Pred. No. 1.5e-37;
Matches 102; Conservative 12; Mismatches 25; Indels 1; Gaps 1;
Qy 1 MGWSWIFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNIHVWKQSH 60
Db 1 MGWSWIFLLSVTAGVHSEVQLQQSGVEQVRTGSSVKMSCKASGYTFTSYGINVWKQRP 60
Qy 61 GKILEWIGYIYPNGVSDYNQNFKSKATLIVDNSSNTAYMELSLTSEDSAVYYCAR-WD 119
Db 61 GQGLEWIGYIHPGKGYIHYSEKFKDKTTLTVDKSSSTAYNQRLSLTSEDSAVYLCARSVY 120
Qy 120 FGSYYFDYWGQGTTLTVSS 139
Db 121 YGGSYYFDYWAQGTTLTVSS 140

RESULT 20
PH1488
Ig heavy chain V region (clone X41-1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C;Accession: PH1488
R;Giusti, A.M.; Manser, T.
J. Exp. Med. 177, 797-809, 1993
A;Title: Hypermutation is observed only in antibody H chain V region transgenes that have
d for somatic mutation.
A;Reference number: PH1482; MUID:93171820; PMID:8436910
A;Accession: PH1488
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-140 <GIU>
A;Cross-references: UNIPARC:UPI0000176BA7
A;Experimental source: hybridoma cell
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 68.7%; Score 520.5; DB 2; Length 140;
Best Local Similarity 71.4%; Pred. No. 1.5e-37;
Matches 100; Conservative 16; Mismatches 23; Indels 1; Gaps 1;
Qy 1 MGWSWIFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNIHVWKQSH 60
Db 1 MGWSWIFLLSVTAGVHSEVQLQQFGAELVRAGSSVKMSCKASGYTFTTYGINVWKQRP 60
Qy 61 GKILEWIGYIYPNGVSDYNQNFKSKATLIVDNSSNTAYMELSLTSEDSAVYYCAR-WD 119
Db 61 GQGLEWIGYINPGYIKYNEKPKGKTTTLTVDKSASTAYMQVRSLSLTSEDSAVYFCRSRVY 120
Qy 120 FGSYYFDYWGQGTTLTVSS 139
Db 121 YGGSYYFDYWGQGTTLTVSS 140

Search completed: March 20, 2006, 07:36:25
Job time : 5.07199 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 20, 2006, 07:32:13 ; Search time 2.60454 Seconds
(without alignments)
1527.558 Million cell updates/sec

Title: US-10-687-035-34

Perfect score: 758

Sequence: 1 MGMSWIFLLSCTAGVHSE.....FGSGYFDYWGQTTITVSS 139

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 169630 seqs, 28622889 residues

Total number of hits satisfying chosen parameters: 169630

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Published Applications_AA_New:*
1: /cgn2_6/ptodata/2/pubppaa/US08_NEW_PUB.pdb:*
2: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pdb:*
3: /cgn2_6/ptodata/2/pubppaa/US07_NEW_PUB.pdb:*
4: /cgn2_6/ptodata/2/pubppaa/PCT_NEW_PUB.pdb:*
5: /cgn2_6/ptodata/2/pubppaa/US09_NEW_PUB.pdb:*
6: /cgn2_6/ptodata/2/pubppaa/US10_NEW_PUB.pdb:*
7: /cgn2_6/ptodata/2/pubppaa/US11_NEW_PUB.pdb:*
8: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pdb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	577	76.1	139	6	US-10-504-389A-28
2	562	74.1	137	7	US-11-074-373-39
3	543.5	71.7	138	7	US-11-125-837-22
4	537.5	70.9	140	7	US-11-193-512-27
5	536	70.7	592	6	US-10-016-686-4
6	518.5	68.4	136	7	US-11-250-411-88
7	518.5	68.4	142	7	US-11-170-453-7
8	513	67.7	293	7	US-11-116-939-10
9	513	67.7	824	7	US-11-116-939-11
10	505.5	66.7	140	7	US-11-193-512-63
11	496.5	65.5	136	7	US-11-250-411-91
12	495.5	65.4	136	7	US-11-250-411-95
13	494.5	65.2	140	7	US-11-183-205-62
14	493.5	65.1	140	7	US-11-193-512-74
15	488	64.4	145	6	US-10-504-389A-45
16	487.5	64.3	140	7	US-11-193-512-78
17	487	64.2	143	6	US-10-932-334-52
18	487	64.2	143	6	US-11-177-648-9
19	485.5	64.1	462	7	US-11-193-512-83
20	482.5	63.7	140	7	US-11-089-872-3
21	478	63.1	138	7	US-11-126-798-4
22	477	62.9	153	7	US-10-016-686-3
23	477	62.9	488	6	US-11-177-648-30
24	475.5	62.7	462	7	US-11-177-648-33
25	475.5	62.7	462	7	US-11-177-648-33

139	7	US-11-226-325-34	Sequence 34, Appl
130	7	US-11-179-820-6	Sequence 6, Appl
119	7	US-11-154-337-2	Sequence 2, Appl
119	7	US-11-182-908-2	Sequence 2, Appl
119	7	US-11-102-120-2	Sequence 2, Appl
119	7	US-11-223-361-2	Sequence 1, Appl
243	6	US-10-016-686-1	Sequence 4, Appl
117	7	US-11-087-528-4	Sequence 4, Appl
117	7	US-11-122-622-4	Sequence 4, Appl
139	7	US-11-226-325-4	Sequence 26, Appl
139	7	US-11-226-325-26	Sequence 26, Appl
139	7	US-11-226-325-44	Sequence 2, Appl
232	7	US-11-173-564-2	Sequence 32, Appl
462	7	US-11-177-648-32	Sequence 30, Appl
139	7	US-11-226-325-30	Sequence 16, Appl
115	7	US-11-165-023-16	Sequence 16, Appl
139	7	US-11-226-325-100	Sequence 100, Appl
139	7	US-11-226-325-36	Sequence 36, Appl
121	7	US-11-107-028-35	Sequence 35, Appl
462	7	US-11-177-648-31	Sequence 31, Appl
462	7	US-11-177-648-97	Sequence 97, Appl
120	6	US-10-932-334-74	Sequence 74, Appl
139	7	US-11-226-325-24	Sequence 24, Appl
114	7	US-11-102-743-7	Sequence 7, Appl
139	7	US-11-226-325-32	Sequence 32, Appl
139	7	US-11-226-325-46	Sequence 46, Appl
139	7	US-11-226-325-50	Sequence 50, Appl
139	7	US-11-226-325-127	Sequence 127, Appl
122	7	US-11-107-028-39	Sequence 39, Appl
139	7	US-11-226-325-18	Sequence 18, Appl
139	7	US-11-226-325-22	Sequence 22, Appl
139	7	US-11-226-325-48	Sequence 48, Appl
467	7	US-11-158-505-72	Sequence 72, Appl
119	7	US-11-097-812-71	Sequence 71, Appl
119	7	US-11-097-812-73	Sequence 73, Appl
119	7	US-11-097-812-74	Sequence 74, Appl
119	7	US-11-097-812-76	Sequence 76, Appl
462	7	US-11-177-648-28	Sequence 28, Appl
120	6	US-10-932-334-72	Sequence 72, Appl
138	7	US-11-250-411-90	Sequence 90, Appl
139	7	US-11-226-325-38	Sequence 38, Appl
117	6	US-10-932-334-76	Sequence 76, Appl
119	6	US-10-507-662-22	Sequence 22, Appl
130	7	US-11-188-187A-3	Sequence 3, Appl
139	7	US-11-226-325-16	Sequence 16, Appl
139	7	US-11-226-325-20	Sequence 20, Appl
471	7	US-11-106-820-25	Sequence 25, Appl
471	7	US-11-106-820-27	Sequence 27, Appl
471	7	US-11-190-364-22	Sequence 22, Appl
471	7	US-11-190-364-23	Sequence 23, Appl
471	7	US-11-147-780-22	Sequence 23, Appl
471	7	US-11-147-780-23	Sequence 23, Appl
139	7	US-11-226-325-28	Sequence 28, Appl
467	7	US-11-158-505-5	Sequence 5, Appl
467	7	US-11-158-505-13	Sequence 13, Appl
467	7	US-11-158-505-15	Sequence 15, Appl
467	7	US-11-158-505-21	Sequence 21, Appl
467	7	US-11-158-505-23	Sequence 23, Appl
467	7	US-11-158-505-29	Sequence 29, Appl
467	7	US-11-158-505-31	Sequence 31, Appl
120	7	US-11-097-812-144	Sequence 144, Appl
138	7	US-11-250-411-86	Sequence 86, Appl
462	7	US-11-177-648-95	Sequence 95, Appl
115	7	US-11-165-023-31	Sequence 31, Appl
119	7	US-11-097-812-66	Sequence 66, Appl
119	7	US-11-097-812-67	Sequence 67, Appl

99 454.5 60.0 120 7 US-11-097-812-136 Sequence 136, App
100 454.5 60.0 120 7 US-11-097-812-145 Sequence 145, App

ALIGNMENTS

RESULT 1
US-10-504-389A-28
; Sequence 28, Application US/10504389A
; Publication No. US20060045876A1
; GENERAL INFORMATION:
; APPLICANT: Renner, Christoph
; APPLICANT: Scott, Andrew
; TITLE OF INVENTION: FUSION PROTEINS OF HUMANIZED G250 SPECIFIC
; TITLE OF INVENTION: ANTIBODIES AND USES THEREOF
; FILE REFERENCE: LUD 5821
; CURRENT APPLICATION NUMBER: US/10/504,389A
; CURRENT FILING DATE: 2004-08-10
; PRIOR APPLICATION NUMBER: PCT/US03/04243
; PRIOR FILING DATE: 2002-02-12
; NUMBER OF SEQ ID NOS: 56
; SEQ ID NO 28
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: amino acid sequence for murine 19/2 heavy chain variable region
US-10-504-389A-28

Query Match 76.1%; Score 577; DB 6; Length 139;
Best Local Similarity 83.6%; Pred. No. 4.7e-41;
Matches 112; Conservative 7; Mismatches 13; Indels 2; Gaps 1;

Qy 6 IFLFLLSGTAGVHSEVOLQQSGPELVKPGASVKISCKASGYTFDYNHIVHWKQSHGKILE 65
Db 4 IMLFLLSGTAGVHSEVOLQQSGPELVKPGASVKISCKASGYTFDYNHIVHWKQSHGKSLD 63

Qy 66 WIGYIYPNGVSDYNQNFKSKATLIVDSSNTAYMELRLSLTSEDSAVYYCARWDFGSGYY 125
Db 64 WIGYIAPVSGGTGYNQFKNRATLTVDKSSSTAYMELRLSLTSDSDSAVYYCARRD--RFPY 121

Qy 126 FDYWGQGTTLTVSS 139
Db 122 FDYWGQGTTLTVSS 135

RESULT 2
US-11-074-373-39
; Sequence 39, Application US/11074373
; Publication No. US20060024302A1
; GENERAL INFORMATION:
; APPLICANT: Achen et al.
; TITLE OF INVENTION: CHIMERIC ANTI-VEGF-D ANTIBODIES AND HUMANIZED ANTI-VEGF-D ANTIBODIES
; TITLE OF INVENTION: AND METHODS OF USING SAME
; FILE REFERENCE: 28967/39969A
; CURRENT APPLICATION NUMBER: US/11/074,373
; CURRENT FILING DATE: 2005-03-07
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 39
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-074-373-39

Query Match 74.1%; Score 562; DB 7; Length 137;
Best Local Similarity 74.8%; Pred. No. 8e-40;
Matches 104; Conservative 15; Mismatches 18; Indels 2; Gaps 1;

Qy 1 MGWSWIFLLSGTAGVHSEVOLQQSGPELVKPGASVKISCKASGYTFDYNHIVHWKQSH 60
Db 1 MGWSGVFLLLSGTAGVHSEIQLQQSGPDLVKPGASVKVSCRASGYSTGYNMYWVKQSH 60

Qy 61 GKLEWIGYIYPNGVSDYNQNFKSKATLIVDSSNTAYMELRLSLTSEDSAVYYCARWDF 120
Db 61 GKLEWIGYIDPNGDTTNNQKFKGKATLTVDKSSSTAFMHLNLSLTSEDSAVYYCARTSY 120

Qy 121 GSGYFDYWGQGTTLTVSS 139
Db 121 YGG--MDYWGQGTSLTVSS 137

RESULT 3
US-11-125-837-22
; Sequence 22, Application US/11125837
; Publication No. US20050266003A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Rong-Hwa
; APPLICANT: Chang, Chung Nan
; APPLICANT: Chen, Pei-Jiun
; APPLICANT: Huang, Chiu-Chen
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 13062-011001
; CURRENT APPLICATION NUMBER: US/11/125,837
; CURRENT FILING DATE: 2005-05-10
; PRIOR APPLICATION NUMBER: US 60/569,892
; PRIOR FILING DATE: 2004-05-10
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-125-837-22

Query Match 71.7%; Score 543.5; DB 7; Length 138;
Best Local Similarity 77.1%; Pred. No. 2.7e-38;
Matches 108; Conservative 7; Mismatches 22; Indels 3; Gaps 2;

Qy 1 MGWSWIFLLSGTAGVHSEVOLQQSGPELVKPGASVKISCKASGYTFDYNHIVHWKQSH 60
Db 1 MEWSWIFLLSVTTGVHSEVOLQQSGPDLVKPGALVKISCKASGYSTFYIHWKQSH 60

Qy 61 GKLEWIGYIYPNGVSDYNQNFKSKATLIVDSSNTAYMELRLSLTSEDSAVYYCARWDF 120
Db 61 GKLEWIGRVNPTGTSYNPKFKKAILNVKSSSTAYMELRLSLTSEDSAVYYCAR--S 118

Qy 121 GSGYFDYWGQGTTLTVSS 139
Db 119 GSPYRYDDWGQGTTLTVSS 138

RESULT 4
US-11-193-512-27
; Sequence 27, Application US/11193512
; Publication No. US20050272918A1
; GENERAL INFORMATION:
; APPLICANT: KOIKE, Masamichi
; FURUYA, Akiko
; NAKAMURA, Kazuyasu
; IIDA, Akihiro
; ANAZAWA, Hideharu
; HANAI, Nobuo
; TAKATSU, Kiyoshi
; TITLE OF INVENTION: Antibody Against Human Interleukin-5
; RECEPTOR ALPHA CHAIN
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:

```
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/11/193,512
;   FILING DATE: 01-AUG-2005
;   CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/10/283,349
;   FILING DATE: 29-Oct-2002
;   APPLICATION NUMBER: US/08/836,561
;   FILING DATE: 09-MAY-1997
;   APPLICATION NUMBER: JP 232384/95
;   FILING DATE: 11-SEP-1995
; ATTORNEY/AGENT INFORMATION:
;   NAME: Lawrence, III, Stanton T
;   REGISTRATION NUMBER: 25,736
;   REFERENCE/DOCKET NUMBER: 7005-115-999
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 212-790-9090
;   TELEFAX: 212-869-9741
;   TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 140 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-11-193-512-27

Query Match          70.9%; Score 537.5; DB 7; Length 140;
Best Local Similarity 76.1%; Pred. No. 8.5e-38;
Matches 108; Conservative 5; Mismatches 24; Indels 5; Gaps 2;

QY 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHWKQSH 60
DB 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTSYVIHWKQRP 60
QY 61 GKILEWIGYIYPNGVDYNQNFKSKATLIVDNSSNTAYMELSLTSEDSAVYICARWDF 120
DB 61 GQGLWIGIYINPDGKTKYKATLTSDRSSSTVYMLSLTSEDSAVYLCGR--E 118
QY 121 GSGYY---FDYWGQGTTLTVSS 139
DB 119 GIRYGLLDGYWGQGTTLTVSS 140

RESULT 5
US-10-016-686-4
; Sequence 4, Application US/10016686
; Publication No. US2006001422A1
; GENERAL INFORMATION:
; APPLICANT: Oxford Biomedica (UK) Limited
; APPLICANT: Kingsman, Alan
; APPLICANT: Kingsman, Susan Mary
; APPLICANT: Bebbington, Christopher Robert
; APPLICANT: Carroll, Miles William
; APPLICANT: Ellard, Fiona Margaret
; APPLICANT: Myers, Kevin Alan
; TITLE OF INVENTION: Antibodies
; FILE REFERENCE: 674523-2012
; CURRENT APPLICATION NUMBER: US/10/016,686
; CURRENT FILING DATE: 2002-11-02
; PRIOR APPLICATION NUMBER: PCT/GB00/04317
; PRIOR FILING DATE: 2000-11-13
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 592
; TYPE: PRT

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: deduced amino acid sequence for the Ig-574 fusion protein
US-10-016-686-4

Query Match          70.7%; Score 536; DB 6; Length 592;
Best Local Similarity 74.8%; Pred. No. 4.2e-37;
Matches 104; Conservative 9; Mismatches 26; Indels 0; Gaps 0;

QY 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHWKQSH 60
DB 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTSYVIHWKQSH 60
QY 61 GKILEWIGYIYPNGVDYNQNFKSKATLIVDNSSNTAYMELSLTSEDSAVYICARWDF 120
DB 61 GKSLEWIGIRINENGVTLNQKFKKAILTVDKSSSTAYMELSLTSEDSAVYICARSTM 120
QY 121 GSGYYFDYWGQGTTLTVSS 139
DB 121 ITNYVMDYWGQVTSVTSS 139

RESULT 6
US-11-250-411-88
; Sequence 88, Application US/11250411
; Publication No. US20060034838A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: ITO, MIKITO
; APPLICANT: HANAI, NOBUO
; APPLICANT: KAWADA, YOKO
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: SHIBUYA, MASABUMI
; TITLE OF INVENTION: ANTI-HUMAN VEGF RECEPTOR FLT-1 MONOCLONAL ANTIBODY
; FILE REFERENCE: 249-107
; CURRENT APPLICATION NUMBER: US/11/250,411
; CURRENT FILING DATE: 2005-10-17
; PRIOR APPLICATION NUMBER: US/09/453,718
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 09/315,051
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/119,014
; PRIOR FILING DATE: 1998-07-20
; PRIOR APPLICATION NUMBER: PCT/JP97/04259
; PRIOR FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 88
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic protein
US-11-250-411-88

Query Match          68.4%; Score 518.5; DB 7; Length 136;
Best Local Similarity 72.7%; Pred. No. 3.1e-36;
Matches 101; Conservative 13; Mismatches 22; Indels 3; Gaps 1;

QY 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHWKQSH 60
DB 1 MGFSRIFLLSVTTGVHSGAFLQSGAELVRPGASVKMSCKASGYTFTSYVHWYKQTP 60
QY 61 GKILEWIGYIYPNGVDYNQNFKSKATLIVDNSSNTAYMELSLTSEDSAVYICARWDF 120
DB 61 RQGLEWIGAIFPGNGFTSYNQKFKKAILTVDKSSSTVYMLSLTSEDSAVYFCAR--- 117
QY 121 GSGYYFDYWGQGTTLTVSS 139
DB 118 DGDYFDYWGQGTTLTVSS 136

RESULT 7
```

```
US-11-170-453-7
; Sequence 7, Application US/111170453
; Publication No. US20060039913A1
; GENERAL INFORMATION:
; APPLICANT: Das, Anuk
; APPLICANT: Carton, Jill
; APPLICANT: Tsui, Ping
; TITLE OF INVENTION: ANTI-MCP1 ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN5068
; CURRENT APPLICATION NUMBER: US/11/170,453
; CURRENT FILING DATE: 2005-06-29
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 7
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Mus sp.
US-11-170-453-7

Query Match      58.4%; Score 518.5; DB 7; Length 142;
Best Local Similarity 70.4%; Pred. No. 3.2e-36;
Matches 100; Conservative 15; Mismatches 24; Indels 3; Gaps 1;

QY 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISKASGYTFTDYNHVKQSH 60
DB 1 MGWSWIFLLSGTAGVHSCVQLKQSGAEVLPKASVKLSCKASGYTFTDYNHVKQRP 60
QY 61 GKLEWIGIYYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRLTSEDSAVYYCARWD- 119
DB 61 GQGLEWIAIYVPGTNYNENPKGKATLTAEKSSSTAYMQLSLSLTSEDSAVYFCARSGS 120
QY 120 --FGSGIYFDYWGQGTTLTVSS 139
DB 121 TVVGNYYGMDYWGQGTSTVTVSS 142

RESULT 8
US-11-116-939-10
; Sequence 10, Application US/11116939
; Publication No. US20050265995A1
; GENERAL INFORMATION:
; APPLICANT: Stephen Tomlinson
; APPLICANT: Richard J. Quigg
; TITLE OF INVENTION: TISSUE TARGETED COMPLEMENT MODULATORS
; FILE REFERENCE: 19113.0115U2
; CURRENT APPLICATION NUMBER: US/11/116,939
; CURRENT FILING DATE: 2005-04-28
; PRIOR FILING DATE: 2005-04-28
; PRIOR FILING DATE: 2004-04-28
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; note=synthetic
; OTHER INFORMATION: construct
US-11-116-939-10

Query Match      67.7%; Score 513; DB 7; Length 293;
Best Local Similarity 69.9%; Pred. No. 1.7e-35;
Matches 100; Conservative 12; Mismatches 27; Indels 4; Gaps 2;

QY 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISKASGYTFTDYNHVKQSH 60
DB 151 MGWSVLMFLVATATGVHSQVQLKQSGPELVKPGVSKISCKSGYFTDYAIHWKQSH 210
QY 61 GKLEWIGIYYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRLTSEDSAVYYCAR- 119
DB 211 AKSLEWIGVISTYGHYTHNQKPKGKATLTVDKSSNTAYMELARLTSEDSAIYYCARPNN 270
QY 120 FGSG---YYPDYWGQGTTLTVSS 139

US-11-116-939-11
; Sequence 11, Application US/11116939
; Publication No. US20050265995A1
; GENERAL INFORMATION:
; APPLICANT: Stephen Tomlinson
; APPLICANT: Richard J. Quigg
; TITLE OF INVENTION: TISSUE TARGETED COMPLEMENT MODULATORS
; FILE REFERENCE: 19113.0115U2
; CURRENT APPLICATION NUMBER: US/11/116,939
; CURRENT FILING DATE: 2005-04-28
; PRIOR FILING DATE: 2005-04-28
; PRIOR FILING DATE: 2004-04-28
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 824
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; note=synthetic
; OTHER INFORMATION: construct
US-11-116-939-11

Query Match      67.7%; Score 513; DB 7; Length 824;
Best Local Similarity 69.9%; Pred. No. 4.4e-35;
Matches 100; Conservative 12; Mismatches 27; Indels 4; Gaps 2;
```

Qy 1 MGMSWIFLLSCTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHMKQSH 60
Db 151 MGMSWIFLLSCTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHMKQSH 210
Qy 61 GKLEWIGIYPYNGVDYQNPKSKATLIVDSSNTAYMELSLTSEDSAVVYCAR-WD 119
Db 211 AKSLWIGVISTYGYGHTYQKPKGKATLIVDSSNTAYMELSLTSEDSAVVYCARPNN 270
Qy 120 FSGG---YFDFYMGQGTTLTVSS 139
Db 271 YGSSPPYANDCWGQGTSTVTVSS 293

RESULT 11

US-11-193-512-63
; Sequence 63, Application US/11193512
; Publication No. US20050272918A1
; GENERAL INFORMATION:
; APPLICANT: KOIKE, Masamichi
; FURUYA, Akiko
; NAKAMURA, Kazuyasu
; IIDA, Akihiro
; ANAZAWA, Hideharu
; HANAI, Nobuo
; TAKATSU, Kiyoshi
; TITLE OF INVENTION: Antibody Against Human Interleukin-5
; Receptor Alpha Chain
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pernie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/193,512
FILING DATE: 01-Aug-2005
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/283,349
FILING DATE: 29-Oct-2002
APPLICATION NUMBER: US/08/836,561
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: JP 232384/95
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lawrence, III, Stanton T
REGISTRATION NUMBER: 25,736
REFERENCE/DOCKET NUMBER: 7005-115-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 140 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 63:
US-11-193-512-63

Query Match 66.7%; Score 505.5; DB 7; Length 140;
Best Local Similarity 69.0%; Pred. No. 3.7e-35;
Matches 98; Conservative 14; Mismatches 25; Indels 5; Gaps 2;

Qy 1 MGMSWIFLLSCTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHMKQSH 60
Db 1 MENSWIFLLSCTAGVHSEVQLVQSGAEVKKPGASVKVSKASGYTFTSYVIHWVQAP 60
Qy 61 GKLEWIGIYPYNGVDYQNPKSKATLIVDSSNTAYMELSLTSEDSAVVYCARWDF 120
Db 61 GQGLEWVGYNPNYDGTQYNERPKGRVTITADTSTSTAYMELSLTSEDSAVVYCAR--E 118
Qy 121 GSGY---FDYMGQGTTLTVSS 139
Db 119 GIRYGLLDYMGQGTTLTVSS 140

RESULT 12

US-11-250-411-91
; Sequence 91, Application US/11250411
; Publication No. US20060034838A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: ITO, MIKITO
; APPLICANT: HANAI, NOBUO
; APPLICANT: KAWADA, YOKO
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: SHIBUYA, MASABUMI
; TITLE OF INVENTION: ANTI-HUMAN VEGF RECEPTOR FLT-1 MONOCLONAL ANTIBODY
; FILE REFERENCE: 249-107
; CURRENT APPLICATION NUMBER: US/11/250,411
; CURRENT FILING DATE: 2005-10-17
; PRIOR APPLICATION NUMBER: US/09/453,718
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 09/315,051
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/119,014
; PRIOR FILING DATE: 1998-07-20
; PRIOR APPLICATION NUMBER: PCT/JP97/04259
; PRIOR FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 91
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic protein
US-11-250-411-91

Query Match 65.5%; Score 496.5; DB 7; Length 136;
Best Local Similarity 67.6%; Pred. No. 2e-34;
Matches 94; Conservative 18; Mismatches 24; Indels 3; Gaps 1;

Qy 1 MGMSWIFLLSCTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHMKQSH 60
Db 1 MGFSRIFLLSVTTGVHSGVQLVQSGAEVKKPGASVKVSKASGYTFTINNMHWVQAP 60
Qy 61 GKLEWIGIYPYNGVDYQNPKSKATLIVDSSNTAYMELSLTSEDSAVVYCARWDF 120
Db 61 GQGLEWVGALFPNGGFTSYNQKPKGRVTITVDKSTSTAYMELSLTSEDSAVVYCAR--- 117
Qy 121 GSGYFDYMGQGTTLTVSS 139
Db 118 DGDYFDYMGQGTTLTVSS 136

RESULT 13

US-11-250-411-95
; Sequence 95, Application US/11250411
; Publication No. US20060034838A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: ITO, MIKITO
; APPLICANT: HANAI, NOBUO
; APPLICANT: KAWADA, YOKO
; APPLICANT: NAKAMURA, KAZUYASU

APPLICANT: SHIBUYA, MASABUMI
TITLE OF INVENTION: ANTI-HUMAN VEGF RECEPTOR FLT-1 MONOCLONAL ANTIBODY
FILE REFERENCE: 249-107
CURRENT APPLICATION NUMBER: US/11/250,411
PRIOR FILING DATE: 2005-10-17
PRIOR APPLICATION NUMBER: US/09/453,718
PRIOR FILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: 09/315,051
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/119,014
PRIOR FILING DATE: 1998-07-20
PRIOR APPLICATION NUMBER: PCT/JP97/04259
PRIOR FILING DATE: 1997-11-21
NUMBER OF SEQ ID NOS: 111
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 95
LENGTH: 136
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic protein
US-11-250-411-95

Query Match 65.4%; Score 495.5; DB 7; Length 136;
Best Local Similarity 66.9%; Pred. No. 2.4e-34;
Matches 93; Conservative 20; Mismatches 23; Indels 3; Gaps 1;

QY 1 MGWSWIFLLSCTAGVHSEVQLQOQSGPELVKPGASVKISKASGYFTDYNHVKQSH 60
DB 1 MGFSRIEFLLSVTTGVHSSQVLQVQSGAEVKKPKASVKVSKASGYFTFINNHHVRQAP 60
QY 61 GKILEWIGYIYPNGVDYQNFKSKATLIVDNNSNTAYMELRSLTSDSAVYYCARWDF 120
DB 61 GQLEWGAIFPGNGFTSYNQKFGKATLTADKSSSTAYMQLSLTSDSAVYYCARWDF 117
QY 121 GSGYFYDYWGQGTTLTVSS 139
DB 118 DGDYFYDYWGQGTTLTVSS 136

RESULT 14
US-11-183-205-62
Sequence 62, Application US/11/183205
Publication No. US2006030521A1
GENERAL INFORMATION:
APPLICANT: Neose Technologies, Inc.
APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Bone, Caryn
APPLICANT: Hakes, David
APPLICANT: Chen, Xi
TITLE OF INVENTION: REMODELING AND GLYCOCONJUGATION OF PEPTIDES
FILE REFERENCE: 040853-01-5052-US01
CURRENT APPLICATION NUMBER: US/11/183,205
CURRENT FILING DATE: 2005-07-15
PRIOR APPLICATION NUMBER: US 11/183,205
PRIOR FILING DATE: 2005-07-15
PRIOR APPLICATION NUMBER: US 60/334,233
PRIOR FILING DATE: 2001-11-28
PRIOR APPLICATION NUMBER: US 60/334,301
PRIOR FILING DATE: 2001-11-28
PRIOR APPLICATION NUMBER: US 60/387,292
PRIOR FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR FILING DATE: 2002-08-28
PRIOR APPLICATION NUMBER: PCT/US2002/032263

PRIOR FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: US 10/287,994
PRIOR FILING DATE: 2002-11-05
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PatentIn version 3.1
SEQ ID NO 62
LENGTH: 140
TYPE: PRT
ORGANISM: Mus musculus
US-11-183-205-62

Query Match 65.2%; Score 494.5; DB 7; Length 140;
Best Local Similarity 68.6%; Pred. No. 3e-34;
Matches 96; Conservative 15; Mismatches 28; Indels 1; Gaps 1;

QY 1 MGWSWIFLLSCTAGVHSEVQLQOQSGPELVKPGASVKISKASGYFTDYNHVKQSH 60
DB 1 MGWSLLILLFLVAVATRVLSQVLQOQPGAEVLKPGASVMSCKASGYFTSYNHHVVKQTP 60
QY 61 GKILEWIGYIYPNGVDYQNFKSKATLIVDNNSNTAYMELRSLTSDSAVYYCARWD- 119
DB 61 GRGLEWIGALYIPNGDTSYNQKFGKATLTADKSSSTAYMQLSLTSDSAVYYCARSTY 120
QY 120 FSGYFYDYWGQGTTLTVSS 139
DB 121 YGDDYFYDYWGQGTTLTVSSA 140

RESULT 15
US-11-193-512-74
Sequence 74, Application US/11/193512
Publication No. US20050272918A1
GENERAL INFORMATION:
APPLICANT: KOIKE, Masamichi
FURUYA, Akiko
NAKAMURA, Kazuyasu
IIDA, Akihiro
ANAZAWA, Hideharu
HANAI, Nobuo
TAKATSU, Kiyoshi
TITLE OF INVENTION: Antibody Against Human Interleukin-5
Receptor Alpha Chain
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/193,512
FILING DATE: 01-AUG-2005
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/283,349
FILING DATE: 29-Oct-2002
APPLICATION NUMBER: US/08/836,561
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: JP 232384/95
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lawrence, III, Stanton T
REGISTRATION NUMBER: 25,736
REFERENCE/DOCKET NUMBER: 7005-115-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741

TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 140 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 74:
US-11-193-512-74

Query Match 65.1%; Score 493.5; DB 7; Length 140;
Best Local Similarity 67.6%; Pred. No. 3.6e-34;
Matches 96; Conservative 14; Mismatches 27; Indels 5; Gaps 2;

QY 1 MGMSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISKCKASGYTFDYNHVKQSH 60
DB 1 MMSWIFLLSGTAGVHSEVQLQSGAEVKKPGASVKCKASGYTFYSYVHWVRQAP 60

QY 61 GKLEWIGYIYPYNGVDYQNFKSKATLIVDSSNTAYMELSLTSEDSAVYYCARWDF 120
DB 61 GQGLEWMGYINPYNDGTYKNERFKGRVTITAD7STSTAYMELSLTSEDSAVYYLCGR--E 118

QY 121 GSGYY---FDYWGQGTTLTVSS 139
DB 119 GIRYGLLDGYWGQGTTLTVSS 140

RESULT 16
US-10-504-389A-45
Sequence 45, Application US/10504389A
Publication No. US2006045876A1
GENERAL INFORMATION:
APPLICANT: Renner, Christoph
APPLICANT: Scott, Andrew
TITLE OF INVENTION: FUSION PROTEINS OF HUMANIZED G250 SPECIFIC
TITLE OF INVENTION: ANTIBODIES AND USES THEREOF
FILE REFERENCE: LUD 5821
CURRENT APPLICATION NUMBER: US/10/504,389A
PRIOR FILING DATE: 2004-08-10
PRIOR APPLICATION NUMBER: PCT/US03/04243
PRIOR FILING DATE: 2002-02-12
NUMBER OF SEQ ID NOS: 56
SEQ ID NO 45
LENGTH: 145
TYPE: PRT
ORGANISM: Mus musculus
FEATURE:
OTHER INFORMATION: amino acid sequence for murine heavy chain variable region
US-10-504-389A-45

Query Match 64.4%; Score 488; DB 6; Length 145;
Best Local Similarity 66.9%; Pred. No. 1.1e-33;
Matches 97; Conservative 12; Mismatches 30; Indels 6; Gaps 3;

QY 1 MGMSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISKCKASGYTFDYNHVK 57
DB 1 MNMTWTFCLLAVAPGAHSAQAQVQLQSGAEELARPGASVKMCKASGYTFYTIHWVR 60

QY 58 QSGKLEWIGYIYPYNGVDYQNFKSKATLIVDSSNTAYMELSLTSEDSAVYYCA- 116
DB 61 QRPGLDLEWIGYINPSSGYSDYQNFKSKATLIVDSSNTAYMELSLTSEDSAVYYCAR 120

QY 117 RDPFGSGYY--FDYWGQGTTLTVSS 139
DB 121 RYDGYEYTWFAWYWGQGTTLTVSS 145

RESULT 17
US-11-193-512-78
Sequence 78, Application US/11193512
Publication No. US20050272918A1
GENERAL INFORMATION:

APPLICANT: KOIKE, Masamichi
FURUYA, Akiko
NAKAMURA, Kazuyasu
IIDA, Akihiko
ANAZAWA, Hideharu
HANAI, Nobuo
TAKATSU, Kiyoshi
TITLE OF INVENTION: Antibody Against Human Interleukin-5
RECEPTOR ALPHA CHAIN
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/193,512
FILING DATE: 01-AUG-2005
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/283,349
FILING DATE: 29-OCT-2002
APPLICATION NUMBER: US/08/836,561
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: JP 232384/95
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lawrence, III, Stanton T
REGISTRATION NUMBER: 25,736
REFERENCE/DOCKET NUMBER: 7005-115-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 140 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 78:
US-11-193-512-78

Query Match 64.3%; Score 487.5; DB 7; Length 140;
Best Local Similarity 66.9%; Pred. No. 1.1e-33;
Matches 95; Conservative 14; Mismatches 28; Indels 5; Gaps 2;

QY 1 MGMSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISKCKASGYTFDYNHVKQSH 60
DB 1 MMSWIFLLSGTAGVHSEVQLQSGAEVKKPGASVKCKASGYTFYSYVHWVRQAP 60

QY 61 GKLEWIGYIYPYNGVDYQNFKSKATLIVDSSNTAYMELSLTSEDSAVYYCARWDF 120
DB 61 GQGLEWMGYINPYNDGTYKNERFKGRVTITAD7STSTAYMELSLTSEDSAVYYLCGR--E 118

QY 121 GSGYY---FDYWGQGTTLTVSS 139
DB 119 GIRYGLLDGYWGQGTTLTVSS 140

RESULT 18
US-10-932-334-52
Sequence 52, Application US/10932334
Publication No. US20050249728A1
GENERAL INFORMATION:

APPLICANT: ImmunoGen, Inc.
TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY
FILE REFERENCE: A8689
CURRENT APPLICATION NUMBER: US/10/932,334
CURRENT FILING DATE: 2004-09-02
PRIOR APPLICATION NUMBER: US/10/729,441
PRIOR FILING DATE: 2003-12-08
PRIOR APPLICATION NUMBER: 10/170,390
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 96
SOFTWARE: PatentIn version 3.2
SEQ ID NO 52
LENGTH: 143
TYPE: PRT
ORGANISM: Mus musculus
US-10-932-334-52

Query Match 64.2%; Score 487; DB 6; Length 143;
Best Local Similarity 68.5%; Pred. No. 1.3e-33;
Matches 98; Conservative 15; Mismatches 26; Indels 4; Gaps 2;
Qy 1 MGWSWIFLLSLGTAGVHSEVQLQSGPELVKPGASVKISKASGYFTFDYNIHWKQSH 60
Db 1 MGWSWIFLLSLGTAGVHSEVQLQSGPELVKPGASVKISKASGYFTFDYNIHWKQSH 60
Qy 61 GKLEWIGYIPYNGVDYNGNFKSKATLIIVDSSNTAYMELSLTSDSAVYYCARW-- 118
Db 61 GQGLEWIGYIPYNGVDYNGNFKSKATLIIVDSSNTAYMELSLTSDSAVYYCARW 120
Qy 119 DF--GSGYYPDYWGQGTTLTVSS 139
Db 121 DYGGSKWYFDVWGAGTTVTSS 143

RESULT 19
US-11-177-648-9
Sequence 9, Application US/11177648
Publication No. US20060029603A1
GENERAL INFORMATION:
APPLICANT: Jonathon Henry ELLIS
APPLICANT: Paul Andrew HAMBLIN
APPLICANT: Paul Alexander WILSON
APPLICANT: Alan Peter LEWIS
TITLE OF INVENTION: IMMUNOGLOBULINS
FILE REFERENCE: PB60608-2
CURRENT APPLICATION NUMBER: US/11/177,648
CURRENT FILING DATE: 2005-07-06
PRIOR APPLICATION NUMBER: PCT/GB2004/005325
PRIOR FILING DATE: 2004-12-20
PRIOR APPLICATION NUMBER: GB0329711.6
PRIOR FILING DATE: 2003-12-22
PRIOR APPLICATION NUMBER: GB0329684.5
PRIOR FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 113
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
LENGTH: 462
TYPE: PRT
ORGANISM: Homo sapien
US-11-177-648-9

Query Match 64.1%; Score 485.5; DB 7; Length 462;
Best Local Similarity 69.1%; Pred. No. 4.8e-33;
Matches 96; Conservative 13; Mismatches 23; Indels 7; Gaps 2;
Qy 1 MGWSWIFLLSLGTAGVHSEVQLQSGPELVKPGASVKISKASGYFTFDYNIHWKQSH 60
Db 1 MGWSWIFLLSLGTAGVHSEVQLQSGPELVKPGASVKISKASGYFTFDYNIHWKQSH 60
Qy 61 GKLEWIGYIPYNGVDYNGNFKSKATLIIVDSSNTAYMELSLTSDSAVYYCARWDF 120
Db 61 GQGLEWIGYIPYNGVDYNGNFKSKATLIIVDSSNTAYMELSLTSDSAVYYCARW 117

Qy 121 GSGYYPDYWGQGTTLTVSS 139
Db 118 GQG-----YWGQGTTLTVSS 132
RESULT 20
US-11-193-512-83
Sequence 83, Application US/11193512
Publication No. US20050272918A1
GENERAL INFORMATION:
APPLICANT: KOIKE, Masamichi
FURUYA, Akiko
NAKAMURA, Kazuyasu
IIDA, Akihiko
ANAZAWA, Hideharu
HANAI, Nobuo
TAKATSU, Kiyoshi
TITLE OF INVENTION: Antibody Against Human Interleukin-5
Receptor Alpha Chain
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/193,512
FILING DATE: 01-Aug-2005
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/283,349
FILING DATE: 29-Oct-2002
APPLICATION NUMBER: US/08/836,561
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: JP 232384/95
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lawrence, III, Stanton T
REGISTRATION NUMBER: 25,736
REFERENCE/DOCKET NUMBER: 7005-115-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 140 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 83:
US-11-193-512-83

Query Match 63.7%; Score 482.5; DB 7; Length 140;
Best Local Similarity 66.9%; Pred. No. 2.9e-33;
Matches 95; Conservative 12; Mismatches 30; Indels 5; Gaps 2;
Qy 1 MGWSWIFLLSLGTAGVHSEVQLQSGPELVKPGASVKISKASGYFTFDYNIHWKQSH 60
Db 1 MGWSWIFLLSLGTAGVHSEVQLQSGPELVKPGASVKISKASGYFTFDYNIHWKQSH 60
Qy 61 GKLEWIGYIPYNGVDYNGNFKSKATLIIVDSSNTAYMELSLTSDSAVYYCARWDF 120
Db 61 GQGLEWIGYIPYNGVDYNGNFKSKATLIIVDSSNTAYMELSLTSDSAVYYCARW 118

Qy 121 GSGY---FDYWGQTTTLTVSS 139
Db 119 GIRYGLLDYWGQTTTLTVSS 140

Search completed: March 20, 2006, 07:32:42
Job time : 2.60454 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 20, 2006, 07:31:52 ; Search time 24.6746 Seconds
(without alignments)
2353.772 Million cell updates/sec

Title: US-10-687-035-34

Perfect score: 758

Sequence: 1 MGWSWIFLLSCTAGVHSE.....FGSGYFYDYGQGTTLTVSS 139

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	758	100.0	139	5	US-10-687-035-34
2	625	82.5	135	4	US-10-389-155-60
3	625	82.5	135	4	US-10-389-417-60
4	625	82.5	135	4	US-10-452-357-69
5	616	81.3	137	4	US-10-462-062-153
6	615	81.3	137	4	US-10-462-062-154
7	613.5	80.9	132	3	US-09-982-107-14
8	613.5	80.9	132	5	US-10-781-989-14
9	600.5	79.2	438	3	US-09-903-327A-6
10	600.5	79.2	456	3	US-09-903-327A-2
11	600.5	79.2	493	3	US-09-903-327A-13
12	600.5	79.2	510	3	US-09-903-327A-12
13	600.5	79.2	597	3	US-09-903-327A-11
14	600.5	79.2	613	3	US-09-903-327A-14
15	585.5	77.2	136	4	US-10-768-193-7
16	578.5	76.3	138	4	US-10-774-076-9
17	577	76.1	139	4	US-10-365-123-28
18	568	74.9	137	4	US-10-462-062-158
19	567	74.8	135	5	US-10-837-504-27
20	565.5	74.6	138	4	US-10-389-155-72
21	565.5	74.6	138	4	US-10-389-417-72
22	565.5	74.6	138	4	US-10-452-357-85
23	564	74.4	143	3	US-09-301-593-26
24	564	74.4	143	4	US-10-159-006-26
25	564	74.4	472	3	US-09-301-593-30
26	564	74.4	472	4	US-10-159-006-30
27	559	73.7	137	4	US-10-462-062-157

28	557	73.5	133	5	US-10-810-861A-79	Sequence 79, Appl
29	555.5	73.3	462	5	US-10-828-782A-18	Sequence 18, Appl
30	552	72.8	467	5	US-10-500-696-2	Sequence 2, Appl
31	551.5	72.8	136	4	US-10-138-505-12	Sequence 12, Appl
32	551.5	72.8	136	4	US-10-257-864A-88	Sequence 88, Appl
33	551.5	72.8	136	4	US-10-221-131-93	Sequence 93, Appl
34	551.5	72.8	136	4	US-10-399-518-117	Sequence 117, App
35	551.5	72.8	136	5	US-10-399-585-117	Sequence 117, App
36	551.5	72.8	136	5	US-10-645-085A-88	Sequence 88, Appl
37	550	72.6	152	4	US-10-642-120-2	Sequence 2, Appl
38	550	72.6	152	4	US-10-642-060-2	Sequence 2, Appl
39	550	72.6	152	4	US-10-642-122-2	Sequence 2, Appl
40	550	72.6	152	4	US-10-642-059-2	Sequence 2, Appl
41	550	72.6	152	4	US-10-642-124-2	Sequence 2, Appl
42	550	72.6	152	4	US-10-621-269-2	Sequence 2, Appl
43	550	72.6	152	4	US-10-620-850-2	Sequence 2, Appl
44	550	72.6	152	4	US-10-642-118-2	Sequence 2, Appl
45	550	72.6	152	4	US-10-642-119-2	Sequence 2, Appl
46	550	72.6	152	4	US-10-642-117-2	Sequence 2, Appl
47	550	72.6	152	5	US-10-642-099-2	Sequence 2, Appl
48	550	72.6	152	5	US-10-642-064-2	Sequence 2, Appl
49	550	72.6	152	5	US-10-642-116-2	Sequence 2, Appl
50	550	72.6	152	5	US-10-642-100-2	Sequence 2, Appl
51	550	72.6	152	5	US-10-642-058-2	Sequence 2, Appl
52	550	72.6	152	5	US-10-642-121-2	Sequence 2, Appl
53	550	72.6	152	5	US-10-642-065-2	Sequence 2, Appl
54	550	72.6	152	5	US-10-642-071-2	Sequence 2, Appl
55	545.5	72.0	142	3	US-09-772-120-8	Sequence 8, Appl
56	545	71.9	144	4	US-10-195-752-112	Sequence 112, App
57	540.5	71.3	136	4	US-10-138-505-8	Sequence 8, Appl
58	540.5	71.3	136	4	US-10-257-864A-86	Sequence 86, Appl
59	540.5	71.3	136	4	US-10-221-131-91	Sequence 91, Appl
60	540.5	71.3	136	4	US-10-399-518-115	Sequence 115, App
61	540.5	71.3	136	5	US-10-399-585-115	Sequence 115, App
62	540.5	71.3	136	5	US-10-645-085A-86	Sequence 86, Appl
63	539.5	71.2	138	5	US-10-723-003-8	Sequence 8, Appl
64	539.5	71.2	138	6	US-11-004-639-8	Sequence 8, Appl
65	539.5	71.2	468	5	US-10-723-003-12	Sequence 12, Appl
66	539.5	71.2	468	6	US-11-004-639-12	Sequence 12, Appl
67	539.5	71.2	624	5	US-10-723-003-30	Sequence 30, Appl
68	539.5	71.2	624	6	US-11-004-639-30	Sequence 30, Appl
69	539.5	71.2	639	5	US-10-723-003-32	Sequence 32, Appl
70	539.5	71.2	639	5	US-11-004-639-32	Sequence 32, Appl
71	538	71.0	137	5	US-10-687-035-30	Sequence 30, Appl
72	537.5	70.9	136	5	US-09-956-206A-47	Sequence 47, Appl
73	537.5	70.9	136	5	US-10-965-616-47	Sequence 47, Appl
74	537.5	70.9	140	4	US-10-283-349-27	Sequence 27, Appl
75	537	70.8	139	4	US-10-006-773-13	Sequence 13, Appl
76	536	70.7	600	4	US-10-334-235-38	Sequence 38, Appl
77	531	70.1	135	4	US-10-389-155-32	Sequence 32, Appl
78	531	70.1	135	4	US-10-389-417-32	Sequence 32, Appl
79	531	70.1	135	4	US-10-452-357-19	Sequence 19, Appl
80	529.5	69.9	138	2	US-08-779-784-31	Sequence 31, Appl
81	529.5	69.9	138	4	US-10-010-729-67	Sequence 67, Appl
82	526.5	69.5	146	3	US-09-791-551-111	Sequence 111, App
83	525.5	69.3	130	3	US-09-929-665-4	Sequence 4, Appl
84	525.5	69.3	130	3	US-09-929-546-4	Sequence 4, Appl
85	522	68.9	118	4	US-10-462-062-139	Sequence 139, App
86	522	68.9	118	4	US-10-462-062-140	Sequence 140, App
87	521.5	68.8	138	4	US-10-682-845-40	Sequence 40, Appl
88	521.5	68.8	147	3	US-09-797-481-4	Sequence 4, Appl
89	521.5	68.8	147	3	US-09-844-736-6	Sequence 6, Appl
90	521.5	68.8	147	4	US-10-162-396-6	Sequence 6, Appl
91	521.5	68.8	147	5	US-10-819-493-6	Sequence 6, Appl
92	521.5	68.8	669	3	US-09-807-721-2	Sequence 2, Appl
93	519.5	68.5	140	5	US-10-723-003-36	Sequence 36, Appl
94	519.5	68.5	140	6	US-11-004-639-36	Sequence 36, Appl
95	519.5	68.5	152	3	US-09-881-823-20	Sequence 20, Appl
96	519.5	68.5	470	5	US-10-723-003-40	Sequence 40, Appl
97	519.5	68.5	470	6	US-11-004-639-40	Sequence 40, Appl
98	519.5	68.5	626	5	US-10-723-003-44	Sequence 44, Appl
99	519.5	68.5	626	6	US-11-004-639-44	Sequence 44, Appl
100	519.5	68.5	641	5	US-10-723-003-46	Sequence 46, Appl

ALIGNMENTS

RESULT 1

US-10-687-035-34
; Sequence 34, Application US/10687035
; Publication No. US20050064518A1
; GENERAL INFORMATION:
; APPLICANT: Albione, Earl F.
; APPLICANT: Soltis, Daniel A.
; TITLE OF INVENTION: ANTIBODIES THAT BIND CELL-ASSOCIATED
; TITLE OF INVENTION: CA 125/0772P AND METHODS OF USE THEREOF
; FILE REFERENCE: 6750-214-999
; CURRENT APPLICATION NUMBER: US/10/687,035
; CURRENT FILING DATE: 2003-10-15
; PRIOR FILING DATE: 2003-07-10
; PRIOR FILING DATE: 2003-07-10
; PRIOR FILING DATE: 2003-07-10
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 776.1 heavy chain polypeptide variable region (776.1H)
US-10-687-035-34

Query Match 100.0%; Score 758; DB 5; Length 139;
Best Local Similarity 100.0%; Pred. No. 4.4e-59;
Matches 139; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGWSWIFLLSLGAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHVKQSH 60
Db 1 MGWSWIFLLSLGAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHVKQSH 60
Qy 61 GKLEWIGIYYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRLTSEDSAVYYCARWDF 120
Db 61 GKLEWIGIYYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRLTSEDSAVYYCARWDF 120
Qy 121 GSGYFDYWGQGTTLTVSS 139
Db 121 GSGYFDYWGQGTTLTVSS 139

RESULT 2

US-10-389-155-60
; Sequence 60, Application US/10389155
; Publication No. US20030229208A1
; GENERAL INFORMATION:
; APPLICANT: Queen, Cary L.
; Co. Man Sung
; Schneider, William P.
; Landolfi, Nicholas F.
; Coelingh, Kathleen L.
; Selick, Harold E.
; TITLE OF INVENTION: Improved Humanized Immunoglobulins
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/389,155
FILING DATE: 13-Mar-2003
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/325,000
FILING DATE: 01-JUN-1999
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 08/484,537
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 011823-002650US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 60:
US-10-389-155-60
Query Match 82.5%; Score 625; DB 4; Length 135;
Best Local Similarity 84.9%; Pred. No. 2.3e-47;
Matches 118; Conservative 7; Mismatches 10; Indels 4; Gaps 1;
Qy 1 MGWSWIFLLSLGAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHVKQSH 60
Db 1 MGWSWIFLLSLGAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHVKQSH 60
Qy 61 GKLEWIGIYYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRLTSEDSAVYYCARWDF 120
Db 61 GKLEWIGIYYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRLTSEDSAVYYCARWDF 120
Qy 121 GSGYFDYWGQGTTLTVSS 139
Db 118 -GRPMDYWGQGTTLTVSS 135

RESULT 3

US-10-389-417-60
; Sequence 60, Application US/10389417
; Publication No. US20040049014A1
; GENERAL INFORMATION:
; APPLICANT: Queen, Cary L.
; Co. Man Sung
; Schneider, William P.
; Landolfi, Nicholas F.
; Coelingh, Kathleen L.
; Selick, Harold E.
; TITLE OF INVENTION: Improved Humanized Immunoglobulins
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/389,417
FILING DATE: 13-Mar-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/325,000
FILING DATE: 01-JUN-1999
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 08/484,537
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 011823-002650US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 60:
US-10-389-417-60

Query Match 82.5%; Score 625; DB 4; Length 135;
Best Local Similarity 84.9%; Pred. No. 2.3e-47;
Matches 118; Conservative 7; Mismatches 10; Indels 4; Gaps 1;
QY 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISKASGYTFTDYNHVKQSH 60
DB 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISKASGYTFTDYNHVKQSH 60
QY 61 GKLEWIGIYPYNGVDYQNPKSKATLIVDNSSNTAYMELSLTSEDSAVYYCARWDF 120
DB 61 GKSLEWIGIYPYNGGTYNQKPKSKATLIVDNSSNTAYMELSLTSEDSAVYYCAR--- 117
QY 121 GSGYYPDYWGQGTTLTVSS 139
DB 118 -GRPAMDYWGQGTSTVTVSS 135

RESULT 4
US-10-452-357-69
Sequence 69, Application US/10452357
Publication No. US20040058414A1
GENERAL INFORMATION:
APPLICANT: Queen, Cathy
APPLICANT: Co, Man Sung
APPLICANT: Schneider, William
APPLICANT: Landolfi, Nicholas
APPLICANT: Coeligh, Kathleen
APPLICANT: Selick, Harold
TITLE OF INVENTION: Improved Humanized Immunoglobulins
FILE REFERENCE: 05882.0078.CNUS01
CURRENT APPLICATION NUMBER: US/10/452,357
CURRENT FILING DATE: 2003-05-30
PRIOR FILING DATE: 09/718,993
PRIOR FILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: 09/487,200
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 07/634,278
PRIOR FILING DATE: 1990-12-19
PRIOR APPLICATION NUMBER: 07/590,275

PRIOR FILING DATE: 1990-09-28
PRIOR APPLICATION NUMBER: 07/310,252
PRIOR FILING DATE: 1989-02-13
PRIOR APPLICATION NUMBER: 07/290,975
PRIOR FILING DATE: 1988-12-28
NUMBER OF SEQ ID NOS: 113
SOFTWARE: PatentIn version 3.2
SEQ ID NO 69
LENGTH: 135
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Heavy chain M195 antibody
US-10-452-357-69

Query Match 82.5%; Score 625; DB 4; Length 135;
Best Local Similarity 84.9%; Pred. No. 2.3e-47;
Matches 118; Conservative 7; Mismatches 10; Indels 4; Gaps 1;
QY 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISKASGYTFTDYNHVKQSH 60
DB 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISKASGYTFTDYNHVKQSH 60
QY 61 GKLEWIGIYPYNGVDYQNPKSKATLIVDNSSNTAYMELSLTSEDSAVYYCARWDF 120
DB 61 GKSLEWIGIYPYNGGTYNQKPKSKATLIVDNSSNTAYMELSLTSEDSAVYYCAR--- 117
QY 121 GSGYYPDYWGQGTTLTVSS 139
DB 118 -GRPAMDYWGQGTSTVTVSS 135

RESULT 5
US-10-462-062-153
Sequence 153, Application US/10462062
Publication No. US20040044187A1
GENERAL INFORMATION:
APPLICANT: SATO, KOH
APPLICANT: ADACHI, HIDEKI
TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN TISSUE FACTOR (TF)
TITLE OF INVENTION: AND PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODIES
FILE REFERENCE: 053466-0360
CURRENT APPLICATION NUMBER: US/10/462,062
CURRENT FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: PCT/JP99/01768
PRIOR FILING DATE: 1999-04-02
PRIOR APPLICATION NUMBER: JP 10-91850
PRIOR FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 183
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 153
LENGTH: 137
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Full-length amino acid
OTHER INFORMATION: sequence for H chain V region of anti-TF mouse monoclonal
OTHER INFORMATION: antibody ATR-2
US-10-462-062-153

Query Match 81.3%; Score 616; DB 4; Length 137;
Best Local Similarity 82.7%; Pred. No. 1.4e-46;
Matches 115; Conservative 8; Mismatches 14; Indels 2; Gaps 1;
QY 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISKASGYTFTDYNHVKQSH 60
DB 1 MEWSWIFLLSGTGTGCHSEIQLQSGPELVKPGASVKISKASGYTFTDYNHVKQSH 60
QY 61 GKLEWIGIYPYNGVDYQNPKSKATLIVDNSSNTAYMELSLTSEDSAVYYCARWDF 120
DB 61 GKSLEWIGIYPYNGGTYNQKPKSKATLIVDNSSNTAYMELSLTSEDSAVYYCAR-- 118
QY 121 GSGYYPDYWGQGTTLTVSS 139

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 6

LENGTH: 438

TYPE: PRT

ORGANISM: Mouse

FEATURE:

NAME/KEY: PEPTIDE

LOCATION: (0)...(0)

OTHER INFORMATION: Portion of DAV-1 heavy chain used for fusion protein

OTHER INFORMATION: bifunctional antibody

US-09-903-327A-6

Query Match 79.2%; Score 600.5; DB 3; Length 438;

Best Local Similarity 82.0%; Pred. No. 1.2e-44;

Matches 114; Conservative 6; Mismatches 12; Indels 7; Gaps 1;

QY 1 MGSMIFLLSGLTAGVHSEVQLQSGPELVKPGASVKISKASGYTFTDYNHVKQSH 60

DB 1 MGSMIFLLSGLTAGVHSEVQLQSGPELVKPGASVKISKASGYTFTDYNHVKQSH 60

QY 61 GKLEWIGIYYPNGVDYQNFKSKATLIVDSSNTAYMELSLTSDSNAVYCARWDF 120

DB 61 GKLEWIGIYYPNGVDYQNFKSKATLIVDSSNTAYMELSLTSDSNAVYCARWDF 120

QY 121 GSGYYPDYMGQGTTLTVSS 139

DB 119 -----IAYWGQGLTVTSA 132

RESULT 10

US-09-903-327A-2

Sequence 2, Application US/09903327A

Patent No. US20020164333A1

GENERAL INFORMATION:

APPLICANT: Nemerow, Glen R.

APPLICANT: Li, Erluang

TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGET

TITLE OF INVENTION: GENE

TITLE OF INVENTION: DELIVERY

FILE REFERENCE: 22908-1228

CURRENT APPLICATION NUMBER: US/09/903,327A

PRIOR FILING DATE: 2001-07-10

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 33

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 2

LENGTH: 456

TYPE: PRT

ORGANISM: Mouse

FEATURE:

NAME/KEY: PEPTIDE

LOCATION: (0)...(0)

OTHER INFORMATION: DAV-1 heavy chain, penton base monoclonal antibody

US-09-903-327A-2

Query Match

Best Local Similarity 79.2%; Score 600.5; DB 3; Length 456;

Matches 114; Conservative 6; Mismatches 12; Indels 7; Gaps 1;

QY 1 MGSMIFLLSGLTAGVHSEVQLQSGPELVKPGASVKISKASGYTFTDYNHVKQSH 60

DB 1 MGSMIFLLSGLTAGVHSEVQLQSGPELVKPGASVKISKASGYTFTDYNHVKQSH 60

QY 61 GKLEWIGIYYPNGVDYQNFKSKATLIVDSSNTAYMELSLTSDSNAVYCARWDF 120

DB 61 GKLEWIGIYYPNGVDYQNFKSKATLIVDSSNTAYMELSLTSDSNAVYCARWDF 120

QY 121 GSGYYPDYMGQGTTLTVSS 139

DB 119 -----IAYWGQGLTVTSA 132

RESULT 11

US-09-903-327A-13

Sequence 13, Application US/09903327A

Patent No. US20020164333A1

GENERAL INFORMATION:

APPLICANT: Nemerow, Glen R.

APPLICANT: Li, Erluang

TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGET

TITLE OF INVENTION: GENE

TITLE OF INVENTION: DELIVERY

FILE REFERENCE: 22908-1228

CURRENT APPLICATION NUMBER: US/09/903,327A

PRIOR FILING DATE: 2001-07-10

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 33

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 13

LENGTH: 493

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Fusion protein with N-terminal portion of DAV-1 heavy chain

OTHER INFORMATION: and EGF mature peptide

US-09-903-327A-13

Query Match

Best Local Similarity 79.2%; Score 600.5; DB 3; Length 493;

Matches 114; Conservative 6; Mismatches 12; Indels 7; Gaps 1;

QY 1 MGSMIFLLSGLTAGVHSEVQLQSGPELVKPGASVKISKASGYTFTDYNHVKQSH 60

DB 1 MGSMIFLLSGLTAGVHSEVQLQSGPELVKPGASVKISKASGYTFTDYNHVKQSH 60

QY 61 GKLEWIGIYYPNGVDYQNFKSKATLIVDSSNTAYMELSLTSDSNAVYCARWDF 120

DB 61 GKLEWIGIYYPNGVDYQNFKSKATLIVDSSNTAYMELSLTSDSNAVYCARWDF 120

QY 121 GSGYYPDYMGQGTTLTVSS 139

DB 119 -----IAYWGQGLTVTSA 132

RESULT 12

US-09-903-327A-12

Sequence 12, Application US/09903327A

Patent No. US20020164333A1

GENERAL INFORMATION:

APPLICANT: Nemerow, Glen R.

APPLICANT: Li, Erluang

TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGET

TITLE OF INVENTION: GENE

TITLE OF INVENTION: DELIVERY

FILE REFERENCE: 22908-1228

CURRENT APPLICATION NUMBER: US/09/903,327A

PRIOR FILING DATE: 2001-07-10

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 33

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 12

LENGTH: 510

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Fusion protein with N-terminal portion of DAV-1 heavy chain

OTHER INFORMATION: and IGF-1 mature peptide

US-09-903-327A-12

Query Match

Best Local Similarity 79.2%; Score 600.5; DB 3; Length 510;

Matches 114; Conservative 6; Mismatches 12; Indels 7; Gaps 1;

```
QY 1 MGWSWIFLLSGTAGVHSEVLOQSGPELVKPGASVKISKASGYFTDYNHVKQSH 60
DB 1 MGWSWIFLLSGTAGVHSEVLOQSGPELVKPGASVKISKASGYFTDYNHVKQSH 60
QY 61 GKILEWIGYIYPYNGVDYQNFQKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
DB 61 GKILEWIGYIYPYNGVDYQNFQKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 118
QY 121 GSGYFDYWGQGTTLTVSS 139
DB 119 -----IAYWGQGTTLTVSA 132

RESULT 13
US-09-903-327A-11
; Sequence 11, Application US/09903327A
; Patent No. US20020164333A1
; GENERAL INFORMATION:
; APPLICANT: Nemerow, Glen R.
; TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGET
; TITLE OF INVENTION: GENE
; FILE REFERENCE: 22908-1228
; CURRENT APPLICATION NUMBER: US/09/903,327A
; CURRENT FILING DATE: 2001-07-10
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 597
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Fusion protein with N-terminal portion of DAV-1 heavy chain
; OTHER INFORMATION: and TNF alpha mature peptide
US-09-903-327A-11

Query Match 79.2%; Score 600.5; DB 3; Length 597;
Best Local Similarity 82.0%; Pred. No. 1.6e-44;
Matches 114; Conservative 6; Mismatches 12; Indels 7; Gaps 1;

QY 1 MGWSWIFLLSGTAGVHSEVLOQSGPELVKPGASVKISKASGYFTDYNHVKQSH 60
DB 1 MGWSWIFLLSGTAGVHSEVLOQSGPELVKPGASVKISKASGYFTDYNHVKQSH 60
QY 61 GKILEWIGYIYPYNGVDYQNFQKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
DB 61 GKILEWIGYIYPYNGVDYQNFQKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 118
QY 121 GSGYFDYWGQGTTLTVSS 139
DB 119 -----IAYWGQGTTLTVSA 132

RESULT 14
US-09-903-327A-14
; Sequence 14, Application US/09903327A
; Patent No. US20020164333A1
; GENERAL INFORMATION:
; APPLICANT: Nemerow, Glen R.
; TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGET
; TITLE OF INVENTION: GENE
; FILE REFERENCE: 22908-1228
; CURRENT APPLICATION NUMBER: US/09/903,327A
; CURRENT FILING DATE: 2001-07-10
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 14
; LENGTH: 613
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion protein with N-terminal portion of DAV-1 heavy chain
; OTHER INFORMATION: and SCF mature peptide
US-09-903-327A-14

Query Match 79.2%; Score 600.5; DB 3; Length 613;
Best Local Similarity 82.0%; Pred. No. 1.7e-44;
Matches 114; Conservative 6; Mismatches 12; Indels 7; Gaps 1;

QY 1 MGWSWIFLLSGTAGVHSEVLOQSGPELVKPGASVKISKASGYFTDYNHVKQSH 60
DB 1 MGWSWIFLLSGTAGVHSEVLOQSGPELVKPGASVKISKASGYFTDYNHVKQSH 60
QY 61 GKILEWIGYIYPYNGVDYQNFQKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
DB 61 GKILEWIGYIYPYNGVDYQNFQKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 118
QY 121 GSGYFDYWGQGTTLTVSS 139
DB 119 -----IAYWGQGTTLTVSA 132

RESULT 15
US-10-768-193-7
; Sequence 7, Application US/10768193
; Publication No. US20040181042A1
; GENERAL INFORMATION:
; APPLICANT: MEDICAL & BIOLOGICAL LABORATORIES CO., LTD.
; APPLICANT: The director of Chubu National Hospital
; APPLICANT: SHIBATA, Masao
; APPLICANT: YANAGISAWA, Katsuhiko
; TITLE OF INVENTION: Antibody recognizing GM1 ganglioside-bound
; FILE REFERENCE: P0102402
; CURRENT APPLICATION NUMBER: US/10/768,193
; CURRENT FILING DATE: 2004-02-02
; PRIOR APPLICATION NUMBER: JP P2001-235700
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: PCT/JP02/07874
; PRIOR FILING DATE: 2002-08-01
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 7
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-768-193-7

Query Match 77.2%; Score 585.5; DB 4; Length 136;
Best Local Similarity 79.9%; Pred. No. 6.9e-44;
Matches 111; Conservative 7; Mismatches 18; Indels 3; Gaps 1;

QY 1 MGWSWIFLLSGTAGVHSEVLOQSGPELVKPGASVKISKASGYFTDYNHVKQSH 60
DB 1 MGWSWIFLLSGTAGVHSEVLOQSGPELVKPGASVKISKASGYFTDYNHVKQSH 60
QY 61 GKILEWIGYIYPYNGVDYQNFQKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
DB 61 GKILEWIGYIYPYNGVDYQNFQKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 117
QY 121 GSGYFDYWGQGTTLTVSS 139
DB 118 GANWVFDYWGQGTTLTVSS 136

RESULT 16
US-10-774-076-9
; Sequence 9, Application US/10774076
; Publication No. US20040210040A1
```

GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; TITLE OF INVENTION: Amphiregulin Antibodies and Their Use to Treat Cancer and
; FILE REFERENCE: 05882.0064.NFUS01
; CURRENT APPLICATION NUMBER: US/10/774.076
; CURRENT FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 138
; TYPE: PRT
; ORGANISM: mus sp.
US-10-774-076-9

Query Match 76.3%; Score 578.5; DB 4; Length 138;
Best Local Similarity 79.1%; Pred. No. 2.9e-43;
Matches 110; Conservative 7; Mismatches 21; Indels 1; Gaps 1;
QY 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISKASGYTFTDYNHWWKQSH 60
DB 1 MEWRWIFLLSGTTGVHSDIQQLQSGPELVKPGASVKVSKASGYAFTNYYNWWKQSH 60
QY 61 GKLEWIGYIYPYNGVSDYNQNFKSKATLIVDSSNTAYMELSLTSEDSAVYYCARWDF 120
DB 61 GKSLEWIGYIDPYVDPGYSQKFGKATLTVDKSSSTAYMHLNLSLTSEDSAVYYCARRG- 119
QY 121 GSGYFDYWGQGTTLTVSS 139
DB 120 NFPPYFDYWGQGTTLTVSS 138

RESULT 17

US-10-365-123-28
; Sequence 28, Application US/10365123
; Publication No. US20040053365A1
; GENERAL INFORMATION:
; APPLICANT: Renner, Christoph
; APPLICANT: Scott, Andrew
; APPLICANT: Burgess, Antony
; TITLE OF INVENTION: HUMANIZED GM-CSF ANTIBODIES
; FILE REFERENCE: LUD 5729.1
; CURRENT APPLICATION NUMBER: US/10/365.123
; CURRENT FILING DATE: 2003-02-12
; NUMBER OF SEQ ID NOS: 56
; SEQ ID NO 28
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: amino acid sequence for murine 19/2 heavy chain variable region
US-10-365-123-28

Query Match 76.1%; Score 577; DB 4; Length 139;
Best Local Similarity 83.6%; Pred. No. 4e-43;
Matches 112; Conservative 7; Mismatches 13; Indels 2; Gaps 1;
QY 6 IFLFLLSGTAGVHSEVQLQSGPELVKPGASVKISKASGYTFTDYNHWWKQSHKILE 65
DB 4 IMLFLLSGTAGVHSEVQLQSGPELVKPGASVKISKASGYTFTDYNHWWKQSHGKSLD 63
QY 66 WIGYIYPYNGVSDYNQNFKSKATLIVDSSNTAYMELSLTSEDSAVYYCARWDFGSGY 125
DB 64 WIGYIAPYSGGTGYNEPKNRATLTVDKSSSTAYMELSLTSDSAVYYCARRD--RFPY 121
QY 126 FDYWGQGTTLTVSS 139
DB 122 FDYWGQGTTLTVSS 135

RESULT 18

US-10-462-062-158

; Sequence 158, Application US/10462062
; Publication No. US20040044187A1
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: ADACHI, HIDEKI
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN TISSUE FACTOR (TF)
; FILE REFERENCE: 053466-0360
; CURRENT APPLICATION NUMBER: US/10/462.062
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: PCT/JP99/01768
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: JP 10-91850
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 158
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Full-length amino acid
; OTHER INFORMATION: sequence for H chain V region of anti-TP mouse monoclonal
; OTHER INFORMATION: antibody ATR-8
US-10-462-062-158

Query Match 74.9%; Score 568; DB 4; Length 137;
Best Local Similarity 75.4%; Pred. No. 2.4e-42;
Matches 107; Conservative 11; Mismatches 16; Indels 8; Gaps 2;
QY 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISKASGYTFTDYNHWWKQSH 60
DB 1 MEWSWIFLLSGTTGVHSDIQQLQSGPELVKPGASVKVSKASGYFTDYNIFWVKQSH 60
QY 61 GKLEWIGYIYPYNGVSDYNQNFKSKATLIVDSSNTAYMELSLTSEDSAVYYCARWDF 120
DB 61 GKSLEWIGYIDPYTGTGTGYNQKFNKATLTVDKSSSTAFMHLNLSLTSEDSAVYYCAR--- 117
QY 121 GSGYFDYWGQGTTLTVSS 139
DB 118 --GFTYDYCYWGQGTTLTVSA 137

RESULT 19

US-10-837-904-27
; Sequence 27, Application US/10837904
; Publication No. US20050142635A1
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary Margaret
; APPLICANT: JONES, Steven Tarran
; APPLICANT: SALDANHA, Jose William
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 134
; CORRESPONDENCE ADDRESS:
; ADDRESS: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/10/837,904
; FILING DATE: 04-May-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/114,285
FILING DATE: 13-Jul-1998
APPLICATION NUMBER: US 08/436,717
FILING DATE: 08-MAY-1995
APPLICATION NUMBER: US 08/137,117
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Wegner, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/234
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-10-837-904-27

Query Match 74.8%; Score 567; DB 5; Length 135;
Best Local Similarity 78.4%; Pred. No. 2.9e-42;
Matches 109; Conservative 8; Mismatches 18; Indels 4; Gaps 1;

Qy 1 MGMSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYFTFDYNIHWKQSH 60
Db 1 MGMSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYFTSYIHWKQSH 60

Qy 61 GKILEWIGYIPYNGVSDYNQFKSKATLIVDSSNTAYMELSLTSDSAVYYCARWDF 120
Db 61 GKLEWIGYIPYNGVSDYNQFKSKATLIVDSSNTAYMELSLTSDSAVYYCARWDF 120

Qy 121 GSGYFDYWGQGTTLTVSS 139
Db 118 -GGNFAYWGQGTTLTVSA 135

RESULT 20
US-10-389-155-72
Sequence 72, Application US/10389155
Publication No. US20030229208A1
GENERAL INFORMATION:
APPLICANT: Queen, Cary L.
Co, Man Sung
Schneider, William P.
Landolfi, Nicholas F.
Coelling, Kathleen L.
Seltick, Harold E.
TITLE OF INVENTION: Improved Humanized Immunoglobulins
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/389,155
FILING DATE: 13-Mar-2003

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/325,000
FILING DATE: 01-JUN-1999
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 08/484,537
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 011823-002650US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 138 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 72:
US-10-389-155-72

Query Match 74.6%; Score 565.5; DB 4; Length 138;
Best Local Similarity 78.4%; Pred. No. 4.1e-42;
Matches 109; Conservative 8; Mismatches 21; Indels 1; Gaps 1;

Qy 1 MGMSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYFTFDYNIHWKQSH 60
Db 1 MGMSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYFTGYTMWVKQSH 60

Qy 61 GKILEWIGYIPYNGVSDYNQFKSKATLIVDSSNTAYMELSLTSDSAVYYCARWDF 120
Db 61 GKLEWIGYIPYNGVSDYNQFKSKATLIVDSSNTAYMELSLTSDSAVYYCTTRGF 120

Qy 121 GSGYFDYWGQGTTLTVSS 139
Db 121 -RDYSMDYWGQGTSTVTVSS 138

Search completed: March 20, 2006, 07:35:11
Job time : 26.6746 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 20, 2006, 07:30:27 ; Search time 7.40237 Seconds
(without alignments)
1552.466 Million cell updates/sec

Title: US-10-687-035-34

Perfect score: 758

Sequence: 1 MGWSWIFLLSCTAGVHSE.....FGSGYFYDVGQGTTLTVSS 139

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5_COMB.pep.*

2: /cgn2_6/ptodata/1/iaa/6_COMB.pep.*

3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*

4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*

5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	625	82.5	135	1	US-07-634-278-69
2	625	82.5	135	1	US-08-477-728-69
3	625	82.5	135	1	US-08-474-040-69
4	625	82.5	135	1	US-08-487-200-69
5	625	82.5	135	2	US-08-484-537-69
6	616	81.3	137	2	US-09-647-468-153
7	616	81.3	137	2	US-09-647-468-154
8	613.5	80.9	132	2	US-08-434-000A-14
9	613.5	80.9	132	2	US-09-312-157-14
10	613.5	80.9	132	2	US-09-717-888-14
11	604	79.7	139	1	US-08-116-778E-1
12	604	79.7	139	1	US-08-438-562-1
13	604	79.7	139	1	US-08-483-528B-91
14	586	77.3	137	1	US-08-116-778B-3
15	586	77.3	137	1	US-08-438-562-3
16	586	77.3	137	1	US-08-483-528B-93
17	568	74.9	137	2	US-09-647-468-158
18	567	74.8	135	1	US-08-137-117D-27
19	567	74.8	135	1	US-08-436-717-27
20	566.5	74.7	140	4	PCT-US93-11612-4
21	565.5	74.6	138	1	US-07-634-278-85
22	565.5	74.6	138	1	US-08-477-728-85
23	565.5	74.6	138	1	US-08-474-040-85
24	565.5	74.6	138	1	US-08-487-200-85
25	565.5	74.6	138	2	US-08-484-537-85
26	564	74.4	143	2	US-09-301-593-26
27	564	74.4	472	2	US-09-301-593-30
28	560	73.9	233	2	US-08-444-644-33
29	560	73.9	233	2	US-08-232-246A-33
30	560	73.9	235	2	US-08-444-644-19
31	560	73.9	235	2	US-08-444-644-28
32	560	73.9	235	2	US-08-444-644-42
33	560	73.9	235	2	US-08-232-246A-19
34	560	73.9	235	2	US-08-232-246A-28
35	560	73.9	235	2	US-08-232-246A-42
36	559	73.7	137	2	US-09-647-468-157
37	556.5	73.4	140	2	US-08-579-378A-4
38	553	73.0	137	2	US-08-444-644-17
39	553	73.0	137	2	US-08-232-246A-17
40	545.5	72.0	142	1	US-08-678-194-8
41	545.5	72.0	142	2	US-08-890-011-8
42	545.5	72.0	142	2	US-09-262-724-8
43	545	71.9	144	2	US-09-393-385B-112
44	545	71.9	144	2	US-10-195-752-112
45	544	71.8	137	1	US-08-379-057-18
46	539	71.1	137	1	US-08-392-419-2
47	537.5	70.9	136	2	US-08-525-539A-47
48	537.5	70.9	140	2	US-08-836-561-27
49	537.5	70.9	140	2	US-09-434-122-27
50	531	70.1	135	1	US-07-634-278-19
51	531	70.1	135	1	US-08-477-728-19
52	531	70.1	135	1	US-08-474-040-19
53	531	70.1	135	1	US-08-487-200-19
54	531	70.1	135	1	US-08-303-569B-31
55	531	70.1	135	2	US-08-484-537-19
56	525.5	69.3	130	2	US-08-838-682-4
57	525.5	69.3	130	2	US-08-895-914-4
58	525.5	69.3	130	2	US-09-357-710A-4
59	525.5	69.3	130	2	US-09-357-707-4
60	525.5	69.3	130	2	US-09-357-708-4
61	524	69.1	139	1	US-08-202-047-3
62	524	69.1	139	2	US-08-564-690-3
63	522.5	68.9	136	4	PCT-US93-11611-11
64	522	68.9	118	2	US-09-647-468-139
65	522	68.9	118	2	US-09-647-468-140
66	521.5	68.8	147	1	US-08-579-940-4
67	521.5	68.8	147	2	US-08-838-692-6
68	519	68.5	116	1	US-07-634-278-56
69	519	68.5	116	1	US-08-477-728-56
70	519	68.5	116	1	US-08-474-040-56
71	519	68.5	116	1	US-08-487-200-56
72	519	68.5	116	2	US-08-484-537-56
73	517.5	68.3	163	4	PCT-US91-02942-5
74	513.5	67.7	468	1	US-08-303-569B-7
75	513.5	67.7	468	1	US-08-116-247-7
76	513.5	67.7	468	2	US-09-795-515-7
77	513.5	67.7	468	2	US-09-348-224-7
78	510.5	67.3	140	1	US-07-946-421-24
79	510	67.3	139	1	US-08-253-877C-8
80	510	67.3	139	1	US-08-556-586-8
81	510	67.3	139	1	US-08-452-164A-8
82	509	67.2	138	2	US-08-603-024-2
83	506.5	66.8	138	1	US-08-482-882-78
84	506.5	66.8	138	1	US-08-483-389-78
85	506.5	66.8	138	1	US-08-487-113D-78
86	506.5	66.8	138	1	US-08-473-503-78
87	506.5	66.8	138	1	US-08-483-932-78
88	506.5	66.8	138	1	US-08-720-420A-78
89	506.5	66.8	138	2	US-08-714-017-78
90	506.5	66.8	138	2	US-08-475-680-78
91	505.5	66.7	140	2	US-08-836-561-63
92	505.5	66.7	140	2	US-09-434-122-63
93	504	66.5	141	1	US-08-461-284-4
94	504	66.5	141	1	US-08-462-939-4
95	504	66.5	141	1	US-08-253-877C-4
96	504	66.5	141	1	US-08-452-164A-4
97	502	66.2	139	1	US-08-137-117D-35
98	502	66.2	139	1	US-08-436-717-35
99	501.5	66.2	143	1	US-08-236-520-7
100	501.5	66.2	143	4	PCT-US95-05262-7

ALIGNMENTS

RESULT 1

US-07-634-278-69
; Sequence 69, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO. Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; NAME: Smith, William M
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-634-278-69

Query Match 82.5%; Score 625; DB 1; Length 135;

Best Local Similarity 84.9%; Pred. No. 2e-57;
Matches 118; Conservative 7; Mismatches 10; Indels 4; Gaps 1;

Qy	1	MGWSWIFLLSGTAGVHSEVQLQSGPGLVKPGASVKISCKASGYTFTDYNHVKQSH	60
Db	1	MGWSWIFLLSGTAGVHSEVQLQSGPGLVKPGASVKISCKASGYTFTDYNHVKQSH	60
Qy	61	GKLEWIGYIYPNGVDYQNFKSKATLIVDNSNTAYMELRSLTSDSAVYYCARWDF	120
Db	61	GKLEWIGYIYPNGVDYQNFKSKATLIVDNSNTAYMELRSLTSDSAVYYCARWDF	117
Qy	121	GSYYFDYWGQGTTLTVSS	139
Db	118	-GRPAMDYWGQGTSTVTVSS	135

RESULT 2

US-08-477-728-69
; Sequence 69, Application US/08477728
; Patent No. 5585089
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,728
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; NAME: Smith, William M
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-477-728-69

Query Match 82.5%; Score 625; DB 1; Length 135;

Best Local Similarity 84.9%; Pred. No. 2e-57;
Matches 118; Conservative 7; Mismatches 10; Indels 4; Gaps 1;

Qy	1	MGWSWIFLLSGTAGVHSEVQLQSGPGLVKPGASVKISCKASGYTFTDYNHVKQSH	60
Db	1	MGWSWIFLLSGTAGVHSEVQLQSGPGLVKPGASVKISCKASGYTFTDYNHVKQSH	60
Qy	61	GKLEWIGYIYPNGVDYQNFKSKATLIVDNSNTAYMELRSLTSDSAVYYCARWDF	120
Db	61	GKLEWIGYIYPNGVDYQNFKSKATLIVDNSNTAYMELRSLTSDSAVYYCARWDF	117
Qy	121	GSYYFDYWGQGTTLTVSS	139
Db	118	-GRPAMDYWGQGTSTVTVSS	135

RESULT 3

US-08-474-040-69

; Sequence 69, Application US/08474040
; Patent No. 5693761
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO. Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,040
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-474-040-69

Query Match 82.5%; Score 625; DB 1; Length 135;
Best Local Similarity 84.3%; Pred. No. 2e-57;
Matches 118; Conservative 7; Mismatches 10; Indels 4; Gaps 1;

Qy	1	MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFDTYNHWKQSH 60
Db	1	MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFDTYNHWKQSH 60
Qy	61	GKLEWIGIYYPNGVSDYNQPKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
Db	61	GKLEWIGIYYPNGVSDYNQPKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
Qy	121	GSGYFDYWGQGTTLTVSS 139
Db	118	-GRPAMDYWGQGTSLTVSS 135

RESULT 4
US-08-487-200-69

; Sequence 69, Application US/08487200
; Patent No. 5693762

; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO. Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew

; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,200
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-487-200-69

Query Match 82.5%; Score 625; DB 1; Length 135;
Best Local Similarity 84.9%; Pred. No. 2e-57;
Matches 118; Conservative 7; Mismatches 10; Indels 4; Gaps 1;

Qy	1	MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFDTYNHWKQSH 60
Db	1	MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFDTYNHWKQSH 60
Qy	61	GKLEWIGIYYPNGVSDYNQPKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
Db	61	GKLEWIGIYYPNGVSDYNQPKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
Qy	121	GSGYFDYWGQGTTLTVSS 139
Db	118	-GRPAMDYWGQGTSLTVSS 135

RESULT 5
US-08-484-537-69

Sequence 69, Application US/08484537
Patent No. 6180370
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO. Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08484,537
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-484-537-69

Query Match 82.5%; Score 625; DB 2; Length 135;
Best Local Similarity 84.9%; Pred. NO. 2e-57;
Matches 118; Conservative 7; Mismatches 10; Indels 4; Gaps 1;
QY 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFDYNHVKQSH 60
DB 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFDYNHVKQSH 60
QY 61 GKLEWIGIYIPYNGVSDYNQNFKSKATLIVDSSNTAYMELSLTSEDSAVYYCARWDF 120
DB 61 GKLEWIGIYIPYNGVSDYNQNFKSKATLIVDSSNTAYMELSLTSEDSAVYYCARWDF 120
QY 121 GSGYFDYWGQGTTLTVSS 139
DB 119 GEGYFDYWGQGTTLTVSS 137

RESULT 7
US-09-647-468-154
Sequence 154, Application US/09647468
Patent No. 6677436
GENERAL INFORMATION:
APPLICANT: SATO, KOH
APPLICANT: ADACHI, HIDEKI
APPLICANT: YABUTA, NAOKIRO
TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
FILE REFERENCE: 053466/0289
CURRENT APPLICATION NUMBER: US/09/647,468
CURRENT FILING DATE: 2000-09-29
PRIORITY APPLICATION NUMBER: PCT/JP99/01768
PRIORITY FILING DATE: 1999-04-02
PRIORITY APPLICATION NUMBER: JP 10-91850
PRIORITY FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 183
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 154
LENGTH: 137
TYPE: PRT
ORGANISM: Mus sp.
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Amino acid
OTHER INFORMATION: sequence coding for H chain V region of ant-TF
OTHER INFORMATION: mouse monoclonal antibody ATR-3
US-09-647-468-154

Query Match 81.3%; Score 616; DB 2; Length 137;
Best Local Similarity 82.7%; Pred. NO. 1.7e-56;
Matches 115; Conservative 8; Mismatches 14; Indels 2; Gaps 1;
QY 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFDYNHVKQSH 60
DB 1 MEWSWIFLLSGTTGVHSEIQLQSGPELVKPGASVKYSCASGYSFDDYNNYWKQSH 60
QY 61 GKLEWIGIYIPYNGVSDYNQNFKSKATLIVDSSNTAYMELSLTSEDSAVYYCARWDF 120
DB 61 GKLEWIGIYIPYNGVSDYNQNFKSKATLIVDSSNTAYMELSLTSEDSAVYYCARWDF 120
QY 121 GSGYFDYWGQGTTLTVSS 139
DB 119 GEGYFDYWGQGTTLTVSS 137

Query Match 81.3%; Score 616; DB 2; Length 137;
Best Local Similarity 82.7%; Pred. NO. 1.7e-56;
Matches 115; Conservative 8; Mismatches 14; Indels 2; Gaps 1;
QY 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFDYNHVKQSH 60
DB 1 MEWSWIFLLSGTTGVHSEIQLQSGPELVKPGASVKYSCASGYSFDDYNNYWKQSH 60
QY 61 GKLEWIGIYIPYNGVSDYNQNFKSKATLIVDSSNTAYMELSLTSEDSAVYYCARWDF 120
DB 61 GKLEWIGIYIPYNGVSDYNQNFKSKATLIVDSSNTAYMELSLTSEDSAVYYCARWDF 120
QY 121 GSGYFDYWGQGTTLTVSS 139
DB 119 GEGYFDYWGQGTTLTVSS 137

Sequence 69, Application US/08484537
Patent No. 6180370
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO. Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08484,537
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-484-537-69

Query Match 82.5%; Score 625; DB 2; Length 135;
Best Local Similarity 84.9%; Pred. NO. 2e-57;
Matches 118; Conservative 7; Mismatches 10; Indels 4; Gaps 1;
QY 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFDYNHVKQSH 60
DB 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFDYNHVKQSH 60
QY 61 GKLEWIGIYIPYNGVSDYNQNFKSKATLIVDSSNTAYMELSLTSEDSAVYYCARWDF 120
DB 61 GKLEWIGIYIPYNGVSDYNQNFKSKATLIVDSSNTAYMELSLTSEDSAVYYCARWDF 120
QY 121 GSGYFDYWGQGTTLTVSS 139
DB 119 GEGYFDYWGQGTTLTVSS 135

RESULT 6
US-09-647-468-153
Sequence 153, Application US/09647468

Best Local Similarity 82.7%; Pred. No. 1.7e-56;
Matches 115; Conservative 8; Mismatches 14; Indels 2; Gaps 1;

QY 1 MGWSWFLFLSAGTGVHSGVQLQSGPDLVKPGASVKISCKASGYTFTDYNHVKQSH 60

Db 1 MEWSWFLFLSAGTGVHSGVQLQSGPDLVKPGASVKISCKASGYTFTDYNHVKQSH 60

QY 61 GKLEWIGIYYPNGVDYQNFKSKATLIVDSSNTAYMELSLTSEDSAVYYCARWDF 120

Db 61 GKSLEWIGIYYPNGVDYQNFKSKATLIVDSSNTAYMELSLTSEDSAVYYCARWDF 120

QY 121 GSGYFDYNGQGTTLTVSS 139

Db 119 GEGYFDYNGQGTTLTVSS 137

RESULT 8

US-08-434-000A-14

; Sequence 14, Application US/08434000A

; Patent No. 6046037

; GENERAL INFORMATION:

; APPLICANT: ANDREW C. HIATT, JULIAN

; APPLICANT: K.-C. MA, THOMAS LEHNER

; TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; SUITE: Suite 4700

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA: US/08/434,000A

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA: including application

; PRIOR APPLICATION DATA: described below: 1

; APPLICATION NUMBER: 08/367,395

; FILING DATE: 12/30/94

; ATTORNEY/AGENT INFORMATION:

; NAME: Guise, Jeffrey W.

; REGISTRATION NUMBER: 34,613

; REFERENCE/DOCKET NUMBER: 212/127

; TELEPHONE: (619) 552-8400

; TELEFAX: (619) 552-0159

; TELEX: 67-3510

; SEQUENCE LISTING

; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 132 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; TOPOLOGY: DESCRIPTION: Guy's 13 Gamma 1

; US-08-434-000A-14

Query Match 80.9%; Score 613.5; DB 2; Length 132;

Best Local Similarity 83.5%; Pred. No. 3e-56;

Matches 116; Conservative 6; Mismatches 10; Indels 7; Gaps 1;

QY 1 MGWSWFLFLSAGTGVHSGVQLQSGPDLVKPGASVKISCKASGYTFTDYNHVKQSH 60

Db 1 MEWSWFLFLSAGTGVHSGVQLQSGPDLVKPGASVKISCKASGYTFTDYNHVKQSH 60

QY 61 GKLEWIGIYYPNGVDYQNFKSKATLIVDSSNTAYMELSLTSEDSAVYYCARWDF 120

Db 61 GKSLEWIGIYYPNGVDYQNFKSKATLIVDSSNTAYMELSLTSEDSAVYYCARWDF 120

Db 1 MEWTWVFLFLSAGTGVHSGVQLQSGPDLVKPGASVKISCKASGYTFTDYNHVKQSR 60

QY 61 GKLEWIGIYYPNGVDYQNFKSKATLIVDSSNTAYMELSLTSEDSAVYYCARWDF 120

Db 61 GKSLEWIGIYYPNGVDYQNFKSKATLIVDSSNTAYMELSLTSEDSAVYYCARWDF 120

QY 121 GSGYFDYNGQGTTLTVSS 139

Db 118 ---YFDYNGQGTTLTVSS 132

RESULT 9

US-09-312-157-14

; Sequence 14, Application US/09312157

; Patent No. 6303341

; GENERAL INFORMATION:

; APPLICANT: ANDREW C. HIATT, JULIAN

; APPLICANT: K.-C. MA, THOMAS LEHNER

; TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; SUITE: Suite 4700

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA: US/09/312,157

; FILING DATE: 14-May-1999

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/434,000

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Guise, Jeffrey W.

; REGISTRATION NUMBER: 34,613

; REFERENCE/DOCKET NUMBER: 212/127

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619) 552-8400

; TELEFAX: (619) 552-0159

; TELEX: 67-351

; SEQUENCE LISTING

; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 132 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; TOPOLOGY: DESCRIPTION: Guy's 13 Gamma 1

; US-09-312-157-14

Query Match 80.9%; Score 613.5; DB 2; Length 132;

Best Local Similarity 83.5%; Pred. No. 3e-56;

Matches 116; Conservative 6; Mismatches 10; Indels 7; Gaps 1;

QY 1 MGWSWFLFLSAGTGVHSGVQLQSGPDLVKPGASVKISCKASGYTFTDYNHVKQSH 60

Db 1 MEWTWVFLFLSAGTGVHSGVQLQSGPDLVKPGASVKISCKASGYTFTDYNHVKQSR 60

QY 61 GKLEWIGIYYPNGVDYQNFKSKATLIVDSSNTAYMELSLTSEDSAVYYCARWDF 120

Db 61 GKSLEWIGIYYPNGVDYQNFKSKATLIVDSSNTAYMELSLTSEDSAVYYCAT--- 117

Qy 121 GSGYFDYWGQGTTLTVSS 139
 Db 118 ----YFDYWGQGTTLTVSS 132

RESULT 10
 US-09-717-888-14
 ; Sequence 14, Application US/09717888
 ; Patent No. 6808709
 ; GENERAL INFORMATION:
 ; APPLICANT: ANDREW C. HIATT, JULIAN
 ; K.-C. MA, THOMAS LEHNER
 ; TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION
 ; PROTEINS IN PLANTS AND THEIR USES
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; Suite 4700
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90071
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; COMPUTER READABLE FORM:
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0
 ; SOFTWARE: Word Perfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/717.888
 ; FILING DATE: 20-No. 6808709-2000
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/434.000
 ; FILING DATE: <Unknown>
 ; APPLICATION NUMBER: 08/367.395
 ; FILING DATE: 30-Dec-94
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Guise, Jeffrey W.
 ; REGISTRATION NUMBER: 34,613
 ; REFERENCE/DOCKET NUMBER: 212/127
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619) 552-8400
 ; TELEFAX: (619) 552-0159
 ; TELEX: 67-3510

SEQUENCE LISTING
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 132 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 DESCRIPTION: Guy's 13 Gamma 1
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Query Match 80.9%; Score 613.5; DB 2; Length 132;
 Best Local Similarity 83.5%; Pred. No. 3e-56;
 Matches 116; Conservative 6; Mismatches 10; Indels 7; Gaps 1;

Qy 1 MGWNIPLFLSLGAGVHSEVLOQSGPELVKPGASVKISCKASGYTFDYNIIHWKQSH 60
 Db 1 MEWTVFLFLSLGAGVHSEVLOQSGPELVKPGASVKISCKASGYTFDYNIIHWKQSR 60
 Qy 61 GKLEWIGIYYPNGVSDYNQFNKSKATLIIVDNSNTAYMELRSITSDSAVYTCARWDF 120
 Db 61 KSLIEWIGIYYPNGNTYQNFKNKATLIVDNSSTSAYMELRSITSDSAVYTCAT--- 117
 Qy 121 GSGYFDYWGQGTTLTVSS 139
 Db 118 ----YFDYWGQGTTLTVSS 132

RESULT 11
 US-08-116-778E-1
 ; Sequence 1, Application US/08116778E
 ; Patent No. 5830470
 ; GENERAL INFORMATION:
 ; APPLICANT: NAKAMURA, KAZUYASU
 ; APPLICANT: KOIKE, MASAMICHI
 ; APPLICANT: SHITARA, KENYA
 ; APPLICANT: HANAI, NOBUO
 ; APPLICANT: KAWANA, YOSHIHISA
 ; APPLICANT: HASEGAWA, MAMORU
 ; TITLE OF INVENTION: HUMANIZED ANTIBODIES
 ; NUMBER OF SEQUENCES: 49
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: NIXON & VANDERHYE P.C.
 ; STREET: 1100 NORTH GLEBE ROAD
 ; CITY: ARLINGTON
 ; STATE: VIRGINIA
 ; COUNTRY: U.S.A.
 ; ZIP: 22201-4714
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/116,778E
 ; FILING DATE: 07-SEP-93
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: WILSON, MARY J.
 ; REGISTRATION NUMBER: 32,955
 ; REFERENCE/DOCKET NUMBER: 249-59
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703)816-4000
 ; TELEFAX: (703)816-4100
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 139 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; FEATURE:
 ; NAME/KEY: sig_peptide
 ; LOCATION: -19...-1
 ; IDENTIFICATION METHOD: BY SIMILARITY
 ; IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN
 ; IDENTIFICATION METHOD: ESTABLISHED CONSENSUS
 ; FEATURE:
 ; NAME/KEY: domain
 ; LOCATION: 31..35
 ; IDENTIFICATION METHOD: BY SIMILARITY
 ; IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
 ; IDENTIFICATION METHOD: CONSENSUS
 ; OTHER INFORMATION: /product= "HYPERVARIABLE REGION 1"
 ; FEATURE:
 ; NAME/KEY: domain
 ; LOCATION: 50..66
 ; IDENTIFICATION METHOD: BY SIMILARITY
 ; IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
 ; IDENTIFICATION METHOD: CONSENSUS
 ; OTHER INFORMATION: /product= "HYPERVARIABLE REGION 2"
 ; FEATURE:
 ; NAME/KEY: domain
 ; LOCATION: 99..109
 ; IDENTIFICATION METHOD: BY SIMILARITY
 ; IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
 ; IDENTIFICATION METHOD: CONSENSUS
 ; OTHER INFORMATION: /product= "HYPERVARIABLE REGION 3"
 ; US-08-116-778E-1
 Query Match 79.7%; Score 604; DB 1; Length 139;


```
/
/
/ NAME/KEY: sig_peptide
/ LOCATION: -19..-1
/ IDENTIFICATION METHOD: BY SIMILARITY WITH KNOWN SEQUENCE OR TO AN
/ IDENTIFICATION METHOD: ESTABLISHED CONSENSUS
/
/ FEATURE:
/
/ NAME/KEY: domain
/ LOCATION: 31..35
/ IDENTIFICATION METHOD: BY SIMILARITY
/ IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
/ IDENTIFICATION METHOD: CONSENSUS
/ OTHER INFORMATION: /product= "HYPERVARIABLE REGION 1"
/
/ FEATURE:
/
/ NAME/KEY: domain
/ LOCATION: 50..66
/ IDENTIFICATION METHOD: BY SIMILARITY
/ IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
/ IDENTIFICATION METHOD: CONSENSUS
/ OTHER INFORMATION: /product= "HYPERVARIABLE REGION 2"
/
/ FEATURE:
/
/ NAME/KEY: domain
/ LOCATION: 99..109
/ IDENTIFICATION METHOD: BY SIMILARITY
/ IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
/ IDENTIFICATION METHOD: CONSENSUS
/ OTHER INFORMATION: /product= "HYPERVARIABLE REGION 3"
/
/ US-08-483-528B-91
/
/ Query Match 79.7%; Score 604; DB 1; Length 139;
/ Best Local Similarity 82.7%; Pred. No. 3.2e-55;
/ Matches 115; Conservative 6; Mismatches 18; Indels 0; Gaps 0;
/
/ Qy 1 MGWSWIFLLISGTVAGVHSEYVQLQSGPELVKPGASVKISKASGYTFDYNHVKQSH 60
/ Db 1 MGWSWIFLLISGTVAGVHSEYVQLQSGPELVKPGASVKISKASGYTFDYNHVKQSH 60
/
/ Qy 61 GKLEWIGYIYPNGVDYQNFKSKATLIVDNSNTAYMELRLTSDSAVYTCARWDF 120
/ Db 61 GKLEWIGYIYPNGVDYQNFKSKATLIVDNSNTAYMELRLTSDSAVYTCARWDF 120
/
/ Qy 121 GSGYFEDYWGQGTTLTVSS 139
/ Db 121 YGYMFAYWGQGTTLTVSA 139
/
/ RESULT 14
/ US-08-116-778E-3
/ Sequence 3, Application US/08116778E
/ Patent No. 5830470
/ GENERAL INFORMATION:
/ APPLICANT: NAKAMURA, KAZUYASU
/ APPLICANT: KOIKE, MASAMICHI
/ APPLICANT: SHITARA, KENYA
/ APPLICANT: HANAI, NOBUO
/ APPLICANT: KAWANA, YOSHIHISA
/ APPLICANT: HASEGAWA, NAMORU
/ TITLE OF INVENTION: HUMANIZED ANTIBODIES
/ NUMBER OF SEQUENCES: 49
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: NIXON & VANDERHYE P.C.
/ STREET: 1100 NORTH GLEBE ROAD
/ CITY: ARLINGTON
/ STATE: VIRGINIA
/ COUNTRY: U.S.A.
/ ZIP: 22201-4714
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/116,778E
```

```
/
/
/ FILING DATE: 07-SEP-93
/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: WILSON, MARY J.
/ REGISTRATION NUMBER: 32,955
/ REFERENCE/DOCKET NUMBER: 249-59
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (703)816-4000
/ TELEFAX: (703)816-4100
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 137 amino acids
/ TYPE: amino acids
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ FEATURE:
/
/ NAME/KEY: sig_peptide
/ LOCATION: -19..-1
/ IDENTIFICATION METHOD: BY SIMILARITY
/ IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
/ IDENTIFICATION METHOD: CONSENSUS
/ OTHER INFORMATION: /product= "HYPERVARIABLE REGION 1"
/
/ FEATURE:
/
/ NAME/KEY: domain
/ LOCATION: 31..35
/ IDENTIFICATION METHOD: BY SIMILARITY
/ IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
/ IDENTIFICATION METHOD: CONSENSUS
/ OTHER INFORMATION: /product= "HYPERVARIABLE REGION 2"
/
/ FEATURE:
/
/ NAME/KEY: domain
/ LOCATION: 55..66
/ IDENTIFICATION METHOD: BY SIMILARITY
/ IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
/ IDENTIFICATION METHOD: CONSENSUS
/ OTHER INFORMATION: /product= "HYPERVARIABLE REGION 3"
/
/ US-08-116-778E-3
/
/ Query Match 77.3%; Score 586; DB 1; Length 137;
/ Best Local Similarity 82.7%; Pred. No. 2.3e-53;
/ Matches 115; Conservative 5; Mismatches 17; Indels 2; Gaps 1;
/
/ Qy 1 MGWSWIFLLISGTVAGVHSEYVQLQSGPELVKPGASVKISKASGYTFDYNHVKQSH 60
/ Db 1 MGWSWIFLLISGTVAGVHSEYVQLQSGPELVKPGASVKISKASGYTFDYNHVKQSH 60
/
/ Qy 61 GKLEWIGYIYPNGVDYQNFKSKATLIVDNSNTAYMELRLTSDSAVYTCARWDF 120
/ Db 61 GKLEWIGYIYPNGVDYQNFKSKATLIVDNSNTAYMELRLTSDSAVYTCARWDF 120
/
/ Qy 121 GSGYFEDYWGQGTTLTVSS 139
/ Db 119 GRYTAWDYGQGTTLTVSA 137
/
/ RESULT 15
/ US-08-438-562-3
/ Sequence 3, Application US/08438562
/ Patent No. 5874255
/ GENERAL INFORMATION:
/ APPLICANT: NAKAMURA, KAZUYASU
/ APPLICANT: KOIKE, MASAMICHI
/ APPLICANT: SHITARA, KENYA
/ APPLICANT: HANAI, NOBUO
/ APPLICANT: KAWANA, YOSHIHISA
/ APPLICANT: HASEGAWA, NAMORU
/ TITLE OF INVENTION: HUMANIZED ANTIBODIES
```


Query Match 77.3%; Score 586; DB 1; Length 137;
Best Local Similarity 82.7%; Pred. No. 2.3e-53;
Matches 115; Conservative 5; Mismatches 17; Indels 2; Gaps 1;

Qy 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHWKQSH 60
Db 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHWKQSH 60

Qy 61 GKLEWIGIYIPYNGVSDYNQNFKSKATLIVDNSNTAYMELRSLTSEDSAVYYCARWDF 120
Db 61 GKLEWIGIYIPYNGVSDYNQNFKSKATLIVDNSNTAYMELRSLTSEDSAVYYCARWDF 120

Qy 121 GSGYFYDWGQGTTLTVSS 139
Db 119 GRYIYAWDWGQGTTLTVSA 137

RESULT 17

US-09-647-468-158
; Sequence 158, Application US/09647468
; Patent No. 6677436
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: ADACHI, HIDEKI
; APPLICANT: YABUCHI, NAOTIRO
; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
; TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
; FILE REFERENCE: 053466/0289
; CURRENT APPLICATION NUMBER: US/09/647,468
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: PCT/JP99/01768
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: JP 10-91850
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 158
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
; OTHER INFORMATION: sequence coding for H chain V region of ant-TF
; OTHER INFORMATION: mouse monoclonal antibody ATR-8
US-09-647-468-158

Query Match 74.9%; Score 568; DB 2; Length 137;
Best Local Similarity 75.4%; Pred. No. 1.7e-51;
Matches 107; Conservative 11; Mismatches 16; Indels 8; Gaps 2;

Qy 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHWKQSH 60
Db 1 MEWSWIFLLSGTAGVHSDIQLQSGPELVKPGASVKISCKASGYTFTDYNHWKQSH 60

Qy 61 GKLEWIGIYIPYNGVSDYNQNFKSKATLIVDNSNTAYMELRSLTSEDSAVYYCARWDF 120
Db 61 GKLEWIGIYIPYNGVSDYNQNFKSKATLIVDNSNTAYMELRSLTSEDSAVYYCARWDF 120

Qy 121 GSGYFYDWGQGTTLTVSS 139
Db 118 --GFYIDYDCYWGQGTTLTVSA 137

RESULT 18

US-08-137-117D-27
; Sequence 27, Application US/08137117D
; Patent No. 5795965
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, KOH
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose

; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,117D
; FILING DATE: 20-DEC-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JP92/00544
; FILING DATE: 24-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-32084
; FILING DATE: 19-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-95476
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/126/AAOK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-137-117D-27

Query Match 74.8%; Score 567; DB 1; Length 135;
Best Local Similarity 78.4%; Pred. No. 2.2e-51;
Matches 109; Conservative 8; Mismatches 18; Indels 4; Gaps 1;

Qy 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHWKQSH 60
Db 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHWKQSH 60

Qy 61 GKLEWIGIYIPYNGVSDYNQNFKSKATLIVDNSNTAYMELRSLTSEDSAVYYCARWDF 120
Db 61 GKLEWIGIYIPYNGVSDYNQNFKSKATLIVDNSNTAYMELRSLTSEDSAVYYCARWDF 120

Qy 121 GSGYFYDWGQGTTLTVSS 139
Db 118 -GGRFAYWGQGTTLTVSA 135

RESULT 19

US-08-436-717-27
; Sequence 27, Application US/08436717
; Patent No. 5817790
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, KOH
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN

TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,717
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-436-717-27

Query Match 74.8%; Score 567; DB 1; Length 135;
Best Local Similarity 78.4%; Pred. No. 2.2e-51;
Matches 109; Conservative 8; Mismatches 18; Indels 4; Gaps 1;
Qy 1 MGMSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYFTDYNHIVKQSH 60
Db 1 MGMSGIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYFTSYIHVVKQSH 60
Qy 61 GKLEWIGYIYPYNGVDYQNGPKSKATLIVDSSNTAYMELSLTSEDSAVVYCARWDF 120
Db 61 GKLEWIGYIDPENGGSYQNGPKSKATLIVDSSNTAYMELSLTSEDSAVVYCARWDF 120
Qy 121 GSGYFDYWGQGTTLTVSS 139
Db 118 -GGRFAYWGQGTTLTVSSA 135

RESULT 20
PCT-US93-11612-4
Sequence 4, Application PC/TUS9311612
GENERAL INFORMATION:
APPLICANT: Co, Man Sung
TITLE OF INVENTION: Humanized Antibodies Reactive with
TITLE OF INVENTION: L-Selectin
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000

CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11612
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/983,946
FILING DATE: 01-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 140 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-11612-4

Query Match 74.7%; Score 566.5; DB 4; Length 140;
Best Local Similarity 77.1%; Pred. No. 2.6e-51;
Matches 108; Conservative 11; Mismatches 20; Indels 1; Gaps 1;
Qy 1 MGMSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYFTDYNHIVKQSH 60
Db 1 MGMSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYFTSYVHIVKQKP 60
Qy 61 GKLEWIGYIYPYNGVDYQNGPKSKATLIVDSSNTAYMELSLTSEDSAVVYCARWDF 120
Db 61 GQGLEWIGYIYPYNGDTKYNKPKGKATLTSDKSSSTAYMELSLTSEDSAVVYCARWDF 120
Qy 121 GSGY-YFDYWGQGTTLTVSS 139
Db 121 GNYVRYFDYWGAGTTLTVSS 140

Search completed: March 20, 2006, 07:31:35
Job time : 8.40237 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 20, 2006, 07:28:19 ; Search time 50.3087 Seconds

(without alignments)
1213.978 Million cell updates/sec

Title: US-10-687-035-34

Perfect score: 758

Sequence: 1 MGSWIFLFLSCTAGVHSE.....FGSGYFDYWGQQTTLTVSS 139

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 100 summaries

Database : A Geneseq_21.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	758	100.0	139	ADS94335	Ads94335 Antibody
2	644	85.0	135	AAW50866	AAW50866 Variable
3	644	85.0	135	AAW80293	AAW80293 IGM chime
4	644	85.0	590	AAW31751	AAW31751 H chain s
5	644	85.0	590	AAW1888	AAW1888 Anti-huma
6	644	85.0	590	AAW12908	AAW12908 Anti-huma
7	625	82.5	135	AAW68548	AAW68548 Anti-CD33
8	625	82.5	135	AAW69682	AAW69682 Murine M1
9	625	82.5	135	ADO47773	ADO47773 Mouse M19
10	623	82.2	137	AAW05090	AAW05090 Heavy cha
11	613.5	80.9	132	AAW03183	AAW03183 Guy's 13
12	604	79.7	139	AAW33328	AAW33328 KM-796 he
13	604	79.7	139	AAW28356	AAW28356 Antibody
14	604	79.7	139	AAW28384	AAW28384 Anti-GM2
15	600.5	79.2	438	AAE18372	AAE18372 Human pen
16	600.5	79.2	438	ABG76347	ABG76347 Portion o
17	600.5	79.2	456	AAE18370	AAE18370 Human pen
18	600.5	79.2	456	ABG76345	ABG76345 Mouse DAV
19	600.5	79.2	456	ABG76354	ABG76354 DAV-1 ant
20	600.5	79.2	493	AAE18379	AAE18379 Human N-t
21	600.5	79.2	493	ABG76354	ABG76354 Mouse DAV
22	600.5	79.2	510	AAE18378	AAE18378 Human N-t
23	600.5	79.2	510	ABG76353	ABG76353 Mouse DAV
24	600.5	79.2	597	AAE18377	AAE18377 Human N-t

25	600.5	79.2	597	5	ABG76352	ABG76352 Mouse DAV
26	600.5	79.2	613	5	AAE18380	AAE18380 Human N-t
27	600.5	79.2	613	5	ABG76355	ABG76355 Mouse DAV
28	593	78.2	588	3	AAW1881	AAW1881 Anti-huma
29	593	78.2	588	3	AAW12918	AAW12918 Anti-huma
30	587	77.4	130	2	AAW71886	AAW71886 Anti-Pas
31	586	77.3	137	2	AAW53330	AAW53330 KM-750 he
32	586	77.3	137	2	AAW28386	AAW28386 Anti-GM2
33	586	77.3	137	2	AAW28358	AAW28358 Antibody
34	585.5	77.2	136	6	ABU08927	ABU08927 Mouse amy
35	585.5	77.2	140	7	ADC24943	ADC24943 Mouse 19/
36	585.5	77.2	140	7	ADK51711	ADK51711 Murine 19
37	578.5	76.3	138	8	ADR73595	ADR73595 Anti-AR a
38	574	75.7	588	2	AAW71880	AAW71880 Anti-huma
39	574	75.7	588	2	AAW12917	AAW12917 Anti-huma
40	573.5	75.7	151	9	AAE31602	AAE31602 Murine in
41	566.5	74.7	140	2	AAW55554	AAW55554 DREG-200
42	565.5	74.6	138	4	ABG69688	ABG69688 Murine CM
43	565.5	74.6	138	8	ADO47789	ADO47789 Mouse CMV
44	564	74.4	135	2	AAW28669	AAW28669 p12-h2. 3
45	564	74.4	143	2	AAW50155	AAW50155 Murine mo
46	564	74.4	472	2	AAW50157	AAW50157 Chimeric
47	562	74.1	137	2	AAW03724	AAW03724 Anti-huma
48	560	73.9	139	2	AAW38259	AAW38259 Chimeric
49	560	73.9	141	2	AAW12356	AAW12356 Heavy cha
50	560	73.9	233	2	AAW41710	AAW41710 Murine 12
51	560	73.9	235	2	AAW41707	AAW41707 Murine 12
52	560	73.9	235	2	AAW41682	AAW41682 Cimeric a
53	560	73.9	235	2	AAW41715	AAW41715 Murine 12
54	559	73.7	140	2	AAW12234	AAW12234 Mouse MAB
55	559	73.7	167	9	ADY94496	ADY94496 Human/mou
56	559	73.7	469	2	AAW40384	AAW40384 Monoclonal
57	557.5	73.5	140	2	AAW06213	AAW06213 MAB Co-1
58	557.5	73.5	140	2	AAW85061	AAW85061 Mouse Co-
59	557.5	73.5	140	6	ABU58895	ABU58895 Mouse ant
60	557	73.5	133	8	ADO00820	ADO00820 Antibody
61	557	73.5	133	8	ADO43850	ADO43850 Heavy cha
62	557	73.5	133	8	ADO43846	ADO43846 Heavy cha
63	557	73.5	133	9	ADO08854	ADO08854 Mammalian
64	557	73.5	144	2	AAW73188	AAW73188 Fragment
65	556.5	73.4	278	6	ABJ19277	ABJ19277 Anti-huma
66	555.5	73.3	140	2	AAW09425	AAW09425 Co-1 Heav
67	555.5	73.3	462	9	ADU70079	ADU70079 Mouse/hum
68	552	72.8	467	6	AAE38408	AAE38408 Mouse vir
69	551.5	72.8	136	3	AAW23815	AAW23815 Plasmid p
70	551.5	72.8	136	4	AAW67491	AAW67491 Amino aci
71	551.5	72.8	136	5	AAW47629	AAW47629 Murine MA
72	551.5	72.8	136	5	ABG97806	ABG97806 Mouse MAB
73	551.5	72.8	136	5	ABG35309	ABG35309 Thrombopo
74	551	72.7	144	2	AAW73189	AAW73189 Fragment
75	551	72.7	144	2	AAW73186	AAW73186 Fragment
76	550	72.6	152	8	ADJ57084	ADJ57084 3G4 antib
77	550	72.6	159	8	ADJ57088	ADJ57088 3G4-2BVH-
78	546	72.0	137	3	AAW99845	AAW99845 Mouse par
79	545.5	72.0	142	2	AAW48249	AAW48249 A77 anti-
80	545.5	72.0	142	4	AAW74622	AAW74622 A77 anti-
81	545.5	72.0	142	4	AAE08555	AAE08555 Murine A7
82	545.5	72.0	460	9	ADW97108	ADW97108 Murine M1
83	545	71.9	144	2	AAW73187	AAW73187 Fragment
84	545	71.9	144	2	AAW73175	AAW73175 Heavy cha
85	544	71.8	135	3	AAW80288	AAW80288 Humanised
86	541.5	71.4	459	9	ADW97104	ADW97104 Murine MA
87	541.5	71.4	460	9	ADW97139	ADW97139 Murine MA
88	540.5	71.3	136	3	AAW23813	AAW23813 Plasmid p
89	540.5	71.3	136	4	AAW67489	AAW67489 Amino aci
90	540.5	71.3	136	5	AAW47627	AAW47627 Murine MA
91	540.5	71.3	136	5	ABG97804	ABG97804 Thrombopo
92	540.5	71.3	136	5	ABG35307	ABG35307 Thrombopo
93	539.5	71.2	138	9	ADW92464	ADW92464 Mouse SM5
94	539.5	71.2	138	9	ADW98527	ADW98527 Novel chi
95	539.5	71.2	468	9	ADW92458	ADW92458 SM5-1 chi
96	539.5	71.2	468	9	ADW98531	ADW98531 Novel chi
97	539.5	71.2	624	9	ADW92486	ADW92486 chSMVH/FC

98 539.5 71.2 624 9 ADV98549
99 539.5 71.2 639 9 ADV92488
100 539.5 71.2 639 9 ADV98551

ALIGNMENTS

RESULT 1
ID ADS94335 standard; protein; 139 AA.

AC ADS94335;

XX 02-DEC-2004 (first entry)

XX Antibody 776.1 heavy chain variable region (776.1H) SEQ ID NO:34.

XX antibody; antigen-binding antibody fragment;
KW cell-associated CA 125/O772P; monoclonal antibody; cytostatic;
KW immunostimulant; mediator of lysis; tumour; cell proliferative disorder;
KW cancer; cervical cancer; uterine cancer; breast cancer; lung cancer;
KW ovarian cancer.

XX Synthetic.

XX WO2004035537-A2.

XX 29-APR-2004.

XX 15-OCT-2003; 2003WO-US032945.

XX 16-OCT-2002; 2002US-0418828P.

XX 10-JUL-2003; 2003US-0485986P.

XX (EURO-) EUROCELTIQUE SA.

XX Albone EF, Soltis DA;

XX WPI; 2004-357171/33.

XX N-PSDB; ADS94342.

XX Novel isolated antibody, or antigen-binding antibody fragment binding
PT with cell-associated CA 125/O772P polypeptide relative to shed CA
PT 125/O772 polypeptide, useful for ameliorating cervical or ovarian cancer.

XX Claim 38; SEQ ID NO 34; 153pp; English.

XX The present invention describes an isolated antibody, or an antigen-
CC binding antibody fragment (I), that preferentially binds cell-associated
CC CA 125/O772P polypeptide relative to shed CA 125/O772 polypeptide. Also
CC described: (1) a monoclonal antibody (II) produced by hybridoma 4E7; (2)
CC as monoclonal antibody that competes with binding of (II); (3) a hybridoma
CC as deposited in (II); (4) an isolated nucleic acid molecule (III)
CC comprising a nucleotide sequence that encodes a variable chain region of
CC (I); (5) a pharmaceutical composition comprising an antibody or an
CC antigen-binding antibody fragment that preferentially binds cell-
CC associated CA 125/O772P polypeptide relative to shed CA 125/O772P
CC polypeptide, and a carrier; (6) a pharmaceutical composition comprising a
CC monoclonal antibody or an antigen-binding monoclonal antibody fragment
CC that preferentially binds cell-associated CA 125/O772P polypeptide
CC relative to shed CA 125/O772P polypeptide, and a carrier; (7) an article
CC of manufacture (IV) comprising packaging material and a composition
CC comprising an antibody, or an antigen-binding antibody fragment that
CC preferentially binds cell-associated CA 125/O772P relative to shed CA
CC 125/O772P, and a carrier contained within the packaging material, and
CC composition in a form suitable for administration to a subject; (8) a
CC fusion polypeptide (V) comprising an antibody, or an antigen-binding
CC antibody fragment, which preferentially binds cell-associated CA
CC 125/O772P relative to shed CA 125/O772P operably linked to a heterologous
CC agent; (9) ameliorating (MI) a symptom of a CA 125/O772P-related disorder
CC; (10) a monoclonal antibody (VI) chosen from 325.1, 621.1, 633.1, 654.1,
CC 725.1, 8G9, 7F10, 8A1, 8AC3, 15C9, 8E3, 8B5, 7G10, 16C7, 7H1, 16H9,

CC 7A11, 4E7, 117.1, 368.1, 446.1, 501.1, and 776.1 or its antigen-binding
CC antibody fragment; (11) an antibody or antigen binding antibody fragment
CC that competes with (VI); and (12) a pharmaceutical composition comprising
CC (VI) and a carrier. (I) has cytostatic activity, and can be used as an
CC immunostimulant and a mediator of lysis of positive tumour cell. (I) is
CC useful for ameliorating a symptom of a CA 125/O772P-related disorder which
CC is a cell proliferative disorder such as cancer, cervical or uterine
CC cancer, breast or lung cancer or ovarian cancer. (V) is useful
CC diagnostically for monitoring the development or progression of cancer or
CC tumour as part of clinical testing procedure. The present sequence
CC represents an antibody heavy chain variable region amino acid sequence,
CC which is used in the exemplification of the present invention.

XX Sequence 139 AA;

Query Match 100.0%; Score 758; DB 8; Length 139;

Best Local Similarity 100.0%; Pred. No. 6.9e-56;

Matches 139; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGMSWIFLFLSCTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHWKQSH 60

Db 1 MGMSWIFLFLSCTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHWKQSH 60

QY 61 GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDSSNTAYNELSLTSEDSAVVYCARWDF 120

Db 61 GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDSSNTAYNELSLTSEDSAVVYCARWDF 120

QY 121 GSGYFDYWGQGTTLTVSS 139

Db 121 GSGYFDYWGQGTTLTVSS 139

RESULT 2

AAW60866

ID AAW60866 standard; protein; 135 AA.

XX AC AAW60866;

XX 10-SEP-1998 (first entry)

XX Variable region of an anti-Fas antibody heavy chain.

XX Variable region; heavy chain; anti-Fas antibody; human; mouse;
KW immunoglobulin G; IgG; light chain; treatment; diagnosis;
KW autoimmune disease.

XX Mus sp.

XX JPI0165178-A.

XX 23-JUN-1998.

XX 01-JUL-1997; 97JP-00191769.

XX 02-JUL-1996; 96JP-00172228.

XX 09-OCT-1996; 96JP-00268737.

XX (IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK.

XX WPI; 1998-406105/35.

XX N-PSDB; AAV37264.

XX DNA encoding, e.g. variable region of anti-Fas antibody - useful for,
PT e.g. diagnosis and treatment of auto-immune diseases.

XX Claim 7; Page 13; 16pp; Japanese.

XX The present sequence represents a variable region of the heavy chain of
CC an anti-Fas antibody. The constant region of the heavy chain is derived
CC from human immunoglobulin G (IgG). The anti-Fas antibody can be used for
CC the treatment and diagnosis of autoimmune diseases

XX Sequence 135 AA;

Query Match 85.0%; Score 644; DB 2; Length 135;
Best Local Similarity 87.8%; Pred. No. 2.5e-46;
Matches 122; Conservative 5; Mismatches 8; Indels 4; Gaps 1;

QY 1 MGMSWIFLLSAGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHWKQSH 60
DB 1 MGMSWIFLLSAGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHWKQSH 60

QY 61 GKLEWIGYIYPYNGVDYQNFKSKATLVDNNSNTAYMELSLTSEDSAVYYCARWDF 120
DB 61 GKLEWIGYIYPYNGGTGYNQKPKSKATLVDNNSSTAYMELSLTSEDSAVYYCAR--- 117

QY 121 GSGYFDYWGQGTTLTVSS 139
DB 118 -SYANDYWGQGTSTVTVSS 135

RESULT 4
AAW31751
ID AAW31751 standard; protein; 590 AA.
XX
AC AAW31751;
XX
XX 15-APR-1998 (first entry)
XX
XX H chain subunit of Fas specific antibody.
XX
XX Fas; antibody; human; immunoglobulin; variable region; rheumatism;
KW autoimmune disease; rheumatoid arthritis; therapy; CDR; heavy chain;
KW complementarity determining region.
XX
XX Mus musculus.
XX
XX
XX Key Location/Qualifiers
XX Peptide 1-19
XX FT /note= "signal peptide"
XX FT Protein 20..590
XX FT /note= "mature protein"
XX
XX EP799891-A1.
XX
XX
XX 08-OCT-1997.
XX
XX 27-MAR-1997; 97EP-00302415.
XX
XX 01-APR-1996; 96JP-00078570.
XX
XX (SANY) SANKYO CO LTD.
XX
XX Serizawa N, Ichikawa K, Nakahara K, Yonehara S;
XX WPI: 1997-482673/45.
XX N-PSDB; AAT88869.
XX
XX Anti-Fas recombinant antibodies - useful for treating auto-immune
PT diseases, especially rheumatoid arthritis.
XX
XX Claim 11; Page 29-31; 72pp; English.
XX
XX This sequence represents the heavy chain of the protein of the invention.
CC The protein of the invention is a recombinant protein (A), that comprises
CC at least one region corresponding to an immunoglobulin (Ig) variable
CC region which enables the protein to recognise and specifically bind to an
CC antigen, preferably human Fas, and has substantially no more
CC immunogenicity in a human patient than a human antibody. The proteins are
CC useful for treating autoimmune diseases, especially rheumatism
CC (rheumatoid arthritis). (A) is based on a murine monoclonal antibody. As
CC the protein lacks the constant region, it has substantially no more
CC immunogenicity in the human patient than a human antibody
XX
SQ Sequence 590 AA;

Query Match 85.0%; Score 644; DB 2; Length 590;
Best Local Similarity 87.8%; Pred. No. 1.2e-45;
Matches 122; Conservative 5; Mismatches 8; Indels 4; Gaps 1;

QY 1 MGMSWIFLLSAGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHWKQSH 60
DB 1 MGMSWIFLLSAGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHWKQSH 60

QY 61 GKLEWIGYIYPYNGVDYQNFKSKATLVDNNSNTAYMELSLTSEDSAVYYCARWDF 120
DB 61 GKLEWIGYIYPYNGGTGYNQKPKSKATLVDNNSSTAYMELSLTSEDSAVYYCAR--- 117

QY 121 GSGYFDYWGQGTTLTVSS 139
DB 118 -SYANDYWGQGTSTVTVSS 135

RESULT 3
AAW80293
ID AAW80293 standard; protein; 135 AA.
XX
AC AAW80293;
XX
XX 30-MAY-2000 (first entry)
XX
XX IGM chimeric antibody heavy chain variable region SEQ ID NO:1.
XX
XX Humanised; anti-Fas antibody; mouse hybridoma; autoimmune disease;
KW diagnosis; CDR; complementarity determining region; apoptosis;
KW immunosuppressive.
XX
XX Mus sp.
XX
XX Synthetic.
XX
XX JP2000014383-A.
XX
XX 18-JAN-2000.
XX
XX 03-JUL-1998; 98JP-00204318.
XX
XX 03-JUL-1998; 98JP-00204318.
XX
XX (IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK.
XX
XX WPI: 2000-199626/18.
XX N-PSDB; AAZ95282.
XX
XX Novel recombinant antibody used for treating and diagnosing autoimmune
PT diseases - is humanized anti-Fas antibody which controls and induces
PT apoptosis in cells expressing fas antigen.
XX
XX Example 1; Page 9-10; 25pp; Japanese.
XX
XX The present invention describes a recombinant antibody (A) which binds to
CC fas antigen, and controls and induces apoptosis in cells which expressed
CC fas antigen. The complementarity determining regions (CDR) of (A) contain
CC amino acid sequences obtained from a mammal other than human, other
CC regions contain amino acid sequences from human and they partly contain
CC modified amino acids. (A) has immunosuppressive activity. (A) is used for
CC treating and/or diagnosing autoimmune diseases. The present sequence
CC represents an immunoglobulin M chimeric antibody heavy chain variable
CC region from an example from the present invention
XX
SQ Sequence 135 AA;

Query Match 85.0%; Score 644; DB 3; Length 135;
Best Local Similarity 87.8%; Pred. No. 2.5e-46;
Matches 122; Conservative 5; Mismatches 8; Indels 4; Gaps 1;

QY 1 MGMSWIFLLSAGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHWKQSH 60
DB 1 MGMSWIFLLSAGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHWKQSH 60

QY	61	GKLEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF	120
Db	61	GKLEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF	117
QY	121	GSYYFYDYGQGTTLTVSS	139
Db	118	-SYAMDYWGQGTSTVTVSS	135
RESULT 5			
AAW71888			
ID	AAW71888	standard; protein; 590 AA.	
XX	AAW71888;		
DT	18-JAN-1999	(first entry)	
DE	Anti-human Fas monoclonal antibody CH11 heavy chain.		
XX	Humanised antibody; Fas; CH11; monoclonal antibody; MAb; apoptosis;		
KW	autoimmune disease; rheumatoid arthritis; therapy; human; mouse;		
KW	antibody engineering.		
XX	Synthetic.		
OS	Mus musculus.		
XX	Key	Location/Qualifiers	
PH	Peptide	1. .19	
FT	Protein	/label= Sig_peptide	
FT	Protein	20. .590	
FT	Region	/label= Mat_protein	
FT	Region	50. .54	
FT	Region	/label= CDR1	
FT	Region	69. .84	
FT	Region	/label= CDR2	
FT	Region	118. .124	
FT	Region	/label= CDR3	
XX	EP866131-A2.		
XX	23-SEP-1998.		
XX	20-MAR-1998;	98EP-00302113.	
XX	21-MAR-1997;	97JP-00067938.	
XX	(SANY) SANKYO CO LTD.		
XX	Serizawa N, Haruyama H, Takahashi T, Nakahara K, Yonehara S;		
XX	WPI; 1998-482965/42.		
DR	N-PSDB; AAV66735.		
XX	Production of anti-Fas protein humanised antibodies - for use in inducing		
PT	apoptosis on Fas expressing cells in the treatment of auto-immune		
PT	diseases, especially rheumatoid arthritis.		
XX	Example 4; Page 58-60; 187pp; English.		
XX	This is the amino acid sequence of the heavy chain of the mouse anti-		
CC	human Fas monoclonal antibody CH11, as deduced from an amplified cDNA		
CC	clone (see AAV66735). The invention relates to novel humanised antibodies		
CC	comprising humanised light and heavy chains (see AAW71876-81) of CH11.		
CC	These humanised anti-human Fas antibodies are capable of inducing		
CC	apoptosis in cells expressing Fas (e.g. synovocytes) and are useful in		
CC	the treatment of autoimmune disease and chronic rheumatoid arthritis		
XX	Sequence 590 AA;		
XX	Query Match	85.0%; Score 644; DB 2; Length 590;	
XX	Best Local Similarity	87.8%; Pred. No. 1.2e-45;	
XX	Matches 122; Conservative	5; Mismatches 8; Indels 4; Gaps 1;	
QY	1	MGMSWIFLLSCTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHVKQSH	60
Db	1	MGMSWIFLLSCTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHVKQSH	60
QY	61	GKLEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF	120
Db	61	GKLEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF	117
QY	121	GSYYFYDYGQGTTLTVSS	139
Db	118	-SYAMDYWGQGTSTVTVSS	135
RESULT 6			
AAW71888			
ID	AAW71888	standard; protein; 590 AA.	
XX	AAW71888;		
DT	16-NOV-2000	(first entry)	
DE	Anti-human Fas antibody CH11 H chain protein sequence SEQ ID #8.		
XX	Antirheumatic agent; immunoglobulin M; IgM; apoptosis inducer;		
KW	immunosuppression; autoimmune disease; treatment; rheumatism;		
KW	anti-Fas antibody.		
XX	Synthetic.		
OS	JP2000154149-A.		
XX	06-JUN-2000.		
XX	17-SEP-1999;	99JP-00263984.	
XX	18-SEP-1998;	98JP-00264598.	
XX	(SANY) SANKYO CO LTD.		
XX	WPI; 2000-454476/40.		
DR	N-PSDB; AAA78202.		
XX	Anti-human Fas humanizing antibody-containing antirheumatic agents.		
XX	Disclosure; Page 47-48; 109pp; Japanese.		
XX	The present invention relates to antirheumatic agents which comprise as		
CC	active ingredients an immunoglobulin M (IgM) protein. The IgM protein		
CC	does not include a J segment, has apoptosis inducing activity, and		
CC	consists of a light and heavy chain polypeptide produced synthetically.		
CC	The agents of the invention exhibit antirheumatic and immunosuppressive		
CC	activity and can be used to treat autoimmune diseases, especially		
CC	rheumatism. The IgM molecule used in the invention has human Fas-antigen		
CC	binding properties. Included in the invention are nucleotide sequences of		
CC	the IgM light and heavy chains (see AAA78267-A78272) and the		
CC	corresponding protein sequences (see AAA12913-B12918 and AAA12919), and		
CC	nucleotide sequences of the humanised anti-human Fas Ig CH11 (see		
CC	AAA78202-A78206) and protein sequences (see AAA12908-B12910). Also		
CC	included are anti-human Fas antibody CDR peptides (AAW78213-78217).		
CC	Primers specific for the anti-human Fas antibody, light, heavy and kappa		
CC	chains used in the invention are represented by sequences AAA78213-		
CC	A78266. Primers used for sequencing the human Ig DNA used in the		
CC	invention are represented by sequences AAA78277-A78318 and AAA78335-		
CC	A78337, while humanised anti-Fas Ig DNA sequencing primers are		
CC	represented by sequences AAA78321-A78334 and AAA78338-A78367. Primer		
CC	sequences AAA78207-A78212 are specific for murine Ig DNA, and are used in		
CC	the production of the agent of the invention		
XX	Sequence 590 AA;		
XX	Query Match	85.0%; Score 644; DB 3; Length 590;	
XX	Best Local Similarity	87.8%; Pred. No. 1.2e-45;	
XX	Matches 122; Conservative	5; Mismatches 8; Indels 4; Gaps 1;	

QY 1 MGMSWIFLLSCTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHVKQSH 60
 |||||
 Db 1 MGMSWIFLLSCTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHVKQSH 60
 |||||
 QY 61 GKLEWIGIYYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELSLTSEDSAVYYCARWDF 120
 |||||
 Db 61 GKLEWIGIYYPYNGGTYGNGKPKSKATLIVDNSSNTAYMELSLTSEDSAVYYCARWDF 120
 |||||
 QY 121 GSGYFDYWGQGTTLTVSS 139
 |||||
 Db 118 -SYAMDYWGQGTSTVTVSS 135
 |||||
 RESULT 7
 AAW68548
 ID AAW68548 standard; protein; 135 AA.
 XX AAW68548;
 AC AAW68548;
 XX
 DT 27-AUG-2003 (revised)
 DT 15-FEB-1999 (first entry)
 XX
 XX Anti-CD33 antibody heavy chain.
 XX
 XX Panconi anaemia complementation group C; FAC; apoptosis; haematopoiesis;
 KW bone marrow; chemotherapy; gene therapy; CD33; antibody.
 XX
 XX Mammalia.
 XX
 PN WO9851792-A1.
 XX
 XX 19-NOV-1998.
 XX
 XX 15-MAY-1998; 98WO-US0009975.
 XX
 XX 15-MAY-1997; 97US-0046546P.
 PR
 XX (BGHM) BRIGHAM & WOMENS HOSPITAL.
 PA
 XX Youssoufian H;
 PI
 XX WPI; 1999-009774/01.
 DR N-PSDB; AAV33947.
 DR
 XX
 XX New conjugate of Panconi anaemia molecule and peptide selective for
 PT haematopoietic precursor cells - inhibits apoptosis of these cells, for
 PT treating Panconi anaemia and patients undergoing high-dose chemotherapy
 PT for cancer.
 PT
 XX
 XX Example 1; Page 50-51; 72pp; English.
 PS
 XX This is the amino acid sequence of the heavy chain of the M195 anti-CD33
 CC antibody. This antibody selectively binds to surface of haematopoietic
 CC progenitor cells (HPC) and is transported into the cells by endocytosis.
 CC The invention provides conjugates of human Panconi anaemia
 CC complementation group C (PAC) protein (see AAW68546) and anti-CD33
 CC antibody (preferably a single chain antibody). A nucleic acid (see
 CC AAV33947) encoding the heavy chain can be ligated with vector pBB6 and
 CC with PAC cDNA (see AAV33945) to provide a fusion protein. Alternatively,
 CC nucleic acids encoding the heavy and light chains (see AAW68549) of M195
 CC are ligated into a bicistronic vector, antibody molecule is isolated from
 CC transfected cells, and chemically crosslinked to FAC protein (see
 CC AAW68546) to form a conjugate. The conjugate or fusion protein, or a
 CC nucleic acid encoding it, can be used to deliver FAC to an HPC,
 CC specifically to inhibit apoptosis, particularly in patients exposed to
 CC high doses of chemotherapy for treatment of non-myeloid cancers, also to
 CC treat Panconi anaemia (by complementation of the genetic defect).
 CC Treatment of HPC is done in vitro, ex vivo (e.g. for recombination
 CC production of conjugate in cell cultures) or in vivo. Treatment with FAC
 CC may eliminate the need for extensive bone marrow transplants to restore
 CC haematopoiesis after chemotherapy. (Updated on 27-AUG-2003 to correct OS
 CC field.)

XX
 SQ Sequence 135 AA;
 Query Match 82.5%; Score 625; DB 2; Length 135;
 Best Local Similarity 84.9%; Pred. No. 9.7e-45;
 Matches 118; Conservative 7; Mismatches 10; Indels 4; Gaps 1;
 QY 1 MGMSWIFLLSCTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHVKQSH 60
 |||||
 Db 1 MGMSWIFLLSCTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHVKQSH 60
 |||||
 QY 61 GKLEWIGIYYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELSLTSEDSAVYYCARWDF 120
 |||||
 Db 61 GKLEWIGIYYPYNGGTYGNGKPKSKATLIVDNSSNTAYMELSLTSEDSAVYYCARWDF 120
 |||||
 QY 121 GSGYFDYWGQGTTLTVSS 139
 |||||
 Db 118 -GRPAMDYWGQGTSTVTVSS 135
 |||||
 RESULT 8
 AAB69682
 ID AAB69682 standard; protein; 135 AA.
 XX AAB69682;
 AC AAB69682;
 XX
 DT 30-APR-2001 (first entry)
 XX
 XX Murine M195 antibody heavy chain SEQ ID NO: 69.
 DE
 XX Humanised immunoglobulin; mouse; human; antibody; heavy chain; diabetes;
 KW light chain; graft versus host disease; transplant; autoimmune disease;
 KW multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus;
 KW myasthenia gravis; herpes infection; myeloid leukaemia; CMV infection.
 XX
 OS Mus sp.
 XX
 XX US6180370-B1.
 PN
 XX 30-JAN-2001.
 PD
 XX
 XX 07-JUN-1995; 95US-00484537.
 PF
 XX 28-DEC-1988; 88US-00290975.
 PR 13-FEB-1989; 89US-00310252.
 PR 28-SEP-1990; 90US-00590274.
 PR 19-DEC-1990; 90US-00634278.
 PR
 XX (PROT-) PROTEIN DESIGN LABS INC.
 PA
 XX Queen CL, Sellick HE;
 PI
 XX WPI; 2001-190856/19.
 DR N-PSDB; AAF58738.
 DR
 XX Producing humanized immunoglobulin, involves producing a cell containing
 PT DNA segments encoding humanized heavy and light chain variable regions,
 PT and expressing the DNA segments in the cell.
 XX
 XX Example 7; Fig 34; 145pp; English.
 PS
 XX The present invention describes a method of producing humanised
 CC immunoglobulins involving expressing in a cell a nucleic acid encoding a
 CC humanised version of an immunoglobulin. This is obtained by comparing a
 CC donor and human immunoglobulin and producing a combined antibody which
 CC contains part of each. These are useful in the treatment of graft-versus-
 CC host disease, transplant rejection, autoimmune diseases such as diabetes,
 CC rheumatoid arthritis, myasthenia gravis, multiple sclerosis and systemic
 CC lupus erythematosus, herpes infections, CMV virus infections and myeloid
 CC leukaemia. The present sequence is an antibody used to demonstrate the
 CC method of the invention
 XX
 XX Sequence 135 AA;

Query Match 82.5%; Score 625; DB 4; Length 135;
 Best Local Similarity 84.9%; Pred. No. 9.7e-45;
 Matches 118; Conservative 7; Mismatches 10; Indels 4; Gaps 1;

QY 1 MGWSWIFLLSGTAGVHSEVOLQSGPELVKPGASVKISCKASGYFTDYNHWKQSH 60
 DB 1 MGWSWIFLLSGTAGVHSEVOLQSGPELVKPGASVKISCKASGYFTDYNHWKQSH 60

QY 61 GKLEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
 DB 61 GKLEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120

QY 121 GSGYFDYWGQGTTLTVSS 139
 DB 118 -GRPAMDYWGQGTSTVTVSS 135

RESULT 9
 ADO47773
 ID ADO47773 standard; protein; 135 AA.
 AC ADO47773;
 XX
 DT 15-JUN-2004 (first entry)
 DE Mouse M195 antibody heavy chain variable region #2.
 XX
 KW humanised immunoglobulin; Ig; immunoglobulin; framework; acceptor Ig;
 KW donor Ig; CDR; complementarity determining region; interleukin-2; IL-2;
 KW IL-2 receptor; T-cell mediated disorder; mouse; M195 antibody;
 KW heavy chain variable region.
 XX
 OS Mus sp.
 XX
 XX US2004058414-A1.
 XX
 PD 25-MAR-2004.
 XX
 XX 30-MAY-2003; 2003US-00452357.
 XX
 PR 28-DEC-1988; 88US-00290975.
 PR 13-FEB-1989; 89US-00310252.
 PR 28-SEP-1990; 90US-00590274.
 PR 07-JUN-1995; 95US-00484537.
 PR 22-NOV-2000; 2000US-00718993.
 XX
 PA (QUEE/) QUEEN C L.
 PA (COMS/) CO M S.
 PA (SCHN/) SCHNEIDER W P.
 PA (LAND/) LANDOLFI N F.
 PA (COEL/) COELINGH K L.
 PA (SELI/) SELICK H E.
 XX
 PI Queen CL, Co MS, Schneider WP, Landolfi NF, Coelingh KL;
 PI Selick HE;
 XX
 XX WPI; 2004-304235/28.
 DR N-PSDB; ADO47772.
 XX
 XX Designing humanized immunoglobulin chain comprises substituting human
 FT framework amino acids of acceptor immunoglobulin with corresponding amino
 FT acid from donor immunoglobulin at position in immunoglobulin.
 XX
 PS Disclosure; Fig 41; 130pp; English.
 XX
 CC The invention describes a method of designing a humanised immunoglobulin
 CC (Ig) chain. The method comprises substituting human framework amino acids
 CC of the acceptor Ig with a corresponding amino acid from the donor Ig at a
 CC position in the Ig, where the amino acid is immediately adjacent to one
 CC of the CDR's or the amino acid is predicted to have a side chain atom
 CC whose Van der Waals surface is 3 angstroms from the CDR's in three-
 CC dimensional Ig model and is capable of interacting with the antigen or

CC with the CDR's of the humanised Ig that when the chain is a heavy chain,
 CC substituted amino acid(s) is capable of interacting with CDR's 2 or 3.
 CC Also described are: an Ig comprising two light/heavy chains; a DNA
 CC sequence which upon expression encodes a humanised Ig chain; a
 CC polynucleotide comprising a DNA sequence coding for a
 CC humanised Ig; a composition comprising a pure humanised immunoglobulin
 CC capable of inhibiting binding of human interleukin-2 (IL-2) to a human IL
 CC -2 receptor; treating T-cell mediated disorders in a human patient
 CC comprising administering to the patient a therapeutic dose of an Ig; and
 CC a composition comprising a pure humanised Ig reactive with the p75 chain
 CC of the human IL-2 receptor. The method is used for designing a humanised
 CC immunoglobulin chain, useful for treating T-cell mediated disorders in a
 CC human patient. The invented method produces an Ig chain that is easily
 CC and economically produced. This is the amino acid sequence of mouse M195
 CC antibody heavy chain variable region. Residues in the human antibody
 CC framework can be replaced with residues from the mouse antibody to create
 CC a humanised antibody.
 XX
 SQ Sequence 135 AA;

Query Match 82.5%; Score 625; DB 8; Length 135;
 Best Local Similarity 84.9%; Pred. No. 9.7e-45;
 Matches 118; Conservative 7; Mismatches 10; Indels 4; Gaps 1;

QY 1 MGWSWIFLLSGTAGVHSEVOLQSGPELVKPGASVKISCKASGYFTDYNHWKQSH 60
 DB 1 MGWSWIFLLSGTAGVHSEVOLQSGPELVKPGASVKISCKASGYFTDYNHWKQSH 60

QY 61 GKLEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
 DB 61 GKLEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120

QY 121 GSGYFDYWGQGTTLTVSS 139
 DB 118 -GRPAMDYWGQGTSTVTVSS 135

RESULT 10
 AAR05090
 ID AAR05090 standard; protein; 137 AA.
 XX
 AC AAR05090;
 XX
 DT 25-MAR-2003 (revised)
 DT 04-OCT-1990 (first entry)
 XX
 DE Heavy chain variable domain of human chorion gonadotropin-binding pptde.
 XX
 KW Human chorionic gonadotropin; antibodies; heavy chain; choriocarcinoma;
 KW abortion; tumour detection; complementary determining regions;
 XX pregnancy prevention.
 OS Mus musculus.
 XX
 PH Key Location/Qualifiers
 FT Binding-site 50..54
 FT /label= CDR 1
 FT Binding-site 70..85
 FT /label= CDR 2
 FT Binding-site 118..126
 FT /label= CDR 3
 XX
 XX EPJ70581-A.
 XX
 PD 30-MAY-1990.
 XX
 PF 21-NOV-1989; 89EP-00202951.
 XX
 PR 25-NOV-1988; 88NL-00002902.
 XX
 PA (ALKU) AKZO NV.
 XX
 PI Vanwezenb PM, Bos ES;

XX WPI; 1990-165307/22.
 DR N-PSDB; AAQ04694.
 XX Polypeptide(s) which specifically bind human chorionic gonadotropin -
 PT contg. antigen-binding domains comprising complementary determining
 PT regions.
 XX Disclosure; Page ?; -pp; English.
 XX Together with the light chain variable domain (AAR05089) the sequence
 CC forms a hCH-binding antibody fragment (PhCG). For the production of Abs
 CC the variable region was fused to a constant region of human origin. The
 CC product can be used to prevent pregnancy or for combatting
 CC choriocarcinomas or other hCG-producing tumours. They also have
 CC diagnostic applications as immune reagents for in vivo diagnosis, eg for
 CC localisation of tumours and for in vitro diagnosis for detection of hCG
 CC in body fluids. (Updated on 25-MAR-2003 to correct PI field.)
 XX Sequence 137 AA;
 SQ

Query Match 82.2%; Score 623; DB 2; Length 137;
 Best Local Similarity 84.2%; Pred. No. 1.5e-44;
 Matches 117; Conservative 9; Mismatches 11; Indels 2; Gaps 1;
 QY 1 MGHSWIFLFLSLGTAGVHSEVQLQSGPELVKPGASVKISKASGYTFTDYNHMKQSH 60
 DB 1 MGHSWIFLFLSLGTAGVHSEVQLQSGPELVKPGASVKISKASGYTFTDYNHMKQSH 60
 QY 61 GKILEWIGIYYPNGVSDYNQNFKSKATLIVDNSSNTAYMELSLTSEDSAVYYCARWDF 120
 DB 61 GRLEWIGIYYPNGVSDYNQNFKSKATLIVDNSSNTAYMELSLTSEDSAVYYCAR--E 118
 QY 121 GSGYFDYWGQGTTLTVSS 139
 DB 119 GIFYTDYWGQGTSTVSS 137

RESULT 11
 AA03183
 ID AA03183 standard; protein; 132 AA.
 XX AC AA03183;
 XX 24-FEB-1997 (first entry)
 XX Guy's 13 anti-Streptococcus mutans antibody gamma chain.
 XX Rabbit; immunoglobulin; receptor; protection protein; mutans;
 XX heavy chain; antigen binding domain; protection; pathogen; mucosal;
 XX environment; gastrointestinal; passive; immunisation; Guy's 13 antibody;
 XX prevention; dental caries; Streptococcus; poly; gamma chain.
 XX Mus musculus.
 OS WO9621012-A1.
 PN 11-JUL-1996.
 XX 27-DEC-1995; 95WO-US016889.
 XX 30-DEC-1994; 94US-00367395.
 XX 04-MAY-1995; 95US-00434000.
 XX (PLAN-) PLANET BIOTECHNOLOGY INC.
 XX (UNMR-) UNITED MEDICAL & DENTAL SCHOOLS GUYS.
 XX Hiatt AC, Ma JK, Lehner T;
 XX WPI; 1996-333987/33.
 XX N-PSDB; AAT31293.
 XX Immunoglobulin and protection protein complex and its prodn. in plants -

PT useful for passive immunisation against mucosal antigens, esp. against S.
 XX mutans and S. sorbinus to prevent dental caries.
 PS Claim 23; Page 131; 152pp; English.
 XX The present sequence is the Guy's 13 anti-Streptococcus mutans antibody,
 CC gamma chain. The immunoglobulin (Ig) of the invention comprises a
 CC protection protein (PP), pref. a portion of the rabbit poly-Ig receptor,
 CC in association with an Ig derived light or heavy chain, having at least a
 CC portion of an antigen (Ag) binding domain, specifically the Guy's 13
 CC kappa or gamma chain. The Ig can be used to prevent dental caries by
 CC binding S. mutans serotypes c, e and f, while the PP protects the Ig in
 CC harsh mucosal, e.g. gastrointestinal, environments, therefore enhancing
 CC its effectiveness in passively immunising animals against mucosal
 CC pathogens
 XX Sequence 132 AA;
 SQ

Query Match 80.9%; Score 613.5; DB 2; Length 132;
 Best Local Similarity 83.5%; Pred. No. 8.8e-44;
 Matches 116; Conservative 6; Mismatches 10; Indels 7; Gaps 1;
 QY 1 MGHSWIFLFLSLGTAGVHSEVQLQSGPELVKPGASVKISKASGYTFTDYNHMKQSH 60
 DB 1 MEWTWVFLFLSLGTAGVHSGVQLQSGPDLVRFKASVKISKASGYTFTDYNHMKQSR 60
 QY 61 GKILEWIGIYYPNGVSDYNQNFKSKATLIVDNSSNTAYMELSLTSEDSAVYYCARWDF 120
 DB 61 GKSLEWIGIYYPNGVSDYNQNFKSKATLIVDNSSNTAYMELSLTSEDSAVYYCAT--- 117
 QY 121 GSGYFDYWGQGTTLTVSS 139
 DB 118 ---YFDYWGQGTTLTVSS 132

RESULT 12
 AAR53328
 ID AAR53328 standard; protein; 139 AA.
 XX AC AAR53328;
 XX 17-NOV-1994 (first entry)
 XX KM-796 heavy chain.
 XX Monoclonal antibody; Ab; ganglioside GM2; chimera; chimeric antibody;
 XX expression vector; heavy; light; chain; hypervariable region; CDR; KM-603;
 XX constant region; hybridoma; Ig; immunoglobulin; KM-796; KM-750;
 XX Mus musculus.
 PH Key Location/Qualifiers
 FT Peptide 1..19 /label= sig_peptide
 FT Region 50..54 /label= CDR1
 FT /note= "claim 8"
 FT Region 69..85 /label= CDR2
 FT /note= "claim 8"
 FT Region 118..128 /label= CDR3
 FT /note= "claim 8"
 XX AU9346181-A.
 XX 17-MAR-1994.
 XX 07-SEP-1993; 93AU-00046181.
 XX 07-SEP-1992; 92JP-00238452.

PA (KYOW) KYOWA HAKKO KOGYO KK.
 XX Nakamura K, Koike M, Shitara K, Hanai N, Kuwana Y, Hasegawa M;
 XX WPI; 1994-126857/16.
 DR N-PSDB; AAQ45426.
 XX Humanised antibody specific for ganglioside GM2 - used for producing a
 FT cytotoxic effect on cancers such as melanoma, neuroblastoma and glioma.
 XX Claim 5; Page 104-105; 19ipp; English.
 XX Chimeric human Ab expression vectors are constructed by inserting the Ab
 CC heavy and light chain variable region-encoding cDNA isolated from
 CC hybridomas producing a mouse or rat monoclonal Ab reacting with the
 CC ganglioside GM2 respectively into an expression vector for use in animal
 CC cells which contains the human Ab heavy and light chain constant region-
 CC encoding cDNA. The expression vectors are introduced into animal cells
 CC and the transformant thus obtained is cultured for the prodn. of a
 CC chimeric human Ab reacting with the ganglioside GM2. In contrast to mouse
 CC monoclonal Abs, the chimeric human Abs will not cause anti-mouse Ig Ab
 CC prodn. in the patient's body but show a prolonged blood half-life, with a
 CC reduced frequency of adverse effects, so that it can be expected to be
 CC superior to mouse monoclonal Abs in the efficacy in the treatment of
 CC human cancer, for instance. Mouse anti-GM2 monoclonal Ab KM-796 and KM-
 CC 750 and rat KM-603 heavy and light chain sequences are given in AAQ45426-
 CC 30. CDR regions for use in chimeric Abs are indicated in the Features
 CC Table
 XX SQ Sequence 139 AA;
 Query Match 79.7%; Score 604; DB 2; Length 139;
 Best Local Similarity 82.7%; Pred. No. 5.8e-43;
 Matches 115; Conservative 6; Mismatches 18; Indels 0; Gaps 0;
 QY 1 MGWSWIFLLSLGAGVHSEVQLQSGPELVKPGASVKISKASGYFTDYNHIVKQSH 60
 DB 1 MGWSWIFLLSLGAGVHSEVQLQSGPELVKPGASVKISKASGYFTDYNHIVKQSH 60
 QY 61 GKILEWIGIYYPNGVSDYQNFKSKATLIVDSSNTAYMELSLTSEDSAVVYCARWDF 120
 DB 61 GKILEWIGIYYPNGVSDYQNFKSKATLIVDSSNTAYMELSLTSEDSAVVYCARWDF 120
 QY 121 GSGYFDYWGQGTTLTVSS 139
 DB 121 YGYMFAYWGQGTTLTVTSA 139
 RESULT 13
 AAY28356
 ID AAY28356 standard; protein; 139 AA.
 XX AC AAY28356;
 XX 27-AUG-2003 (revised)
 DT 04-NOV-1999 (first entry)
 XX Antibody chain used to produce Human chimeric antibodies.
 DE antibody; nucleotide; genomic; hypervariable region; chimeric;
 KW light chain; heavy chain; amino acid.
 XX Mammalia.
 OS
 XX Key Location/Qualifiers
 FH Peptide 1..19
 FT /label= Signal peptide
 FT Protein 20..139
 FT /label= Mature antibody chain
 FT Domain 50..55
 FT /label= CDR1
 FT /note= "Complementarity determining region"
 FT Domain 69..86

FT /label= CDR2
 FT /note= "Complementarity determining region"
 FT 118..129
 FT /label= CDR3
 FT /note= "Complementarity determining region"
 PN US939532-A.
 XX 17-AUG-1999.
 XX 07-JUN-1995; 95US-00483528.
 XX 07-SEP-1993; 93US-00116778.
 XX (KYOW) KYOWA HAKKO KOGYO KK.
 XX Nakamura K, Hanai N, Kuwana Y, Hasegawa M, Koike M, Shitara K;
 XX WPI; 1999-468416/39.
 XX N-PSDB; AAX99474.
 XX Chimeric human antibody expression vectors.
 XX Disclosure; Col 81-83; 188pp; English.
 CC This antibody chain is used in the production of Human chimeric
 CC antibodies. The chimeric human antibodies are useful in the treatment of
 CC cancer, especially that which is of neural ectodermal origin. In contrast
 CC to prior art constructs based on mouse monoclonal antibodies, the
 CC chimeric human antibodies do not cause anti-mouse immunoglobulin
 CC production. The chimeric human antibodies have a prolonged half-life and
 CC a reduced frequency of adverse effects when compared to mouse monoclonal
 CC antibodies. (Updated on 27-AUG-2003 to correct OS field.)
 XX SQ Sequence 139 AA;
 Query Match 79.7%; Score 604; DB 2; Length 139;
 Best Local Similarity 82.7%; Pred. No. 5.8e-43;
 Matches 115; Conservative 6; Mismatches 18; Indels 0; Gaps 0;
 QY 1 MGWSWIFLLSLGAGVHSEVQLQSGPELVKPGASVKISKASGYFTDYNHIVKQSH 60
 DB 1 MGWSWIFLLSLGAGVHSEVQLQSGPELVKPGASVKISKASGYFTDYNHIVKQSH 60
 QY 61 GKILEWIGIYYPNGVSDYQNFKSKATLIVDSSNTAYMELSLTSEDSAVVYCARWDF 120
 DB 61 GKILEWIGIYYPNGVSDYQNFKSKATLIVDSSNTAYMELSLTSEDSAVVYCARWDF 120
 QY 121 GSGYFDYWGQGTTLTVSS 139
 DB 121 YGYMFAYWGQGTTLTVTSA 139
 RESULT 14
 AAY28384
 ID AAY28384 standard; protein; 139 AA.
 XX AC AAY28384;
 XX 04-NOV-1999 (first entry)
 DT Anti-GM2 heavy chain from KM796 mouse hybridoma cell line.
 DE antibody; nucleotide; genomic; hypervariable region; chimeric;
 KW light chain; heavy chain; plasmid; hypervariable.
 XX Mus sp.
 XX Key Location/Qualifiers
 FH Peptide 1..19
 FT /label= Signal peptide
 FT Protein 20..139
 FT /label= Mature mouse heavy chain

```

FT Domain 50..54
FT /label= Hypervariable region 1
FT Domain 69..85
FT /label= Hypervariable region 2
FT Domain 118..128
FT /label= Hypervariable region 3
XX US5939532-A.
XX 17-AUG-1999.
XX 07-JUN-1995; 95US-00483528.
XX 07-SEP-1993; 93US-00116778.
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX Nakamura K, Hanai N, Kuwana Y, Hasegawa M, Koike M, Shitara K;
XX WPI; 1999-468416/39.
XX Chimeric human antibody expression vectors.
XX Example 1; Col 151-153; 198pp; English.
XX This amino acid sequence was isolated from mouse hybridoma cell line KM-
XX 796, and encodes for the anti-GM2 heavy chain. Chimeric human antibodies
XX of the invention are useful in the treatment of cancer, especially that
XX which is of neural ectodermal origin. In contrast to prior art constructs
XX based on mouse monoclonal antibodies, the chimeric human antibodies do
XX not cause anti-mouse immunoglobulin production. The chimeric human
XX antibodies have a prolonged half-life and a reduced frequency of adverse
XX effects when compared to mouse monoclonal antibodies
XX Sequence 139 AA;
XX
XX Query Match 79.7%; Score 604; DB 2; Length 139;
XX Best Local Similarity 82.7%; Pred. No. 5.8e-43;
XX Matches 115; Conservative 6; Mismatches 18; Indels 0; Gaps 0;
XX
Qy 1 MGMSWIFLLSCTAGVHSEVQLQSGPELVKPGASVKISKASGYTFTDYNHWKQSH 60
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 MGMSWIFLLSCTAGVHSEVQLQSGPELVKPGASVKISKASGYTFTDYNHWKQSH 60
Qy 61 GKLEWIGIYYPNGVSDYNQPKSKATLIVDSSNTAYMELSLTSEDSAVYYCARWDF 120
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 GKLEWIGIYYPNGVSDYNQPKSKATLIVDSSNTAYMELSLTSEDSAVYYCATYGH 120
Qy 121 GSGYYFDYWGQGTTLTVSS 139
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 YGYMFAVWGQGTTLTVSA 139
XX
XX RESULT 15
XX AAE18372
XX ID AAE18372 standard; protein; 438 AA.
XX AC AAE18372;
XX 07-MAY-2002 (first entry)
XX Human penton base monoclonal antibody, DAV-1 heavy chain fragment.
XX Human; bifunctional molecule; monoclonal antibody; gene therapy; cancer;
XX vascular disorder; diabetic retinopathy; restenosis; ophthalmic disorder;
XX hyperproliferative disorder; hormonal disorder; DAV-1 heavy chain;
XX cytostatic; vasotropic; ophthalmological.
XX Homo sapiens.
XX OS
XX WO200204522-A2.
XX 17-JAN-2002.
XX
XX 09-JUL-2001; 2001WO-EP007878.
XX 10-JUL-2000; 2000US-00613017.
XX (NOVS ) NOVARTIS AG.
XX PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX PA (SCRI ) SCRIPPS RES INST.
XX PI Nemerow GR, Li E;
XX WPI; 2002-171707/22.
XX N-PSDB; AAE18372.
XX
XX New bifunctional molecules comprising an antibody or its antigen-binding
XX portion, and a targeting agent, useful for e.g. gene therapy, or for
XX promoting Adenoviral vector-mediated gene delivery to cells lacking av
XX integrins.
XX Claim 10; Page 96; 106pp; English.
XX
XX The present invention relates to a bifunctional molecule comprising an
XX antibody or its antigen-binding portion, and a targeting agent where the
XX antibody specifically binds to an antigen in a protein that binds to av
XX integrin, and the targeting agent specifically binds to a cell surface
XX protein that activates the phosphatidylinositol 3 (PI3K) signalling
XX pathway. The bifunctional molecules are useful for gene therapy, for
XX promoting Adenoviral (Ad) vector-mediated gene delivery to cells lacking
XX av integrins, for enhancing Ad binding and internalisation, and in gene
XX delivery of by fibreless adenovirus particles. The bifunctional molecules
XX permit targeting of viral and bacterial vectors to cells that express
XX targeted receptors. Diseases that can be targeted include cancers,
XX vascular disorders, diabetic retinopathies, restenosis, ophthalmic
XX disorders, hyperproliferative disorders, and hormonal disorders. The
XX present sequence is human penton base monoclonal antibody, DAV-1 heavy
XX chain fragment
XX
XX Sequence 438 AA;
XX
XX Query Match 79.2%; Score 600.5; DB 5; Length 438;
XX Best Local Similarity 82.0%; Pred. No. 3.9e-42;
XX Matches 114; Conservative 6; Mismatches 12; Indels 7; Gaps 1;
XX
Qy 1 MGMSWIFLLSCTAGVHSEVQLQSGPELVKPGASVKISKASGYTFTDYNHWKQSH 60
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 MGMSWIFLLSCTAGVHSEVQLQSGPELVKPGASVKISKASGYTFTDYNHWKQSH 60
Qy 61 GKLEWIGIYYPNGVSDYNQPKSKATLIVDSSNTAYMELSLTSEDSAVYYCARWDF 120
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 GKLEWIGIYYPNGVSDYNQPKSKATLIVDSSNTAYMELSLTSEDSAVYYCARG-- 118
Qy 121 GSGYYFDYWGQGTTLTVSS 139
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 119 -----IAYWGQGTTLTVSA 132
XX
XX RESULT 16
XX ABG76347
XX ID ABG76347 standard; protein; 438 AA.
XX AC ABG76347;
XX 10-MAY-2003 (first entry)
XX Portion of mouse DAV-1 heavy chain monoclonal antibody.
XX Mouse; bifunctional molecule; antigen-binding portion; alpha integrin;
XX cell surface protein; phosphatidylinositol-3-OH kinase; PI3K;
XX signalling pathway; targeted gene therapy; delivery vector;
XX adenoviral gene delivery particle; viral infection; cancer;
XX rheumatoid arthritis; cardiovascular disorder; diabetic retinopathy;
XX restenosis; ophthalmic disorder; hyperproliferative disorder;
XX hormonal disorder; virucide; antiinflammatory; antirheumatic;

```

KW antiarthritic; ophthalmological; DAV-1 heavy chain;
KW penton base monoclonal antibody.

XX Mus sp.

XX US2002164333-A1.

XX 07-NOV-2002.

XX 10-JUL-2001; 2001US-00903327.

XX 10-JUL-2000; 2000US-00613017.

XX 10-JUL-2000; 2000US-0325781P.

XX (SCRI) SCRIPPS RES INST.

XX Nemerow GR, Li E;

XX WPI; 2002-171707/22.

XX N-PSDB; ABX12746.

XX New bifunctional molecules comprising an antibody or its antigen-binding
XX portion, and a targeting agent, useful for e.g. gene therapy, or for
XX promoting Adenoviral vector-mediated gene delivery to cells lacking av
XX integrins.

XX Claim 10; Page 35-36; 49pp; English.

XX The present invention relates to a bifunctional molecule comprising an
XX antibody or its antigen-binding portion, and a targeting agent. The
XX antibody specifically binds to an antigen in a protein that binds to
XX alpha integrin, and the targeting agent specifically binds to a cell
XX surface protein that activates the phosphatidylinositol-3-OH kinase
XX (PI3K) signalling pathway. The bifunctional molecules are useful for
XX targeted gene therapy using targeting delivery vectors, such as
XX adenoviral gene delivery particles. The bifunctional molecules are useful
XX for treating viral infections, rheumatoid arthritis, cancers, ophthalmic
XX cardiovascular disorders, diabetic retinopathies, restenosis, ophthalmic
XX disorders, hyperproliferative disorders, and hormonal disorders. The
XX present sequence represents a portion of the mouse DAV-1 heavy chain that
XX is used for a fusion protein bifunctional antibody

XX Sequence 438 AA;

Query Match 79.2%; Score 600.5; DB 5; Length 438;

Best Local Similarity 82.0%; Pred. No. 3.9e-42;

Matches 114; Conservative 6; Mismatches 12; Indels 7; Gaps 1;

Qy 1 MGWSWIFLLSLGTAGVHSEVQLQSGPELVKPGASVKISKASGYTFTDYNHWKQSH 60

Db 1 MGWSWIFLLSLGTAGVHSEVQLQSGPELVKPGASVKISKASGYTFTDYNHWKQSH 60

Qy 61 GKILEWIGYIYPYNGVDYNGVSNQNFKSKATLIVDNSNTAYMELRSITSDSAVYTCARWDF 120

Db 61 GKILEWIGYIYPYNGVSNQNFKSKATLIVDNSNTAYMELRSITSDSAVYTCARWDF 120

Qy 121 GSGYFDYWGQGTTLTVSS 139

Db 119 -----IAYWGQGTTLTVSA 132

RESULT 17

AAE18370

ID AAE18370 standard; protein; 456 AA.

XX AAE18370;

XX 07-MAY-2002 (first entry)

XX Human penton base monoclonal antibody, DAV-1 heavy chain.

XX Human; bifunctional molecule; monoclonal antibody; gene therapy; cancer;
XX vascular disorder; diabetic retinopathy; restenosis; ophthalmic disorder;

KW hyperproliferative disorder; hormonal disorder; DAV-1 heavy chain;
KW cystostatic; vasotropic; ophthalmological.

XX Homo sapiens.

XX Key Location/Qualifiers
XX 230..242
XX Region /note= "Hinge region"

XX WO200204522-A2.

XX 17-JAN-2002.

XX 09-JUL-2001; 2001WO-EP007878.

XX 10-JUL-2000; 2000US-00613017.

XX (NOVS) NOVARTIS AG.

XX (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.

XX (SCRI) SCRIPPS RES INST.

XX Nemerow GR, Li E;

XX WPI; 2002-171707/22.

XX N-PSDB; AAD29308.

XX New bifunctional molecules comprising an antibody or its antigen-binding
XX portion, and a targeting agent, useful for e.g. gene therapy, or for
XX promoting Adenoviral vector-mediated gene delivery to cells lacking av
XX integrins.

XX Claim 10; Page 91-92; 106pp; English.

XX The present invention relates to a bifunctional molecule comprising an
XX antibody or its antigen-binding portion, and a targeting agent where the
XX antibody specifically binds to an antigen in a protein that binds to av
XX integrin, and the targeting agent specifically binds to a cell surface
XX protein that activates the phosphatidylinositol 3 (PI3K) signalling
XX pathway. The bifunctional molecules are useful for gene therapy, for
XX promoting Adenoviral (Ad) vector-mediated gene delivery to cells lacking
XX av integrins, for enhancing Ad binding and internalisation, and in gene
XX delivery of by fibreless adenovirus particles. The bifunctional molecules
XX permit targeting of viral and bacterial vectors to cells that express
XX targeted receptors. Diseases that can be targeted include cancers,
XX vascular disorders, diabetic retinopathies, restenosis, ophthalmic
XX disorders, hyperproliferative disorders, and hormonal disorders. The
XX present sequence is human penton base monoclonal antibody, DAV-1 heavy
XX chain

XX Sequence 456 AA;

Query Match 79.2%; Score 600.5; DB 5; Length 456;

Best Local Similarity 82.0%; Pred. No. 4.1e-42;

Matches 114; Conservative 6; Mismatches 12; Indels 7; Gaps 1;

Qy 1 MGWSWIFLLSLGTAGVHSEVQLQSGPELVKPGASVKISKASGYTFTDYNHWKQSH 60

Db 1 MGWSWIFLLSLGTAGVHSEVQLQSGPELVKPGASVKISKASGYTFTDYNHWKQSH 60

Qy 61 GKILEWIGYIYPYNGVDYNGVSNQNFKSKATLIVDNSNTAYMELRSITSDSAVYTCARWDF 120

Db 61 GKILEWIGYIYPYNGVSNQNFKSKATLIVDNSNTAYMELRSITSDSAVYTCARWDF 120

Qy 121 GSGYFDYWGQGTTLTVSS 139

Db 119 -----IAYWGQGTTLTVSA 132

RESULT 18

ABG76345

ID ABG76345 standard; protein; 456 AA.

XX ABG76345;

XX	RESULT 19
DT	AEB96754
XX	ID AEB96754 standard; protein; 456 AA.
XX	AC AEB96754;
XX	20-OCT-2005 (first entry)
XX	DAV-1 antibody heavy chain.
XX	Gene therapy; cancer; vascular disease; diabetic retinopathy; restenosis;
XX	ocular disease; hyperproliferation; hormone metabolism disorder;
XX	cytostatic; vasotropic; antidiabetic; ophthalmological; metabolic-gen.;
XX	DAV-1; heavy chain; antibody.
XX	Synthetic.
XX	WO2005075506-A1.
XX	18-AUG-2005.
XX	29-DEC-2004; 2004WO-IB004324.
XX	09-JAN-2004; 2004US-0535199P.
XX	(SCRI) SCRIPPS RES INST.
XX	Nemerow GR, Li E;
XX	WPI; 2005-555928/56.
XX	New modified adenovirus fiber protein comprising a fiber shaft and a
XX	modified knob, useful for treating cancer, vascular disorders, diabetic
XX	retinopathies, restenosis and vascular, ophthalmic, hyperproliferative or
XX	hormonal disorders.
XX	Example 1; SEQ ID NO 28; 250pp; English.
XX	The invention relates to a modified adenovirus fiber protein comprising a
XX	fiber shaft that contains a sufficient number of shaft repeats to permit
XX	trimerization in the absence of a fiber knob or in the absence of an
XX	extrinsic trimerization domain, and optionally a modified knob, where, if
XX	the knob is included, it is modified to remove or disable the
XX	trimerization domain of the knob. The invention also relates to a
XX	modified adenovirus fiber protein comprising a modified knob, where the
XX	modification of the knob removes or disables a trimerization domain of
XX	the knob, and the modified fiber trimerizes a nucleic acid molecule
XX	comprising a sequence of nucleotides that encodes the modified adenovirus
XX	fiber protein, a cell comprising the nucleic acid, an adenovirus particle
XX	comprising the modified fiber, a composition formulated for
XX	administration to a subject, comprising the adenovirus particle,
XX	detecting an adenoviral vector particle comprising producing the
XX	adenoviral particle, where the binding of the particle to a native
XX	receptor is reduced or eliminated as compared to binding of a particle
XX	containing the unmodified fiber, introducing the adenoviral particle into
XX	cells, introducing the cells into a subject and administering the
XX	composition to the subject. The modified adenovirus fiber protein is
XX	useful for treating cancer, vascular disease, diabetic retinopathy,
XX	restenosis, ocular diseases, hyperproliferative disorders and hormonal
XX	disorders. This sequence represents a DAV-1 antibody heavy chain used in
XX	the scope of the invention.
XX	Sequence 456 AA;
XX	Query Match 79.2%; Score 600.5; DB 9; Length 456;
XX	Best Local Similarity 82.0%; Pred. No. 4.1e-42;
XX	Matches 114; Conservative 6; Mismatches 12; Indels 7; Gaps 1;
QY	1 MGWSWIFLLSAGTGVHSEVLQSGPELVKPGASVKISKASYTTDYNHWKQSH 60
DB	1 MGWSWIFLLSAGTGVHSEVLQSGPELVKPGASVKISKASYTTDYNHWKQSH 60
QY	61 GKILEWIGIYPNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSDSAVYYCARWDF 120
DB	61 GKISLEWIGIYPNGGTYGNQFKSKATLTDDSSNTAYMELRSLTSDSAVYYCARG-- 118
QY	121 GSGYFPDYWGQGTLTVSS 139
DB	119 -----JAYWGQGLTVTSA 132

Db	61	GKSLEWIGYIYPKGGTGYNOKFKSKATLTDTSSNTAYMELRSLTSDASAVYCYARG--	118
Qy	121	GSYYFDYWGQGTTLTVSS	139
Db	119	-----IAYWGQGTTLTVSA	132
RESULT 20			
AAE18379			
ID	AAE18379	standard; protein; 493 AA.	
XX	AAE18379;		
DT	07-MAY-2002	(first entry)	
XX	Human N-terminal DAV-1 heavy chain-mature EGF fusion protein.		
XX	Human; bifunctional molecule; monoclonal antibody; gene therapy; cancer;		
KW	vascular disorder; diabetic retinopathy; restenosis; ophthalmic disorder;		
KW	hyperproliferative disorder; hormonal disorder; DAV-1 heavy chain;		
KW	cytostatic; vasotropic; ophthalmological; epidermal growth factor; EGF;		
XX	fusion protein.		
XX	Homo sapiens.		
OS	Synthetic.		
OS	Chimeric.		
XX			
Key	Location/Qualifiers		
FT	Region	1..439	
FT	/note= "N-terminal portion of DAV-1 heavy chain"		
FT	Region	441..493	
FT	/note= "Human mature EGF"		
XX			
PN	WO200204522-A2.		
XX			
PD	17-JAN-2002.		
XX			
XX	09-JUL-2001; 2001WO-EP007878.		
PF			
XX			
PR	10-JUL-2000; 2000US-00613017.		
XX			
PA	(NOVS) NOVARTIS AG.		
PA	(NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.		
PA	(SCRI) SCRIPPS RES INST.		
XX			
PI	Nemerow GR, Li E;		
XX			
DR	WPI; 2002-171707/22.		
XX			
XX	New bifunctional molecules comprising an antibody or its antigen-binding		
PT	portion, and a targeting agent, useful for e.g. gene therapy, or for		
PT	promoting Adenoviral vector-mediated gene delivery to cells lacking av		
PT	integrins.		
XX			
PS	Claim 15; Page 101-102; 106pp; English.		
XX			
CC	The present invention relates to a bifunctional molecule comprising an		
CC	antibody or its antigen-binding portion, and a targeting agent where the		
CC	antibody specifically binds to an antigen in a protein that binds to av		
CC	integrin, and the targeting agent specifically binds to a cell surface		
CC	protein that activates the phosphatidylinositol 3 (PI3K) signalling		
CC	pathway. The bifunctional molecules are useful for gene therapy, for		
CC	promoting Adenoviral (Ad) vector-mediated gene delivery to cells lacking		
CC	av integrin, for enhancing Ad binding and internalisation, and in gene		
CC	delivery of by fibrolees adenovirus particles. The bifunctional molecules		
CC	permit targeting of viral and bacterial vectors to cells that express		
CC	targeted receptors. Diseases that can be targeted include cancers,		
CC	vascular disorders, diabetic retinopathies, restenosis, ophthalmic		
CC	disorders, hyperproliferative disorders, and hormonal disorders. The		
CC	present sequence is human N-terminal DAV-1 heavy chain-mature epidermal		
CC	growth factor (EGF) fusion protein which is used in the invention		
XX			

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 20, 2006, 07:28:38 ; Search time 23.7968 Seconds
(without alignments)
3765.293 Million cell updates/sec

Title: US-10-687-035-33

Perfect score: 656

Sequence: 1 MDPQVQIFSLISASVMS.....YCOQWSSNPFTGSGTKLEI 127

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	574	87.5	235	2	Q5XFP8_MOUSE
2	533	81.2	235	2	O58EV6_MOUSE
3	526	80.2	134	2	Q8VDD0_MOUSE
4	511.5	78.0	131	2	Q811C3_MOUSE
5	473	72.1	237	2	Q569Y8_MOUSE
6	452	68.9	129	1	KV4A_MOUSE
7	434	66.2	112	2	Q8KIF3_MOUSE
8	429	65.4	107	1	KV6F_MOUSE
9	428	65.2	112	2	Q8KIF2_MOUSE
10	424	64.6	107	1	KV6I_MOUSE
11	423	64.5	107	1	KV6H_MOUSE
12	423	64.5	107	1	KV6J_MOUSE
13	422	64.3	112	2	Q8KIF0_MOUSE
14	421	64.2	106	2	Q9U410_MOUSE
15	420	64.0	107	1	KV6G_MOUSE
16	419.5	63.9	97	2	Q9JL76_MOUSE
17	409	62.3	108	1	KV6K_MOUSE
18	408	62.2	114	2	Q8KIF1_MOUSE
19	395	60.2	107	1	KV6B_MOUSE
20	392	59.8	107	1	KV6A_MOUSE
21	391	59.6	107	1	KV6D_MOUSE
22	390	59.5	107	1	KV6C_MOUSE
23	375	57.2	107	1	KV6E_MOUSE
24	350	53.4	109	2	Q9UL78_HUMAN
25	349	53.2	129	1	KV3M_HUMAN
26	348	53.0	129	1	KV3L_HUMAN
27	345.5	52.7	240	2	Q52164_MOUSE
28	341.5	52.1	101	2	Q9JL78_MOUSE
29	341.5	52.1	236	2	Q7Z3Y4_HUMAN
30	338.5	51.6	237	2	Q7S236_XENLA
31	338	51.5	109	1	KV3B_HUMAN

32	335.5	51.1	236	2	Q6PIH7_HUMAN
33	334	50.9	108	1	KV3A_HUMAN
34	334	50.9	235	2	Q6GMV9_HUMAN
35	333.5	50.8	236	2	Q6PIL8_HUMAN
36	333	50.8	129	1	KV3H_HUMAN
37	332.5	50.7	111	1	KV3M_MOUSE
38	332	50.6	235	2	Q6RPF2_HUMAN
39	331.5	50.5	108	1	KV1V_HUMAN
40	331.5	50.5	109	2	Q9UL70_HUMAN
41	331	50.5	109	1	KV3D_HUMAN
42	330	50.5	109	2	Q9UL86_HUMAN
43	330	50.3	109	1	KV3G_HUMAN
44	329	50.2	109	1	KV3E_HUMAN
45	328.5	50.1	134	1	KV4C_HUMAN
46	327.5	49.9	131	1	KV3I_MOUSE
47	327	49.8	109	1	KV3F_HUMAN
48	326.5	49.8	128	1	KV3K_HUMAN
49	325.5	49.6	108	2	Q9UL79_HUMAN
50	325.5	49.6	111	1	KV3L_MOUSE
51	325.5	49.6	111	1	KV3O_MOUSE
52	325.5	49.6	236	2	Q6GMX9_HUMAN
53	325.5	49.6	236	2	Q6GMX8_HUMAN
54	325.5	49.6	244	2	Q65ZC8_HUMAN
55	325.5	49.6	255	2	Q6XB05_MOUSE
56	324.5	49.5	111	1	KV3Q_MOUSE
57	323.5	49.3	239	2	Q5HZC6_XENLA
58	322.5	49.2	243	2	Q6NTU5_XENLA
59	321.5	49.0	111	1	KV3N_MOUSE
60	321.5	49.0	238	2	O58EU4_MOUSE
61	320.5	48.9	108	1	KV1O_HUMAN
62	320.5	48.9	109	2	Q920E6_MOUSE
63	320.5	48.9	111	1	KV3J_MOUSE
64	320.5	48.9	236	2	Q6P5S8_HUMAN
65	320	48.8	133	1	KV4B_HUMAN
66	319.5	48.7	111	1	KV3H_MOUSE
67	318.5	48.6	108	2	Q9UL83_HUMAN
68	318.5	48.6	114	1	KV4A_HUMAN
69	318.5	48.6	236	2	Q7Z473_HUMAN
70	318.5	48.6	236	2	Q6PIT5_HUMAN
71	318.5	48.6	240	2	Q65ZC9_HUMAN
72	317.5	48.4	108	1	KV1R_HUMAN
73	317.5	48.4	129	1	KV1N_HUMAN
74	316.5	48.2	111	1	KV3K_MOUSE
75	316.5	48.2	132	1	KV3F_MOUSE
76	315.5	48.1	108	1	KV1L_HUMAN
77	315.5	48.1	108	1	KV1Y_HUMAN
78	315.5	48.1	136	1	KV5E_MOUSE
79	315.5	48.1	149	1	KV5A_MOUSE
80	315	48.0	110	1	KV3P_MOUSE
81	314.5	47.9	108	2	Q9UL77_HUMAN
82	314.5	47.9	111	2	Q920E9_MOUSE
83	314.5	47.9	189	2	O56917_HUMAN
84	313	47.7	109	2	Q9UL85_HUMAN
85	312.5	47.6	111	2	Q811U6_MOUSE
86	312	47.6	107	2	Q5FE6A_HUMAN
87	311.5	47.5	234	2	Q5FE6E_HUMAN
88	310.5	47.3	111	1	KV3S_MOUSE
89	309.5	47.2	108	1	KV1E_HUMAN
90	309.5	47.2	108	1	KV1H_HUMAN
91	309.5	47.2	108	1	KV1M_HUMAN
92	309.5	47.2	236	2	Q502W4_HUMAN
93	308.5	47.0	108	1	KV5D_MOUSE
94	308.5	47.0	111	1	KV3R_MOUSE
95	307.5	46.9	236	2	Q7TS98_MOUSE
96	307.5	46.9	240	2	Q6PIH6_HUMAN
97	307	46.8	107	2	Q9UL81_HUMAN
98	306.5	46.7	111	1	KV3U_MOUSE
99	306.5	46.7	127	2	Q925S9_MOUSE
100	306.5	46.7	130	1	KV5G_MOUSE

ALIGNMENTS

```

RESULT 1
Q5XFY8_MOUSE
ID Q5XFY8_MOUSE PRELIMINARY; PRT; 235 AA.
AC Q5XFY8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
NUCLEOTIDE SEQUENCE.
RP STRAIN=FVB/N; TISSUE=Colon;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Datchenko L., Moore T., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Rodriguez S., Sanchez A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Blakesley R.W., Touchman J.W., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Green E.D., Dickinson M.C.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
NUCLEOTIDE SEQUENCE.
RP STRAIN=FVB/N; TISSUE=Colon;
RC NIH MGC Project;
RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC084683; AAH4683.1; -; mRNA.
DR SMR; Q5XFY8; 23-235.
DR GO; GO:0003823; F:antigen binding; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25835 MW; 828E9ED277FDC667 CRC64;

Query Match 87.5%; Score 574; DB 2; Length 235;
Best Local Similarity 89.0%; Pred. No. 4.4e-47;
Matches 113; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

Qy 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTWTCRASSSVIYMCWNOOK 60
Db 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILSGFFGKEKVTWTCRASSSVYMHVYQOK 60
Qy 61 PGSSPKPWYGTSTLASGVPTRFSGSGTSGTYSYLTISRVEADAATYCCQWSSNPFTFG 120
Db 61 PGSSPKPWYATYKSLASGVPARFSGSGTSGTYSYLTISRVEADAATYCCQWSSNPFTFG 120
Qy 121 SGTKEI 127

```

```

Db 121 AGTRLEI 127
:::|::|:
RESULT 2
Q58EV6_MOUSE
ID Q58EV6_MOUSE PRELIMINARY; PRT; 235 AA.
AC Q58EV6;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Igk-C protein.
GN Name=Igk-C;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
NUCLEOTIDE SEQUENCE.
RP STRAIN=FVB/N; TISSUE=Colon;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Datchenko L., Moore T., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Blakesley R.W., Touchman J.W., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Green E.D., Dickinson M.C.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
NUCLEOTIDE SEQUENCE.
RP STRAIN=FVB/N; TISSUE=Colon;
RC NIH MGC Project;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC091738; AAH91738.1; -; mRNA.
DR SMR; Q58EV6; 23-235.
DR GO; GO:0003823; F:antigen binding; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 235 AA; 25719 MW; BE4EABDD2578252 CRC64;

Query Match 81.2%; Score 533; DB 2; Length 235;
Best Local Similarity 81.9%; Pred. No. 3.9e-43;
Matches 104; Conservative 9; Mismatches 14; Indels 0; Gaps 0;

Qy 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTWTCRASSSVIYMCWNOOK 60
Db 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILSGFFGKEKVTWTCRASSSVYMHVYQOK 60
Qy 61 PGSSPKPWYGTSTLASGVPTRFSGSGTSGTYSYLTISRVEADAATYCCQWSSNPFTFG 120

```

```

Db 61 SGTSPKRWIYDTSKLASGVPARFSGSGSGTSYSLTSSMEAEADAATYYCQOWSNPLTFG 120
Qy 121 SGTKLEI 127
   :|||||:
Db 121 AGTKLDL 127

RESULT 3
Q8VDDO MOUSE
ID Q8VDDO MOUSE PRELIMINARY; PRT; 134 AA.
AC Q8VDDO;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-MOG 212 variable light chain (Fragment).
GN Name=Gm1502; Synonyms=anti-MOG kappa;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=MRL/lpr; TISSUE=Spleen;
RX MEDLINE=93156722; PubMed=8429833; DOI=10.1016/0161-5890(93)90089-T;
RA Takahashi S., Itoh J., Nose M., Ono M., Yamamoto T., Kyogoku M.;
RT "Cloning and cDNA sequence analysis of nephritogenic monoclonal
antibodies derived from an MRL/lpr lupus mouse.";
RL Mol. Immunol. 30:177-182(1993)
DR EMBL; D14625; BAA03482.1; -; mRNA.
DR HSP; P01679; 2PBJ.
DR SMR; Q811C3; 23-131.
DR Ensembl; ENSMUSG00000058987; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1_v.
DR PROSITE; PS50835; IG_LIKE; 1.
FT SIGNAL. 1 22 Potential.
FT CHAIN 23 >131 immunoglobulin gamma-3 kappa chain.
FT NON_TER 131 131
SQ SEQUENCE 131 AA; 14083 MW; 5E83656954666B9E CRC64;

Query Match 78.0%; Score 511.5; DB 2; Length 131;
Best Local Similarity 81.5%; Pred. No. 2.4e-41;
Matches 106; Conservative 7; Mismatches 14; Indels 3; Gaps 2;

Qy 1 MDPQVQIFSPFLISASVIMSRGQIVLSQSPAILFASPGETVWTTCRASSV--IYMCWQ 58
   :|||||:
Db 1 MDSQVQIFSPFLISALVIMSRGQIVLTQSPAIMASPGKVTWTCRASSVRSYLHWYQ 60

Qy 59 QKPGSSPKWIYGTSTLASGVPTRFSGSGSGTSYSLTSSVEAEADAATYYCQOWSNP-F 117
   :|||||:
Db 61 QKPGSSPKWIYGTSTLASGVPTRFSGSGSGTSYSLTSSVEAEADAATYYCQOWSNP 120

Qy 118 TFGSGTKLEI 127
   :|||||:
Db 121 TFGAGTKLEI 130

RESULT 5
Q569Y8 MOUSE
ID Q569Y8 MOUSE PRELIMINARY; PRT; 237 AA.
AC Q569Y8;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Igk-C protein.
GN Name=Igk-C;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udgin T.B., Toshiyuki S., Carninci P., Prange C.,

Qy 121 SGTKLEI 127
   :|||||:
Db 121 GGTKLEI 127

RESULT 4
Q811C3 MOUSE
ID Q811C3 MOUSE PRELIMINARY; PRT; 131 AA.
AC Q811C3;

```

```

DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Immunoglobulin gamma-3 kappa chain precursor (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=MRL/lpr; TISSUE=Spleen;
RX MEDLINE=93156722; PubMed=8429833; DOI=10.1016/0161-5890(93)90089-T;
RA Takahashi S., Itoh J., Nose M., Ono M., Yamamoto T., Kyogoku M.;
RT "Cloning and cDNA sequence analysis of nephritogenic monoclonal
antibodies derived from an MRL/lpr lupus mouse.";
RL Mol. Immunol. 30:177-182(1993)
DR EMBL; D14625; BAA03482.1; -; mRNA.
DR HSP; P01679; 2PBJ.
DR SMR; Q811C3; 23-131.
DR Ensembl; ENSMUSG00000058987; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1_v.
DR PROSITE; PS50835; IG_LIKE; 1.
FT SIGNAL. 1 22 Potential.
FT CHAIN 23 >131 immunoglobulin gamma-3 kappa chain.
FT NON_TER 131 131
SQ SEQUENCE 131 AA; 14083 MW; 5E83656954666B9E CRC64;

Query Match 78.0%; Score 511.5; DB 2; Length 131;
Best Local Similarity 81.5%; Pred. No. 2.4e-41;
Matches 106; Conservative 7; Mismatches 14; Indels 3; Gaps 2;

Qy 1 MDPQVQIFSPFLISASVIMSRGQIVLSQSPAILFASPGETVWTTCRASSV--IYMCWQ 58
   :|||||:
Db 1 MDSQVQIFSPFLISALVIMSRGQIVLTQSPAIMASPGKVTWTCRASSVRSYLHWYQ 60

Qy 59 QKPGSSPKWIYGTSTLASGVPTRFSGSGSGTSYSLTSSVEAEADAATYYCQOWSNP-F 117
   :|||||:
Db 61 QKPGSSPKWIYGTSTLASGVPTRFSGSGSGTSYSLTSSVEAEADAATYYCQOWSNP 120

Qy 118 TFGSGTKLEI 127
   :|||||:
Db 121 TFGAGTKLEI 130

RESULT 5
Q569Y8 MOUSE
ID Q569Y8 MOUSE PRELIMINARY; PRT; 237 AA.
AC Q569Y8;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Igk-C protein.
GN Name=Igk-C;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udgin T.B., Toshiyuki S., Carninci P., Prange C.,

```


(3)
 RN NUCLEOTIDE SEQUENCE.
 RX MEDLINE=92381444; PubMed=1512540; DOI=10.1084/jem.176.3.761;
 RA Tillman D.M., Jou N.T., Hill R.J., Marion T.N.;
 RT "Both IgM and IgG anti-DNA antibodies are the products of clonally
 selective B cell stimulation in (NZB x NZW)F1 mice.";
 RL J. Exp. Med. 176:761-779(1992).
 DR EMBL; AF516282; AAM64200.1; -, Genomic_DNA.
 DR PIR; A33933; A33933.
 DR PIR; PH1085; PH1085.
 DR HSSP; P01837; 25C8.
 DR SMR; Q8K1F2; 2-112.
 DR Ensembl; ENSMUSG0000063156; Mus musculus.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 FT NON_TER 112 112
 FT NON_TER 112 112
 SQ SEQUENCE 112 AA; 12017 MW; 22DD75B5414CDB18 CRC64;
 Query Match 66.2%; Score 434; DB 2; Length 112;
 Best Local Similarity 80.8%; Pred. No. 6e-34;
 Matches 84; Conservative 7; Mismatches 13; Indels 0; Gaps 0;
 QY 24 IVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQKPGSSPKPWYGTSTLASGVPTFR 83
 Db 2 IVLTQSPAIMSASPGKVTITCSASSSVYMYWYQKPGSSPKPWYGTSTLASGVPTFR 61
 QY 84 SGSGSGTSYSLTISRVEADAATYYCQWSSNPFTFGSGTKLEI 127
 Db 62 SGSGSGTSYSLTISRMEADAATYYCQVHSYPYTFGGTKLEI 105
 RESULT 8
 KV6F MOUSE STANDARD; PRT; 107 AA.
 ID KV6F MOUSE
 AC P04940;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Ig kappa chain V-J region NQ2-17.4.1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=83271467; PubMed=6877353;
 RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
 RT "mRNA sequences define an unusually restricted IgG response to 2-
 phenyloxazolone and its early diversification.";
 RL Nature 304:320-324(1983).
 CC -!- FUNCTION: Anti-2-phenyl oxazolone (PHOX) Antibody.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC EMBL; K00735; AAA38680.1; -, mRNA.
 DR HSSP; P01679; 2FBJ.
 DR SMR; P04940; 1-107.
 DR Ensembl; ENSMUSG0000062047; Mus musculus.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Hybridoma; Immunoglobulin domain; Immunoglobulin V region.
 FT REGION 1 23
 FT REGION 24 33
 Complementarity-determining-1.

FT REGION 34 48 Framework-2.
 FT REGION 49 55 Complementarity-determining-2.
 FT REGION 56 87 Framework-3.
 FT REGION 88 96 Complementarity-determining-3.
 FT REGION 97 106 Framework-4.
 FT DISULFID 23 87 By similarity.
 FT NON_TER 107 107
 SQ SEQUENCE 107 AA; 11561 MW; 6F694284CEFA68E6 CRC64;
 Query Match 65.4%; Score 429; DB 1; Length 107;
 Best Local Similarity 78.1%; Pred. No. 1.7e-33;
 Matches 82; Conservative 9; Mismatches 14; Indels 0; Gaps 0;
 QY 23 QIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQKPGSSPKPWYGTSTLASGVPTFR 82
 Db 1 QIVLTQSPAIMSASPGKVTITCSASSSVYMYWYQKPGSSPKPWYGTSTLASGVPTFR 60
 QY 83 FSGSGSGTSYSLTISRVEADAATYYCQWSSNPFTFGSGTKLEI 127
 Db 61 FSGSGSGTSYSLTISRMEADAATYYCQWSSNPFTFGAGTKLEI 105
 RESULT 9
 Q8K1F2 MOUSE PRELIMINARY; PRT; 112 AA.
 ID Q8K1F2 MOUSE PRELIMINARY;
 AC Q8K1F2;
 DT 01-OCT-2002 (T-EMBLrel. 22, Created)
 DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
 DE Anti-Vifase light chain variable region (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=2499887;
 RA Baccala R., Quang T.V., Gilbert M., Ternynck T., Avrameas S.;
 RT "Two murine natural polypeptide autoantibodies are encoded by
 RT nonmutated germ-line genes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628(1989).
 DR EMBL; AF516283; AAM64201.1; -, Genomic_DNA.
 DR PIR; H33932; H33932.
 DR HSSP; P01837; 25C8.
 DR SMR; Q8K1F2; 2-112.
 DR Ensembl; ENSMUSG0000064150; Mus musculus.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 FT NON_TER 112 112
 FT NON_TER 112 112
 SQ SEQUENCE 112 AA; 11953 MW; 4716B87FADBS43ED CRC64;
 Query Match 65.2%; Score 428; DB 2; Length 112;
 Best Local Similarity 80.8%; Pred. No. 2.3e-33;
 Matches 84; Conservative 7; Mismatches 13; Indels 0; Gaps 0;
 QY 24 IVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQKPGSSPKPWYGTSTLASGVPTFR 83
 Db 2 IVLTQSPAIMSASPGKVTITCSASSSVYMYWYQKPGSSPKPWYGTSTLASGVPTFR 61
 QY 84 SGSGSGTSYSLTISRVEADAATYYCQWSSNPFTFGSGTKLEI 127
 Db 62 SGSGSGTSYSLTISRMEADAATYYCQWSSNPFTFGAGTKLEI 105

Mon Mar 20 08:49:45 2006

```

NCBI_TaxID=10090;
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted Igg response to 2-
phenyloxazolone and its early diversification.";
RL Nature 304:320-324(1983).
CC -1- FUNCTION: Anti-2-phenyl oxazolone (PHOX) Antibody.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC
CC EMBL; K00739; AAA38684.1; -; mRNA.
DR HSSP; P01679; 2FBJ.
DR SMR; P04942; 1-107.
DR Ensembl; ENSMUSG00000062047; Mus musculus.
DR InterPro; IPR007110; Igg-like.
DR InterPro; IPR003596; Igg_v.
DR SMART; SM00406; Igg; 1.
DR PROSITE; PS0835; IGG LIKE; 1.
KW Hybridoma; Immunoglobulin domain; Immunoglobulin V region.
FT REGION 1 23 Framework-1.
FT REGION 24 33 Framework-2.
FT REGION 34 48 Framework-3.
FT REGION 49 55 Complementarity-determining-1.
FT REGION 56 87 Complementarity-determining-2.
FT REGION 88 96 Complementarity-determining-3.
FT REGION 97 106 Complementarity-determining-4.
FT DISULFID 23 87 By similarity.
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11605 MW; CA6C4284ECFCB550 CRC64;

Query Match 64.6%; Score 424; DB 1; Length 107;
Best Local Similarity 77.1%; Pred. No. 5.2e-33;
Matches 81; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

Oy 23 QIVLSQSPAILFASPGTWTTCRASSSVIYMCWQKPGSPKPIYGTSTLASGVPT 82
Db 1 QIVLTQSPALMSASPGQKVTWTCSSASSVSYMHVYQKSGTSPKRWIYDTSKLDSGVP 60
Oy 83 FSGSGSGTSYSLTISRVEAEDAATYCCQWSSNPFYFGSGTKLEI 127
Db 61 FSGSGSATSYSLTITSMQAEADAATYCCQWSSNPLTFGAGTKLEL 105

RESULT 12
KV6J MOUSE
ID KV6J MOUSE STANDARD; PRT; 107 AA.
AC P04944;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Igg kappa chain V-VI region NQ5-78.2.6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted Igg response to 2-
phenyloxazolone and its early diversification.";
RL Nature 304:320-324(1983).
CC -1- FUNCTION: Anti-2-phenyl oxazolone (PHOX) Antibody.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC
CC EMBL; K00739; AAA38684.1; -; mRNA.
DR HSSP; P01679; 2FBJ.
DR SMR; P04942; 1-107.
DR Ensembl; ENSMUSG00000062047; Mus musculus.
DR InterPro; IPR007110; Igg-like.
DR InterPro; IPR003596; Igg_v.
DR SMART; SM00406; Igg; 1.
DR PROSITE; PS0835; IGG LIKE; 1.
KW Hybridoma; Immunoglobulin domain; Immunoglobulin V region.
FT REGION 1 23 Framework-1.
FT REGION 24 33 Framework-2.
FT REGION 34 48 Framework-3.
FT REGION 49 55 Complementarity-determining-1.
FT REGION 56 87 Complementarity-determining-2.
FT REGION 88 96 Complementarity-determining-3.
FT REGION 97 106 Complementarity-determining-4.
FT DISULFID 23 87 By similarity.
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11573 MW; 6F694824ECF0C8E6 CRC64;

Query Match 64.6%; Score 424; DB 1; Length 107;
Best Local Similarity 77.1%; Pred. No. 5.2e-33;
Matches 81; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

Oy 23 QIVLSQSPAILFASPGTWTTCRASSSVIYMCWQKPGSPKPIYGTSTLASGVPT 82
Db 1 QIVLTQSPALMSASPGQKVTWTCSSASSVSYMHVYQKSGTSPKRWIYDTSKLDSGVP 60
Oy 83 FSGSGSGTSYSLTISRVEAEDAATYCCQWSSNPFYFGSGTKLEI 127
Db 61 FSGSGSATSYSLTITSMQAEADAATYCCQWSSNPLTFGAGTKLEL 105

RESULT 11
KV6H MOUSE
ID KV6H MOUSE STANDARD; PRT; 107 AA.
AC P04942;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Igg kappa chain V-VI region NQ5-61.1.2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.

```


OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted IGG response to 2-
phenylloxazolone and its early diversification.";
RL Nature 304:320-324(1983).
CC -1- FUNCTION: Anti-2-phenyl oxazolone (PHOX) Antibody.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; K00737; AAA38682.1; -; mRNA.
DR HSSP; Q91W12; IAY1.
DR SMR; P04941; 1-103.
DR Ensembl; ENSMUSG00000062047; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IGV; 1.
DR HYDRIOMA; Immunoglobulin domain; Immunoglobulin V region.
KW REGION 1 23
FT REGION 24 33
FT REGION 34 48
FT REGION 49 55
FT REGION 56 87
FT REGION 88 96
FT REGION 97 106
FT DISULFID 23 87
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11557 MW; 72488DA9F354934 CRC64;
Query Match 64.0%; Score 420; DB 1; Length 107;
Best Local Similarity 76.2%; Pred. No. 1.3e-32;
Matches 80; Conservative 10; Mismatches 15; Indels 0; Gaps 0;
Qy 23 QIVLSQSPALFASPGETVTTCRASSSVIYMCNQKPGSSPKPWIYGTSLASGVPT 82
Db 1 QILLTQSPAINMSFGQKVTTCRASSSVSYMHYQKQSGTSPKRWIYDTSKLASGV 60
Qy 83 FSGSGSGTSLTISRVEAEADATYCCQWSSNPFPGSGTKLEI 127
Db 61 FSGSGSATSLTITSMQAEADATYCCQWSSNPLTFGAGTKLXL 105
RESULT 16
Q9JL76_MOUSE PRELIMINARY; PRT; 97 AA.
ID Q9JL76_MOUSE STANDARD; PRT; 108 AA.
AC P04945;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anti-myosin immunoglobulin light chain variable region
(Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=DRB/2;
RX MEDLINE=20448942; PubMed=10992488;
RX DOI=10.1128/TAI.68.10.5803-5808.2000;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of

RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
with cardiac myosin.";
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL; AF206030; AAF69328.1; -; mRNA.
DR HSSP; P01679; 2PBJ.
DR SMR; Q9JL76; 1-97.
DR Ensembl; ENSMUSG00000057015; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IGV; 1.
DR NON_TER 1 1
FT NON_TER 97 97
SQ SEQUENCE 97 AA; 10542 MW; C9EE1FFELF49DA1C CRC64;
Query Match 63.9%; Score 419.5; DB 2; Length 97;
Best Local Similarity 86.5%; Pred. No. 1.3e-32;
Matches 83; Conservative 1; Mismatches 11; Indels 1; Gaps 1;
Qy 33 LFASPGETVTTCRASSSVIYMCNQKPGSSPKPWIYGTSLASGVPT 92
Db 1 LSASPGKVTTCRASSSVSYMHYQKQSGTSPKRWIYATSNLASGVPT 60
Qy 93 SLTISRVEAEADATYCCQWSSN-PFTFGSGTKLEI 127
Db 61 SLTISRVEAEADATYCCQWSSKVMYTFGGTKLEI 96
RESULT 17
KV6K_MOUSE STANDARD; PRT; 108 AA.
ID KV6K_MOUSE STANDARD; PRT; 108 AA.
AC P04945;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-VI region NQ2-6.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted IGG response to 2-
phenylloxazolone and its early diversification.";
RL Nature 304:320-324(1983).
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; K00746; AAA38691.1; -; mRNA.
DR HSSP; Q91W12; IAY1.
DR SMR; P04945; 1-108.
DR Ensembl; ENSMUSG00000062686; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IGV; 1.
DR HYDRIOMA; Immunoglobulin domain; Immunoglobulin V region.
KW REGION 1 23
FT REGION 24 33
FT REGION 34 48
FT REGION 49 55
FT REGION 56 87
FT REGION 88 98
FT REGION 99 108
FT DISULFID 23 87
FT NON_TER 108 108

SQ SEQUENCE 108 AA; 11713 MW; DABF235CD9680AC6 CRC64;
 Query Match 62.3%; Score 409; DB 1; Length 108;
 Best Local Similarity 75.7%; Pred. No. 1.5e-31;
 Matches 81; Conservative 10; Mismatches 14; Indels 2; Gaps 1;
 QY 23 QIVLSQSPAILFASPGETVTMTTCRASSSVIYMCWNQKPGSSPKPWIYGTSTLASGVPT 82
 D 1 QILLTQSPAIMASPGQKVTMTCSASSSVSYMYWYQKPGSPRLLIYDTSNLASGVPT 60
 QY 83 FSGSGSGTSYSLTISRVEADAATYCCQWSSNP--FTFGSGTKLEI 127
 D 61 FSGSGGSATSYSLTITRQAEADAATYCCQWSSYPPMLTFGAGTKLEI 107
 RESULT 18
 QKIF1_MOUSE
 ID QKIF1_MOUSE PRELIMINARY; PRT; 114 AA.
 AC QKIF1;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Anti-VIPase light chain variable region (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=BALB/c; TISSUE=Hyperimmunized spleen;
 RA Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed2499887;
 RA Baccala R., Quang T.V., Gilbert M., Ternynck T., Avrameas S.;
 RT "Two murine natural polyreactive autoantibodies are encoded by
 RT nonmutated germ-line genes";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628 (1989).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=92381444; PubMed=1512540; DOI=10.1084/jem.176.3.761;
 RA Tillman D.M., Jou N.T., Hill R.J., Marion T.N.;
 RT "Both IgM and IgG anti-DNA antibodies are the products of clonally
 RT selective B cell stimulation in (NZB x NZW)F1 mice";
 RL J. Exp. Med. 176:761-779 (1992).
 DR EMBL; AF516284; AAM64202.1; -; Genomic_DNA.
 DR PIR; A33933; A33933.
 DR PIR; PH1058; PH1058.
 DR HSSP; P01837; 25C8.
 DR SMR; Q8KIF1; 2-114.
 DR Ensembl; ENSMUSG0000059896; Mus musculus.
 DR InterPro; IPR007110; Ig-like.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 FT NON_TER 1 114
 FT NON_TER 114 114
 SQ SEQUENCE 114 AA; 12163 MW; 8BD9833DBF3EEFD1 CRC64;
 Query Match 62.2%; Score 408; DB 2; Length 114;
 Best Local Similarity 78.3%; Pred. No. 1.9e-31;
 Matches 83; Conservative 6; Mismatches 15; Indels 2; Gaps 1;
 QY 24 IVLSQSPAILFASPGETVTMTTCRASSSV--IYMCWNQKPGSSPKPWIYGTSTLASGVPT 81
 D 2 IVLTQSPAIMASPGKVTMTTCRASSSVSSYLLHWYQKPGSPKLIYSTSNLASGVA 61
 QY 82 FSGSGSGTSYSLTISRVEADAATYCCQWSSNPFTFGSGTKLEI 127
 D 62 FSGSGSGTSYSLTISMEADAATYCCQWHSYPRFTFGGTKLEI 107

RESULT 19
 KV6B_MOUSE
 ID KV6B_MOUSE STANDARD; PRT; 107 AA.
 AC P01676;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Ig kappa chain V-VI region XRPC 24.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=79082830; PubMed=1035573;
 RA Rao D.N., Rudikoff S., Potter M.;
 RT "k Chain variable regions from three galactan binding myeloma
 RT proteins";
 RL Biochemistry 17:5555-5559 (1978).
 CC -I- MISCELLANEOUS: This chain was isolated from a myeloma protein that
 CC bind galactan.
 CC
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC
 CC HSSP; P01679; 2FBJ.
 DR SMR; P01676; 1-107.
 DR Ensembl; ENSMUSG0000062047; Mus musculus.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; IG_V.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Direct protein sequencing; Immunoglobulin domain;
 KW Immunoglobulin V region.
 FT REGION 1 23
 FT REGION 24 33
 FT REGION 34 48
 FT REGION 49 55
 FT REGION 56 87
 FT REGION 88 96
 FT REGION 97 106
 FT DISULFID 23 87
 FT NON_TER 107 107
 SQ SEQUENCE 107 AA; 11584 MW; 36E6D022A5EC34D7 CRC64;
 Query Match 60.2%; Score 395; DB 1; Length 107;
 Best Local Similarity 75.2%; Pred. No. 3.2e-30;
 Matches 79; Conservative 7; Mismatches 19; Indels 0; Gaps 0;
 QY 23 QIVLSQSPAILFASPGETVTMTTCRASSSVIYMCWNQKPGSSPKPWIYGTSTLASGVPT 82
 D 1 EIVLTQSPAITAASLGQKVTITCSASSSVSYMYWYQKSGTSPKPMIYEISKLASGVPT 60
 QY 83 FSGSGSGTSYSLTISRVEADAATYCCQWSSNPFTFGSGTKLEI 127
 D 61 FSGSGSGTSYSLTISMEADAATYCCQWNYPLITFGSGTKLEI 105
 RESULT 20
 KV6A_MOUSE
 ID KV6A_MOUSE STANDARD; PRT; 107 AA.
 AC P01675;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Ig kappa chain V-VI region XRPC 44.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=79082830; PubMed=103573;
RA Rao D.N., Rudikoff S., Potter M.;
RT "k Chain variable regions from three galactan binding myeloma
RL proteins.";
RL Biochemistry 17:5555-5559 (1978) .
RN [2]
RP PROTEIN SEQUENCE.
RX PubMed=6776525;
RA Rudikoff S., Rao D.N., Glaudemans C.P.J., Potter M.;
RT "Kappa Chain joining segments and structural diversity of antibody
RT combining sites.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:4270-4274 (1980) .
CC -1- MISCELLANEOUS: This chain was isolated from a myeloma protein that
CC bind galactan.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR PIR; A90420; KVMX4.
DR HSP; P01679; 2FBJ.
DR SMR; P01675; 1-107.
DR Ensembl; ENSMUSG0000062047; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG Like; 1.
DR Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23
FT REGION 24 33
FT REGION 34 48
FT REGION 49 55
FT REGION 56 87
FT REGION 88 96
FT REGION 97 106
FT DISULFID 23 87
FT CONFLICT 95 95
FT NON TER 107 107
SQ SEQUENCE 107 AA; 11627 MW; 27A2D022BC0A34D7 CRC64;

Query Match 59.8%; Score 392; DB 1; Length 107;
Best Local Similarity 74.3%; Pred. No. 6.3e-30;
Matches 78; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

Qy 23 QIVLSQSPAILFASPGETVMTTCRASSSVIYMCWNQKPGSSPKPWIYGTSTLASGVPT 82
Db 1 EIVLTQSPAITAASLGKVTITCSASSSVYMHYQKSGTSPKPIWIEISKLASGVPT 60

Qy 83 FSGSGSGTSLTISRVEAEADAATYCCQWSSNPFPGSGTKLEI 127
Db 61 FSGSGSGTSLTISSEAEADAATYCCQWNYPLWTFGGTKLEI 105

Search completed: March 20, 2006, 07:32:04
Job time : 25.7968 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 20, 2006, 07:29:34 ; Search time 4.63412 Seconds
(without alignments)
2636.859 Million cell updates/sec

Title: US-10-687-035-33
Perfect score: 656
Sequence: 1 MRFQVQIFPLLSASVIMS.....YCOQWSSNPFTFGSGTKLEI 127

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

PIR_80.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	536	81.7	130	1 JL0079	Ig kappa chain pre
2	533	81.2	130	2 A32513	Ig kappa chain pre
3	532	81.1	235	2 S25058	Ig kappa chain - m
4	518	79.0	130	2 S04573	Ig kappa chain pre
5	515	78.5	140	2 PL0013	Ig kappa chain pre
6	501	76.4	130	2 B32456	Ig kappa chain pre
7	469	71.5	107	2 A42848	Ig light chain v r
8	462	70.4	106	2 PL0082	Ig kappa chain v r
9	458	69.8	132	2 S05268	Ig kappa chain pre
10	452	68.9	107	2 B30562	Ig kappa chain v r
11	452	68.9	129	1 KVMS7B	Ig kappa chain pre
12	448	68.3	107	2 A30562	Ig kappa chain v r
13	440.5	67.1	108	2 G30560	Ig kappa chain v r
14	438	66.8	104	2 B49049	Ig kappa chain v r
15	437	66.6	103	2 S29591	Ig kappa chain v r
16	437	66.6	107	2 PC4405	Ig kappa chain v r
17	435.5	66.4	108	2 S38720	Ig light chain v r
18	435	66.3	106	2 PS0071	Ig kappa chain v r
19	432	65.9	105	2 S26338	Ig kappa chain v r
20	429	65.4	107	2 PT0406	Ig kappa chain v r
21	425	64.8	106	2 B54378	Ig light chain v r
22	424	64.6	107	2 S11118	Ig kappa chain v r
23	423	64.5	100	2 S29590	Ig kappa chain v r
24	422	64.3	113	2 S03410	Ig kappa chain pre
25	420	64.0	97	2 S26341	Ig light chain v r
26	420	64.0	107	2 S11119	Ig kappa chain v r
27	416	63.4	106	2 G27887	Ig kappa chain v r
28	415	63.3	107	2 PD0011	Ig kappa chain v r
29	412	62.8	107	2 S11121	Ig kappa chain v r

30	411	62.7	123	2 S05269	Ig kappa chain pre
31	410	62.5	97	2 PH1084	Ig light chain v r
32	408	62.2	108	2 S29581	Ig kappa chain v r
33	407	62.0	106	2 PS0070	Ig kappa chain v r
34	405	61.7	107	2 S11117	Ig kappa chain v r
35	404	61.6	108	2 PL0278	Ig kappa chain v r
36	402	61.3	134	2 S05267	Ig kappa chain pre
37	401	61.1	107	2 S11112	Ig kappa chain v r
38	400	61.0	99	2 S29585	Ig kappa chain v r
39	400	61.0	104	2 JC6076	anti-D-dimer monoc
40	400	61.0	108	2 PL0277	Ig kappa chain v r
41	400	61.0	108	2 PL0276	Ig kappa chain v r
42	399	60.8	109	2 PT0405	Ig light chain v r
43	398	60.7	97	2 PH1085	Ig light chain v r
44	397	60.5	107	2 S11113	Ig kappa chain v r
45	393	59.9	95	2 D33730	Ig kappa chain v r
46	392	59.8	107	1 KVMSX4	Ig kappa chain v r
47	390	59.5	107	2 S11122	Ig kappa chain v r
48	388	59.1	104	2 S29592	Ig kappa chain v r
49	387	59.0	109	2 PT0404	Ig light chain v r
50	386	58.8	102	2 S29584	Ig kappa chain v r
51	385	58.7	94	2 S26340	Ig light chain v r
52	384	58.5	108	2 PS0069	Ig kappa chain v r
53	383	58.4	91	2 S17629	Ig kappa chain v r
54	382	58.2	106	2 S11120	Ig kappa chain v r
55	381	58.1	99	2 D38601	Ig kappa chain v r
56	381	58.1	104	2 S26475	Ig kappa chain v r
57	379	57.8	91	2 S17637	Ig kappa chain v r
58	379	57.8	288	2 A56446	Ig heavy chain v r
59	378.5	57.7	106	2 S11114	Ig kappa chain v r
60	377.5	57.5	98	2 PH1061	Ig light chain v r
61	377	57.5	90	2 S26339	Ig kappa chain v r
62	376	57.3	120	2 A34871	Ig kappa chain v r
63	375	57.2	107	1 KVMSJ5	Ig kappa chain v r
64	374	57.0	91	2 S17626	Ig kappa chain v r
65	374	57.0	107	2 PT0401	Ig light chain v r
66	373	56.9	120	2 S66536	Ig light chain v r
67	372	56.7	91	2 S17639	Ig kappa chain v r
68	371	56.6	96	2 C33730	Ig kappa chain v r
69	370	56.4	107	2 S11123	Ig kappa chain v r
70	370	56.4	107	2 PT0398	Ig light chain v r
71	369	56.2	99	2 PH1059	Ig light chain v r
72	368	56.1	108	2 S11125	Ig kappa chain v r
73	367	55.9	91	2 S17627	Ig kappa chain v r
74	367	55.9	91	2 S17630	Ig kappa chain v r
75	366	55.8	98	2 S26342	Ig kappa chain v r
76	366	55.8	99	2 PH1058	Ig light chain v r
77	366	55.8	107	2 PT0402	Ig light chain v r
78	365	55.6	107	2 PT0403	Ig light chain v r
79	364	55.5	109	2 S13699	Ig kappa chain v r
80	363	55.3	91	2 S17638	Ig kappa chain v r
81	362	55.2	107	2 PT0395	Ig light chain v r
82	360	54.9	93	2 S17641	Ig kappa chain v r
83	359.5	54.8	102	2 S11115	Ig kappa chain v r
84	359	54.7	91	2 S17628	Ig kappa chain v r
85	359	54.7	93	2 S17623	Ig kappa chain v r
86	358	54.6	93	2 S17642	Ig kappa chain v r
87	358	54.6	93	2 S17640	Ig kappa chain v r
88	358	54.6	106	2 S29583	Ig kappa chain v r
89	357.5	54.5	145	2 PL0014	Ig kappa chain pre
90	357	54.4	107	2 S11116	Ig kappa chain v r
91	357	54.4	107	2 PT0397	Ig light chain v r
92	356	54.3	107	2 PT0400	Ig light chain v r
93	354	54.0	99	2 PH1060	Ig light chain v r
94	354	54.0	109	2 S40601	Ig kappa chain v-I
95	354	54.0	129	2 S46369	Ig light chain var
96	354	54.0	134	2 S38643	Ig kappa chain v r
97	352	53.7	102	2 S29582	Ig kappa chain v r
98	352	53.7	106	2 PS0072	Ig kappa chain v r
99	352	53.7	108	2 C30608	Ig kappa chain v-I
100	352	53.7	109	2 A30608	Ig kappa chain v-I

A:Molecule type: mRNA
 A:Residues: 1-130 <KOF>
 A:Cross-references: UNIPARC:UPI0000115DFE; EMBL:X14620; NID:G52031; PIDN:CAA32773.1; PII
 A>Note: the authors translated the codon AGC for residue 47 as Aen
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-130/Product: Ig kappa chain V region (fragment) #status predicted <MAT>
 F:38-113/Domain: immunoglobulin homology <IMM>

Query Match 79.0%; Score 518; DB 2; Length 130;
 Best Local Similarity 80.6%; Pred. No. 1.1e-35;
 Matches 104; Conservative 10; Mismatches 13; Indels 2; Gaps 1;

QY 1 MDPQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVI--YMCWNQ 58
 DB 1 MDPQVQIFSFLLISASVIMTRGQIVLTQSPAINASPGKVTMTCSASSSVSKYLNWYQ 60

QY 59 QKPGSPKPMIYGTSTLASGVPTRFSGSGSGTYSYLTISRVEAEDAATYYCQWSSNPFT 118
 DB 61 QRSQSPKLMWYGTSTLASGVPTRFSGSGSGTYSYLTISRVEAEDAATYYCQYHSDPLT 120

QY 119 FGSSTKLEI 127
 DB 121 FGAGTKLEL 129

RESULT 5
 PLO013
 Ig kappa chain precursor V region (4C11) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
 C:Accession: PLO013
 R:Cheng, H.L.; Sood, A.K.; Ward, R.E.; Kieber-Emmons, T.; Kohler, H.
 Mol. Immunol. 25, 33-40, 1988
 A:Title: Structural basis of stimulatory anti-idiotypic antibodies.
 A:Reference number: PLO011; MUID:88142863; PMID:3125424
 A:Accession: PLO013
 A:Molecule type: mRNA
 A:Residues: 1-140 <CHE>
 A:Cross-references: UNIPARC:UPI00001767A6
 A:Experimental source: cell line 4C11
 C:Comment: This protein is an anti-idiotypic antibody that induces an anti-phosphorylch
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-129/Product: Ig heavy chain V region (4C11) #status predicted <MAT>
 F:38-111/Domain: immunoglobulin homology <IMM>
 F:46-55/Region: complementarity-determining 1
 F:71-77/Region: complementarity-determining 2
 F:110-118/Region: complementarity-determining 3
 F:130-140/Domain: constant region (fragment) #status predicted <COR>

Query Match 78.5%; Score 515; DB 2; Length 140;
 Best Local Similarity 82.7%; Pred. No. 2.1e-35;
 Matches 105; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

QY 1 MDPQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQ 60
 DB 1 MDPQVQIFSFLLISASVIMSRGQIVLTQSPAINASPGKVTMTCSASSSVIMHWFOQK 60

QY 61 PGSSPKPMIYGTSTLASGVPTRFSGSGSGTYSYLTISRVEAEDAATYYCQWSSNPFTFG 120
 DB 61 PDSPKLMWYGTSTLASGVPTRFSGSGSGTYSYLTISRVEAEDAATYYCQYHSDPLT 120

QY 121 SGTLEI 127
 DB 121 GGTLEL 127

RESULT 6
 B32456
 Ig kappa chain precursor V region - mouse

C:Species: Mus musculus (house mouse)
 C>Date: 26-Oct-1989 #sequence_revision 26-Oct-1989 #text_change 21-Jan-2000
 C:Accession: B32456
 R:Dombink-Kurtzman, M.A.; Johnson, L.S.; Riordan, G.S.; Bedzyk, W.D.; Voss Jr., E.W.
 J. Biol. Chem. 264, 4513-4522, 1989
 A:Title: Variable region primary structures of a high affinity anti-fluorescein immunogl
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:38-113/Domain: immunoglobulin homology <IMM>

Query Match 76.4%; Score 501; DB 2; Length 130;
 Best Local Similarity 78.3%; Pred. No. 2.8e-34;
 Matches 101; Conservative 9; Mismatches 17; Indels 2; Gaps 1;

QY 1 MDPQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSV--IYMCWNQ 58
 DB 1 MDPQVQIFSFLLISASVIMSRGQIVLTQSPAINASPGKVTMTCRASSSVSSYLHWYQ 60

QY 59 QKPGSPKPMIYGTSTLASGVPTRFSGSGSGTYSYLTISRVEAEDAATYYCQWSSNPFT 118
 DB 61 QKSGASPKLMWYGTSTLASGVPTRFSGSGSGTYSYLTISRVEAEDAATYYCQYSGYPLT 120

QY 119 FGSSTKLEI 127
 DB 121 FGAGTKLEL 129

RESULT 7
 A42848
 Ig light chain V region - mouse (fragment)
 N:Alternate names: L6 anti-tumor antibody
 C:Species: Mus musculus (house mouse)
 C>Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
 C:Accession: A42848; S33902
 R:Fell, H.P.; Gayle, M.A.; Yelton, D.; Lipsich, L.; Schieven, G.L.; Marken, J.S.; Aruffo,
 J. Biol. Chem. 267, 15552-15558, 1992
 A:Title: Chimeric L6 anti-tumor antibody. Genomic construction, expression, and character
 A:Reference number: A42848; MUID:92348410; PMID:1639794
 A:Accession: A42848
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-107 <FEL>
 A:Cross-references: UNIPARC:UPI0000115334; EMBL:M90690
 A>Note: sequence extracted from NCBI backbone (NCBIN:109958, NCBI:109959)
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F:16-89/Domain: immunoglobulin homology <IMM>

Query Match 71.5%; Score 469; DB 2; Length 107;
 Best Local Similarity 85.7%; Pred. No. 9.5e-32;
 Matches 90; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 23 QIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQKPGSSPKPMIYGTSTLASGVPTR 82
 DB 1 QIVLSQSPAILFASPGKVTMTCRASSSVSPMNWYQKPGSSPKPMIYATSNLASGVPR 60

QY 83 FSGSGSGTYSYLTISRVEAEDAATYYCQWSSNPFTFGSTKLEI 127
 DB 61 FSGSGSGTYSYLTISRVEAEDAATYYCQWSSNPFTFGAGTKLEL 105

RESULT 8
 PLO082
 Ig kappa chain V region (2D3) - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 21-Jan-2000
 C:Accession: PLO082

R;Meek, K.; Hasemann, C.; Pollok, B.; Alkan, S.S.; Brait, M.; Slaoui, M.; Urbain, J.; Ca
J. Exp. Med. 169, 519-533, 1989
A;Title: Structural characterization of antiidiotypic antibodies; evidence that Ab2s are
A;Reference number: PLO080; MUID:89094248; PMID:2492056
A;Accession: PLO082
A;Molecule type: mRNA
A;Residues: 1-106 <MEE>
A;Cross-references: UNIPARC:UPI00001767ED
A;Experimental source: strain BALB/c
A;Note: the sequence shown here is from the V kappa region of an antiidiotypic monoclonal
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-89/Domain: immunoglobulin homology <IMM>

Query Match 70.4%; Score 462; DB 2; Length 106;
Best Local Similarity 87.6%; Pred. No. 3.5e-31;
Matches 92; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 23 QIVLSQSPAILFASPGETVMTTCRASSSVIYMCWQKPGSSPKPWIYGTSTLASGVPTTR 82
DB 1 QIVLSQSPAILFASPGETVMTTCRASSSVIYMCWQKPGSSPKPWIYGTSTLASGVPTTR 60

QY 83 FSGSGSGTSYSLTISRVEADAATYYCQWSSNPFTFGSGTKLEI 127
DB 61 FSGSGSGTSYSLTISRVEADAATYYCQWSSNPFTFGSGTKLEI 105

RESULT 9
S05268
Ig kappa chain precursor V-J region (38C13-VI) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 21-Jan-2000
C;Accession: S05268; JLO062; S03846
R;Levy, S.
submitted to the EMBL Data Library, February 1989
A;Reference number: S05267
A;Accession: S05268
A;Molecule type: mRNA
A;Residues: 1-132 <LEV>
A;Cross-references: UNIPARC:UPI000015DEC; EMBL:X14098; NID:952562; PIDN:CAA32260.1; PII
R;Carroll, W.L.; Starnes, C.O.; Levy, R.; Levy, S.
J. Exp. Med. 168, 1607-1620, 1988
A;Title: Alternative V kappa gene rearrangements in a murine B cell lymphoma. An explana
A;Reference number: JLO061; MUID:89035985; PMID:3141553
A;Accession: JLO062
A;Molecule type: mRNA
A;Residues: 1-120 <CAR>
A;Cross-references: UNIPARC:UPI0000176789; EMBL:X14098
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-14/Domain: signal sequence (fragment) #status predicted <SIG>
F;15-132/Product: Ig kappa chain (fragment) #status predicted <MAT>
F;15-108/Domain: V region (V-kappa-1) <VRE>
F;30-103/Domain: immunoglobulin homology <IMM>
F;109-132/Domain: J region (J-kappa-4) (fragment) <JRE>

Query Match 69.8%; Score 458; DB 2; Length 132;
Best Local Similarity 76.3%; Pred. No. 9.2e-31;
Matches 90; Conservative 10; Mismatches 18; Indels 0; Gaps 0;

QY 10 FLLISASVIMSRGQIVLSQSPAILFASPGETVMTTCRASSSVIYMCWQKPGSSPKPWI 69
DB 2 FLLISVTLVINGEIFLQSPAILFASPGETVMTTCRASSSVIYMCWQKPGSSPKIWI 61

QY 70 YGTSTLASGVPTTRFSGSGSGTSYSLTISRVEADAATYYCQWSSNPFTFGSGTKLEI 127
DB 62 YGINLASGVPTTRFSGSGSGTSYSLTISRVEADAATYYCQWSSNPFTFGSGTKLEI 119

RESULT 10
B30562
Ig kappa chain V region (27.10.2) - mouse (fragment)
C;Species: Mus musculus (house mouse)

C;Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 21-Jan-2000
C;Accession: B30562
R;Skder, S.K.; Borden, P.; Gruero, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison, S.L
J. Immunol. 142, 888-893, 1989
A;Title: Amino acid substitutions in V-H CDR2 change the idiotype but not the antigen-bir
A;Reference number: A30562; MUID:89110066; PMID:2464031
A;Accession: B30562
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-107 <SIK>
A;Cross-references: UNIPARC:UPI00001767BA
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-89/Domain: immunoglobulin homology <IMM>

Query Match 68.9%; Score 452; DB 2; Length 107;
Best Local Similarity 82.9%; Pred. No. 2.3e-30;
Matches 87; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

QY 23 QIVLSQSPAILFASPGETVMTTCRASSSVIYMCWQKPGSSPKPWIYGTSTLASGVPTTR 82
DB 1 QIVLSQSPAILFASPGETVMTTCRASSSVIYMCWQKPGSSPKPWIYGTSTLASGVPTTR 60

QY 83 FSGSGSGTSYSLTISRVEADAATYYCQWSSNPFTFGSGTKLEI 127
DB 61 FSGSGSGTSYSLTISRVEADAATYYCQWSSNPFTFGSGTKLEI 105

RESULT 11
KVMS7B
Ig kappa chain precursor V region (S107B) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 17-Dec-1982 #sequence_revision 17-Dec-1982 #text_change 09-Jul-2004
C;Accession: A01943
R;Kwan, S.P.; Max, E.E.; Seidman, J.G.; Leder, P.; Scharff, M.D.
Cell 26, 57-66, 1981
A;Title: Two kappa immunoglobulin genes are expressed in the myeloma S107.
A;Reference number: A01943; MUID:82115300; PMID:6799208
A;Accession: A01943
A;Molecule type: mRNA
A;Residues: 1-129 <KWA>
A;Cross-references: UNIPROT:P01680; UNIPARC:UPI000002A119; GB:V00780; NID:951676; PIDN:CI
A;Note: the sequence was determined from the differentiated gene
C;Comment: This protein, in which there is a deletion of two amino acids at the V-J recomb
al kappa chain S107.
C;Genetics:
A;Introns: 17/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp
hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-129/Product: Ig kappa chain V region (S107B) #status predicted <MAT>
F;38-113/Domain: immunoglobulin homology <IMM>
F;45-111/Disulfide bonds: #status predicted

Query Match 68.9%; Score 452; DB 1; Length 129;
Best Local Similarity 74.4%; Pred. No. 2.8e-30;
Matches 96; Conservative 8; Mismatches 21; Indels 4; Gaps 2;

QY 1 MDFQVQFFSFLILISASVIMSRGQIVLSQSPAILFASPGETVMTTCRASSSV--IYMCWNQ 58
DB 1 MDLQVQIIXFLILISVTVIMSRGENVLTQSPAIMAASLGQKVTWTCRASSSVSSSYLHWYQ 60

QY 59 QKPGSSPKPWIYGTSTLASGVPTTRFSGSGSGTSYSLTISRVEADAATYYCQWSSNPFT 118
DB 61 QKSGASPKPIHRTSNLASGVPTTRFSGSGSGTSYSLTISRVEADAATYYCQWSSNPFT 118

QY 119 FSGSGTKLEI 127
DB 119 FSGSGTKLEI 127

RESULT 12

A30562
Ig kappa chain V regions (27.7.2 and 27.4b.2) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 21-Jan-2000
C;Accession: A30562
R;Skidder, S.K.; Borden, P.; Gruezo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison, S.L.
J. Immunol. 142, 888-893, 1989
A;Title: Amino acid substitutions in V-H CDR2 change the idiotype but not the antigen-binding site
A;Reference number: A30562; MUID:89110066; PMID:2464031
A;Accession: A30562
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-107 <SIK>
A;Cross-references: UNIPARC:UPI00001767B0
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-89/Domain: immunoglobulin homology <IMM>

Query Match 68.3%; Score 448; DB 2; Length 107;
Best Local Similarity 82.9%; Pred. No. 4.9e-30;
Matches 87; Conservative 5; Mismatches 13; Indels 0; Gaps 0;
QY 23 QIVLSQSPAILFASPGETVMTTCRASSSVIYMCWNQKPGSSPKPWIYGTSTLASGVPTTR 82
DB 1 QIVLTQSPALMSASPGKVTMTCSASSSVSYMHYQKSGTSPKRWIYDTSKLASGVPAR 60
QY 83 FSGSGGTSLTISRVEADAATYYCQWSSNPFTFGSGTKLEI 127
DB 61 FSGSGGTSLTISRVEADAATYYCQWSSNPFTFGSGTKLEI 105

RESULT 13

G30560
Ig kappa chain V region (35.8.2H) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 21-Jan-2000
C;Accession: G30560
R;Matsuda, T.; Kabat, E.A.
J. Immunol. 142, 863-870, 1989
A;Title: Variable region cDNA sequences and antigen binding specificity of mouse monoclonal antibody
A;Reference number: A30560; MUID:89110062; PMID:2464028
A;Accession: G30560
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-108 <MAT>
A;Cross-references: UNIPARC:UPI00001767B8
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-89/Domain: immunoglobulin homology <IMM>

Query Match 67.1%; Score 440.5; DB 2; Length 108;
Best Local Similarity 83.0%; Pred. No. 2e-29;
Matches 88; Conservative 4; Mismatches 13; Indels 1; Gaps 1;
QY 23 QIVLSQSPAILFASPGETVMTTCRASSSVIYMCWNQKPGSSPKPWIYGTSTLASGVPTTR 82
DB 1 QIVLTQSPALMSASPGKVTMTCSASSSVSYMHYQKSGTSPKRWIYDTSKLASGVPAR 60
QY 83 FSGSGGTSLTISRVEADAATYYCQWSSNPFTFGSGTKLEI 127
DB 61 FSGSGGTSLTISRVEADAATYYCQWTRNPPFTFGSGTKLEI 106

RESULT 14

B49049
Ig kappa chain V region (anti-idiotypic) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C;Accession: B49049
R;Armandola, E.A.; Mariani, S.M.; Zwickl, M.; Hardman, N.; Ferrone, S.
Eur. J. Immunol. 22, 2893-2899, 1992

A;Title: Molecular analysis of anti-idiotypic monoclonal antibodies in the HLA-DR antigen
A;Reference number: A49049; MUID:93049629; PMID:1425914
A;Accession: B49049
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-104 <ARM>
A;Cross-references: UNIPARC:UPI00001767AD
A;Experimental source: BALB/c
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;16-89/Domain: immunoglobulin homology <IMM>

Query Match 66.8%; Score 438; DB 2; Length 104;
Best Local Similarity 81.7%; Pred. No. 3.2e-29;
Matches 85; Conservative 5; Mismatches 14; Indels 0; Gaps 0;
QY 23 QIVLSQSPAILFASPGETVMTTCRASSSVIYMCWNQKPGSSPKPWIYGTSTLASGVPTTR 82
DB 1 QIVLTQSPALMSASPGKVTMTCSASSSVSYMHYQKSGTSPKRWIYDTSKLASGVPAR 60
QY 83 FSGSGGTSLTISRVEADAATYYCQWSSNPFTFGSGTKLE 126
DB 61 FSGSGGTSLTISRVEADAATYYCQWSSNPFTFGAGTKLE 104

RESULT 15

S29591
Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S29591
R;Kavaler, J.
Submitted to the EMBL Data Library, April 1991
A;Reference number: S26459
A;Accession: S29591
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-103 <KAV>
A;Cross-references: UNIPARC:UPI0000115F57; EMBL:X59094; NID:952227; PIDN:CAA41820.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-88/Domain: immunoglobulin homology <IMM>

Query Match 66.6%; Score 437; DB 2; Length 103;
Best Local Similarity 82.5%; Pred. No. 3.8e-29;
Matches 85; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

QY 24 IVLSQSPAILFASPGETVMTTCRASSSVIYMCWNQKPGSSPKPWIYGTSTLASGVPTTR 83
DB 1 IVLTQSPALMSASPGKVTMTCSASSSVSYMHYQKSGTSPKRWIYDTSKLASGVPAR 60

QY 84 SGSGGTSLTISRVEADAATYYCQWSSNPFTFGSGTKLE 126
DB 61 SGSGGTSLTISRVEADAATYYCQWSSNPFTFGAGTKLE 103

RESULT 16

PC4405
Ig kappa chain V region (F3, anti-AFP) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 10-Nov-1997 #sequence_revision 23-Jan-1998 #text_change 09-Jul-2004
C;Accession: PC4405
R;Deng, J.B.; Han, H.; Su, C.-Z.; Chen, C.Q.
Chinese Biochem. J. 12, 648-653, 1996
A;Title: Generation of a phage display library of the immunoglobulin repertoire from hum
A;Reference number: PC4405
A;Accession: PC4405
A;Molecule type: mRNA
A;Residues: 1-107 <DEN>
A;Cross-references: UNIPROT:Q8K1F0; UNIPARC:UPI00001767BB
A;Experimental source: spleen cell
C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;16-89/Domain: immunoglobulin homology <IMM>

Query Match 66.6%; Score 437; DB 2; Length 107;
Best Local Similarity 81.7%; Pred. No. 3.9e-29;
Matches 85; Conservative 4; Mismatches 15; Indels 0; Gaps 0;

Qy 24 IVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQKPGSSPKPWIYGTSTLASGVPTRF 83
Db 2 IEVLTQSPALMSASPGKVTMTCSASSSISYMHYVQKPGTSPKRWIYDTSKLASGVPAR 61
Qy 84 SGGSGGTSYSLTISRVEAEDAATYCCQWSSNPFTFGSGTKLEI 127
Db 62 SGGSGGTSYSLTISRVEAEDAATYCCQWRDNPFTFGGTKLEI 105

RESULT 17

S38720
Ig light chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
C;Accession: S38720
R;Cimanis, A.Y.
submitted to the EMBL Data Library, November 1993

A;Reference number: S38713
A;Accession: S38720
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-108 <IM>
A;Cross-references: UNIPARC:UPI0000117544; EMBL:X76023; NID:9416104; PIDN:CAA53610.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;16-89/Domain: immunoglobulin homology <IMM>

Query Match 66.4%; Score 435.5; DB 2; Length 108;
Best Local Similarity 80.2%; Pred. No. 5.2e-29;
Matches 85; Conservative 8; Mismatches 12; Indels 1; Gaps 1;

Qy 23 QIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQKPGSSPKPWIYGTSTLASGVPTR 82
Db 1 EIVLTQSPALMSASPGKVTMTCSASSSVSYMHYVQKPRSSPKPWIYLTSTLASGVPLR 60
Qy 83 FSGSGGTSYSLTISRVEAEDAATYCCQWSSNPFTFGSGTKLEI 127
Db 61 FSGSGGTSYSLTISRVEAEDAATYCCQWSSNPFLFGAGTKLQL 106

RESULT 18

PS0071
Ig kappa chain V region (38C13.V8) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000
C;Accession: PS0071
R;Levy, S.; Campbell, M.J.; Levy, R.
J. Exp. Med. 170, 1-13, 1989
A;Title: Functional immunoglobulin light chain genes are replaced by ongoing rearrangeme
A;Reference number: A92781; MUID:89310348; PMID:2501443
A;Accession: PS0071
A;Status: translation not shown

A;Molecule type: DNA
A;Residues: 1-106 <LEV>
A;Cross-references: UNIPARC:UPI00001767C9
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-89/Domain: immunoglobulin homology <IMM>

Query Match 66.3%; Score 435; DB 2; Length 106;
Best Local Similarity 81.0%; Pred. No. 5.7e-29;
Matches 85; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

Qy 23 QIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQKPGSSPKPWIYGTSTLASGVPTR 82
Db 1 QIVLTQSPALMSASPGKVTMTCSASSSVSYMHYVQKSGTSPKRWIYDTSKLASGVPAR 60

Qy 83 FSGSGGTSYSLTISRVEAEDAATYCCQWSSNPFTFGSGTKLEI 127
Db 61 FSGSGGTSYSLTISRVEAEDAATYCCQWSSNPFTFGAPTKLEI 105

RESULT 19

S26338
Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: S26338
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protein e
A;Reference number: S26309; MUID:91341421; PMID:1908510
A;Accession: S26338
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-105 <STA>
A;Cross-references: UNIPARC:UPI0000115F82; EMBL:X59197; NID:952328; PIDN:CAA41907.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-89/Domain: immunoglobulin homology <IMM>

Query Match 65.9%; Score 432; DB 2; Length 105;
Best Local Similarity 81.0%; Pred. No. 9.8e-29;
Matches 85; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

Qy 23 QIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQKPGSSPKPWIYGTSTLASGVPTR 82
Db 1 QIVLTQSPALMSASPGKVTMTCSASSSVSYMHYVQKPGSSPKPWIYRTSNLASGVPAR 60

Qy 83 FSGSGGTSYSLTISRVEAEDAATYCCQWSSNPFTFGSGTKLEI 127
Db 61 FSGSGGTSYSLTISRMEADAATYCCQYHSYPTFTFGGTKLEI 105

RESULT 20

PT0406
Ig kappa chain V region (S107/VH11 group 6-26) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PT0406
R;Behar, S.M.; Lustgarten, D.L.; Corbet, S.; Scharff, M.D.
J. Exp. Med. 173, 731-741, 1991
A;Title: Characterization of somatically mutated S107 VH11-encoded anti-DNA autoantibodi
A;Reference number: PT0376; MUID:91147903; PMID:1900082
A;Accession: PT0406
A;Molecule type: DNA
A;Residues: 1-107 <BEH>

A;Cross-references: UNIPARC:UPI00001767E8
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;16-89/Domain: immunoglobulin homology <IMM>

Query Match 65.4%; Score 429; DB 2; Length 107;
Best Local Similarity 79.0%; Pred. No. 1.8e-28;
Matches 83; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

Qy 23 QIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQKPGSSPKPWIYGTSTLASGVPTR 82
Db 1 QIVLTQSPALMSASPGKVTMTCSASSSVSYMHYVQKSGTSPKRWIYDTSKLASGVPAR 60

Qy 83 FSGSGGTSYSLTISRVEAEDAATYCCQWSSNPFTFGSGTKLEI 127
Db 61 FSGSGGTSYSLTXISMEADAATYCCQWSSNPFTFGGTXXEI 105

Search completed: March 20, 2006, 07:36:25
Job time : 5.63412 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 20, 2006, 07:32:13 ; Search time 2.37968 Seconds
(without alignments)
1527.558 Million cell updates/sec

Title: US-10-687-035-33

Perfect score: 656

Sequence: 1 MDPQVQIFSLISAVIMS.....YCOQSSNPFTFGSGTKLRI 127

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 169630 seqs, 28622889 residues

Total number of hits satisfying chosen parameters: 169630

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Published Applications_AA_New:*
1: /cgn2_6/ptodata/2/pubppa/US08_NEW_PUB.pdb:*
2: /cgn2_6/ptodata/2/pubppa/US06_NEW_PUB.pdb:*
3: /cgn2_6/ptodata/2/pubppa/US07_NEW_PUB.pdb:*
4: /cgn2_6/ptodata/2/pubppa/PCT_NEW_PUB.pdb:*
5: /cgn2_6/ptodata/2/pubppa/US09_NEW_PUB.pdb:*
6: /cgn2_6/ptodata/2/pubppa/US10_NEW_PUB.pdb:*
7: /cgn2_6/ptodata/2/pubppa/US11_NEW_PUB.pdb:*
8: /cgn2_6/ptodata/2/pubppa/US60_NEW_PUB.pdb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	572	87.2	128	7	US-11-193-205-60
2	524	79.9	128	7	US-11-250-411-87
3	494	75.3	130	7	US-11-090-331-4
4	494	75.3	138	7	US-11-090-331-8
5	493	75.2	130	7	US-11-125-837-21
6	478	72.9	126	7	US-11-250-411-89
7	475	72.4	213	7	US-11-124-620-6
8	475	72.4	236	7	US-11-106-820-19
9	475	72.4	236	7	US-11-190-364-17
10	475	72.4	236	7	US-11-147-780-17
11	470	71.6	106	7	US-11-107-028-28
12	470	71.6	107	7	US-11-120-338-1
13	470	71.6	107	7	US-11-106-820-1
14	470	71.6	107	7	US-11-143-077-1
15	470	71.6	107	7	US-11-190-364-1
16	470	71.6	107	7	US-11-147-780-1
17	470	71.6	107	7	US-11-143-386-1
18	467	71.2	106	7	US-11-193-440-89
19	462	70.4	128	7	US-11-250-411-92
20	461	70.3	106	7	US-11-107-028-34
21	457	69.7	235	7	US-11-166-994-2
22	449.5	68.5	110	7	US-11-193-512-33
23	445	67.8	126	7	US-11-250-411-96
24	444	67.7	107	7	US-11-221-900-6
25	440	67.1	126	7	US-11-250-411-94
					Sequence 60, Appl
					Sequence 87, Appl
					Sequence 4, Appl
					Sequence 8, Appl
					Sequence 21, Appl
					Sequence 89, Appl
					Sequence 6, Appl
					Sequence 19, Appl
					Sequence 17, Appl
					Sequence 28, Appl
					Sequence 1, Appl
					Sequence 1, Appl
					Sequence 1, Appl
					Sequence 89, Appl
					Sequence 92, Appl
					Sequence 34, Appl
					Sequence 2, Appl
					Sequence 33, Appl
					Sequence 36, Appl
					Sequence 6, Appl
					Sequence 94, Appl

26	437	66.6	106	6	US-10-507-662-43	Sequence 43, Appl
27	435	66.3	106	6	US-10-507-662-42	Sequence 42, Appl
28	434	66.2	126	7	US-11-250-411-93	Sequence 93, Appl
29	426	64.9	106	7	US-11-097-812-39	Sequence 39, Appl
30	425	64.8	106	7	US-11-250-411-98	Sequence 98, Appl
31	424.5	64.7	107	7	US-11-097-812-101	Sequence 101, Appl
32	422	64.3	106	7	US-11-174-186-1	Sequence 1, Appl
33	421	64.2	110	7	US-11-097-812-99	Sequence 99, Appl
34	421	64.2	110	7	US-11-097-812-100	Sequence 100, Appl
35	421	64.2	110	7	US-11-097-812-171	Sequence 171, Appl
36	418	63.7	110	7	US-11-097-812-207	Sequence 207, Appl
37	417	63.6	106	7	US-11-174-186-8	Sequence 8, Appl
38	415	63.3	110	7	US-11-097-812-174	Sequence 174, Appl
39	414	63.1	110	7	US-11-097-812-110	Sequence 110, Appl
40	413	63.0	110	7	US-11-097-812-114	Sequence 114, Appl
41	411	62.7	106	7	US-11-174-186-9	Sequence 9, Appl
42	411	62.7	213	7	US-11-174-186-42	Sequence 42, Appl
43	409	62.3	106	7	US-11-174-186-16	Sequence 16, Appl
44	408	62.2	108	6	US-10-507-662-44	Sequence 44, Appl
45	404	61.6	106	7	US-11-174-186-15	Sequence 15, Appl
46	403	61.4	241	6	US-10-902-546-6	Sequence 6, Appl
47	400	61.0	106	7	US-11-107-028-36	Sequence 36, Appl
48	400	61.0	110	7	US-11-097-812-97	Sequence 97, Appl
49	400	61.0	111	7	US-11-097-812-112	Sequence 112, Appl
50	400	61.0	248	6	US-10-512-184-36	Sequence 36, Appl
51	400	61.0	615	6	US-10-512-184-50	Sequence 50, Appl
52	399	60.8	241	6	US-10-902-546-5	Sequence 5, Appl
53	398	60.7	108	6	US-10-507-662-45	Sequence 45, Appl
54	398	60.7	110	7	US-11-097-812-96	Sequence 96, Appl
55	398	60.7	110	7	US-11-097-812-114	Sequence 114, Appl
56	397	60.5	111	7	US-11-097-812-180	Sequence 180, Appl
57	396	60.4	237	6	US-10-073-301A-9	Sequence 9, Appl
58	396	60.4	237	7	US-11-203-137-9	Sequence 9, Appl
59	395	60.2	106	7	US-11-174-186-12	Sequence 12, Appl
60	394	60.1	111	7	US-11-097-812-107	Sequence 107, Appl
61	393	59.9	107	7	US-11-009-939-7	Sequence 7, Appl
62	393	59.9	107	7	US-11-107-028-40	Sequence 40, Appl
63	392	59.8	106	7	US-11-174-186-13	Sequence 13, Appl
64	391	59.6	106	7	US-11-174-186-10	Sequence 10, Appl
65	391	59.6	106	7	US-11-174-186-11	Sequence 11, Appl
66	391	59.6	215	7	US-11-174-186-14	Sequence 14, Appl
67	391	59.6	215	7	US-11-102-621-141	Sequence 141, Appl
68	391	59.6	215	7	US-11-166-900-2	Sequence 2, Appl
69	387	59.0	107	7	US-11-221-900-9	Sequence 9, Appl
70	387	59.0	110	7	US-11-097-812-179	Sequence 179, Appl
71	386	58.8	113	7	US-11-097-812-108	Sequence 108, Appl
72	386	58.8	290	7	US-11-032-773-957	Sequence 957, Appl
73	386	58.8	319	7	US-11-032-773-955	Sequence 955, Appl
74	383	58.4	111	7	US-11-097-812-115	Sequence 115, Appl
75	383	58.4	232	7	US-11-106-820-23	Sequence 23, Appl
76	383	58.4	232	7	US-11-190-364-21	Sequence 21, Appl
77	383	58.4	232	7	US-11-147-780-21	Sequence 21, Appl
78	381	58.1	102	7	US-11-097-812-109	Sequence 109, Appl
79	381	58.1	111	7	US-11-097-812-111	Sequence 111, Appl
80	380	57.9	110	7	US-11-097-812-98	Sequence 98, Appl
81	380	57.9	110	7	US-11-097-812-172	Sequence 172, Appl
82	379	57.8	111	7	US-11-097-812-106	Sequence 106, Appl
83	375	57.2	104	7	US-11-250-411-100	Sequence 100, Appl
84	375	57.2	105	7	US-11-250-411-108	Sequence 108, Appl
85	374	57.0	107	7	US-11-120-338-2	Sequence 2, Appl
86	374	57.0	107	7	US-11-107-028-29	Sequence 29, Appl
87	374	57.0	107	7	US-11-106-820-2	Sequence 2, Appl
88	374	57.0	107	7	US-11-143-077-2	Sequence 2, Appl
89	374	57.0	107	7	US-11-190-364-2	Sequence 2, Appl
90	374	57.0	107	7	US-11-147-780-2	Sequence 2, Appl
91	374	57.0	107	7	US-11-143-386-2	Sequence 2, Appl
92	374	57.0	213	7	US-11-120-338-13	Sequence 13, Appl
93	374	57.0	213	7	US-11-107-028-31	Sequence 31, Appl
94	374	57.0	213	7	US-11-106-820-24	Sequence 24, Appl
95	374	57.0	213	7	US-11-143-077-13	Sequence 13, Appl
96	374	57.0	213	7	US-11-143-386-13	Sequence 13, Appl
97	373	56.9	107	7	US-11-221-900-8	Sequence 8, Appl
98	369	56.2	111	7	US-11-097-812-103	Sequence 103, Appl


```
; SEQ ID NO 4
; LENGTH: 130
; TYPE: PRT
; ORGANISM: mus musculus
US-11-090-331-4

Query Match      75.3%; Score 494; DB 7; Length 130;
Best Local Similarity 79.1%; Pred. No. 6.9e-32;
Matches 102; Conservative 7; Mismatches 18; Indels 2; Gaps 1;

QY 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVVTWTCRASSSVI--YMCWNQ 58
Db 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVVTWTCRASSSVSNYLHWYQ 60

QY 59 QKFGSSPKWIYGTSTILASGVPTRFSGSGSGTSGTYSYLSITSRVEAEDAATYYCQWSSNPFT 118
Db 61 QKFGSAPNLWIYSTNLASGVPARFSGSGSGTSGTYSYLSITSSMEAEADAATYYCHQYLSRPPT 120

QY 119 FGSQTKLEI 127
Db 121 FGGGTKLEI 129

RESULT 4
US-11-090-331-8
; Sequence 8, Application US/11090331
; Publication No. US20050260210A1
; GENERAL INFORMATION:
; APPLICANT: PROTEIN DESIGN LABS, INC.
; APPLICANT: RAMAKRISHNAN, Vanitha
; APPLICANT: BHASKAR, Vinay
; APPLICANT: HO, Sun
; APPLICANT: MURRAY, Richard
; APPLICANT: LAW, Debbie
; TITLE OF INVENTION: USE OF ANTI ALPHASBETAL ANTIBODIES TO INHIBIT CANCER CELL
; TITLE OF INVENTION: PROLIFERATION
; FILE REFERENCE: 05882.0156.NPUS11
; CURRENT APPLICATION NUMBER: US/11/090,331
; CURRENT FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/556,421
; PRIOR FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/556,422
; PRIOR FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/625,049
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: 60/651,098
; PRIOR FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: 60/657,514
; PRIOR FILING DATE: 2005-02-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: chimeric antibody
US-11-090-331-8

Query Match      75.3%; Score 494; DB 7; Length 138;
Best Local Similarity 79.1%; Pred. No. 7.3e-32;
Matches 102; Conservative 7; Mismatches 18; Indels 2; Gaps 1;

QY 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVVTWTCRASSSVI--YMCWNQ 58
Db 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVVTWTCRASSSVSNYLHWYQ 60

QY 59 QKFGSSPKWIYGTSTILASGVPTRFSGSGSGTSGTYSYLSITSRVEAEDAATYYCQWSSNPFT 118
Db 61 QKFGSAPNLWIYSTNLASGVPARFSGSGSGTSGTYSYLSITSSMEAEADAATYYCHQYLSRPPT 120

QY 119 FGSQTKLEI 127
Db 121 FGGGTKLEI 129

; SEQ ID NO 129
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-125-837-21

Query Match      75.2%; Score 493; DB 7; Length 130;
Best Local Similarity 77.5%; Pred. No. 8.3e-32;
Matches 100; Conservative 10; Mismatches 17; Indels 2; Gaps 1;

QY 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVVTWTCRASSSV--YMCWNQ 58
Db 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVVTWTCRASSVTNSTYHLWFO 60

QY 59 QKFGSSPKWIYGTSTILASGVPTRFSGSGSGTSGTYSYLSITSRVEAEDAATYYCQWSSNPFT 118
Db 61 QKFGSAPNLWIYSTNLASGVPARFSGSGSGTSGTYSYLSITSSVEAEDAATYYCQYSGYPLT 120

QY 119 FGSQTKLEI 127
Db 121 FGGGTKLEI 129

RESULT 5
US-11-125-837-21
; Sequence 21, Application US/11125837
; Publication No. US20050266003A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Rong-Hwa
; APPLICANT: Chang, Chung Nan
; APPLICANT: Chen, Pei-Jiun
; APPLICANT: Huang, Chia-Chen
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 13062-011001
; CURRENT APPLICATION NUMBER: US/11/125,837
; CURRENT FILING DATE: 2005-05-10
; PRIOR APPLICATION NUMBER: US 60/569,892
; PRIOR FILING DATE: 2004-05-10
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-125-837-21

; SEQ ID NO 129
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```

```
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic protein
US-11-250-411-89

Query Match      72.4%; Score 478; DB 7; Length 126;
Best Local Similarity 78.7%; Pred. No. 1.2e-30;
Matches 100; Conservative 6; Mismatches 19; Indels 2; Gaps 1;

Qy 1 MDFQVQIFSLIISASVIMRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQOK 60
Db 1 MDFQVQIFSLIISASVIMRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQOK 60
Qy 61 PGSSPKWIVGTSTLASGVPTRFSGSGTYSLSLTISRVEADAATYCCQWSSNPFTFG 120
Db 61 SGTSFKLLIYRTSNLASGVPRFSGSGTYSLSLTISRVEADAATYCCQWSSNPFTFG 120
Qy 121 SGTKEI 127
Db 119 GGTKEI 125

RESULT 7
US-11-124-620-6
; Sequence 6, Application US/11124620
; Publication No. US20060024298A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; APPLICANT: Dang, Wei
; APPLICANT: Desjarlais, John R.
; APPLICANT: Karki, Sher Bahadur
; APPLICANT: Vafa, Omid
; APPLICANT: Hayes, Robert
; TITLE OF INVENTION: OPTIMIZED FC VARIANTS
; FILE REFERENCE: A-71386-9
; CURRENT APPLICATION NUMBER: US/11/124,620
; CURRENT FILING DATE: 2005-05-05
; PRIOR APPLICATION NUMBER: US 60/568,440
; PRIOR FILING DATE: 2004-07-15
; PRIOR APPLICATION NUMBER: US 60/589,906
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: US 60/627,026
; PRIOR FILING DATE: 2004-11-09
; PRIOR APPLICATION NUMBER: US 60/626,991
; PRIOR FILING DATE: 2004-11-10
; PRIOR APPLICATION NUMBER: US 60/627,774
; PRIOR FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US 10/822,231
; PRIOR FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: US 10/672,280
; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: US 10/379,392
; PRIOR FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-124-620-6

Query Match      72.4%; Score 475; DB 7; Length 213;
Best Local Similarity 88.6%; Pred. No. 3.1e-30;
Matches 93; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

Qy 23 QIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQOKPGSSPKWIVGTSTLASGVPTR 82
Db 1 QIVLSQSPAILFASPGETVTMTCRASSSVIYHFWQKPGSSPKWIVYATSNLASGVPVR 60
Qy 83 FSGSGTYSLSLTISRVEADAATYCCQWSSNPFTFGSGTKLEI 127
Db 61 FSGSGTYSLSLTISRVEADAATYCCQWSSNPFTFGGKLEI 105

RESULT 8
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic protein
US-11-106-820-19
; Sequence 19, Application US/11106820
; Publication No. US2006002930A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G
; APPLICANT: SEWELL, KATHRYN L.
; TITLE OF INVENTION: Treatment of Disorders
; FILE REFERENCE: P2102R1
; CURRENT APPLICATION NUMBER: US/11/106,820
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/563,227
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/565,098
; PRIOR FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 45
; SEQ ID NO 19
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-106-820-19

Query Match      72.4%; Score 475; DB 7; Length 236;
Best Local Similarity 78.9%; Pred. No. 3.3e-30;
Matches 97; Conservative 4; Mismatches 18; Indels 4; Gaps 1;

Qy 9 SFLIISASVIM----SRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQOKPGSS 64
Db 6 AFLIASMFVFSIATNAYAQIVLSQSPAILFASPGETVTMTCRASSSVIYHFWYQKPGSS 65
Qy 65 PKWIVGTSTLASGVPTRFSGSGTYSLSLTISRVEADAATYCCQWSSNPFTFGSGTK 124
Db 66 PKWIVAPSNLASGVPARFSGSGTYSLSLTISRVEADAATYCCQWSSNPFTFGAGTK 125
Qy 125 LEI 127
Db 126 LEL 128

RESULT 9
US-11-190-364-17
; Sequence 17, Application US/11190364
; Publication No. US20060024300A1
; GENERAL INFORMATION:
; APPLICANT: Adams Et Al.
; TITLE OF INVENTION: Immunoglobulin Variants and Uses Thereof
; FILE REFERENCE: P1990R3C1P1
; CURRENT APPLICATION NUMBER: US/11/190,364
; CURRENT FILING DATE: 2005-07-26
; PRIOR APPLICATION NUMBER: US 60/434,115
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: US 60/526,163
; PRIOR FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: PCT/US03/40426
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: US 11/147,780
; PRIOR FILING DATE: 2005-06-07
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 17
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is chimeric
US-11-190-364-17

Query Match      72.4%; Score 475; DB 7; Length 236;
Best Local Similarity 78.9%; Pred. No. 3.3e-30;
Matches 97; Conservative 4; Mismatches 18; Indels 4; Gaps 1;

Qy 9 SFLIISASVIM----SRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQOKPGSS 64
Db 6 AFLIISASVIM----SRGQIVLSQSPAILFASPGETVTMTCRASSSVIYHFWYQKPGSS 64
```

Db 6 AFLASMFVSIATNAYAQIVLSQSPAILSGPGEKVTMTCRASSSVSYMHYQKQPGSS 65
Qy 65 PKWIYGTSTLASGVPTRFSGSGTYSYLTISRVEADAATYCCQWSSNPFTFGSGTK 124
Db 66 PKWIYAPSNLASGVPARFSGSGTYSYLTISRVEADAATYCCQWSSNPFTFGAGTK 125

Qy 125 LEI 127
Db 126 LEL 128

RESULT 10

US-11-147-780-17

; Sequence 17, Application US/11147780
; Publication No. US20060034835A1
; GENERAL INFORMATION:
; APPLICANT: Adams Et Al.
; TITLE OF INVENTION: Immunoglobulin Variants and Uses Thereof
; FILE REFERENCE: P1990R3C1
; CURRENT APPLICATION NUMBER: US/11/147,780
; CURRENT FILING DATE: 2005-06-07
; PRIOR APPLICATION NUMBER: US 60/434,115
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: US 60/526,163
; PRIOR FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: PCT/US03/40426
; PRIOR FILING DATE: 2003-12-16
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 17
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is chimeric

US-11-147-780-17

Query Match 72.4%; Score 475; DB 7; Length 236;
Best Local Similarity 78.9%; Pred. No. 3.3e-30;
Matches 97; Conservative 4; Mismatches 18; Indels 4; Gaps 1;

Qy 9 SFLLISASVIM---SRGQIVLSQSPAILSPGEGTVMTCRASSSVSYMHYQKQPGSS 64
Db 6 AFLASMFVSIATNAYAQIVLSQSPAILSGPGEKVTMTCRASSSVSYMHYQKQPGSS 65

Qy 65 PKWIYGTSTLASGVPTRFSGSGTYSYLTISRVEADAATYCCQWSSNPFTFGSGTK 124
Db 66 PKWIYAPSNLASGVPARFSGSGTYSYLTISRVEADAATYCCQWSSNPFTFGAGTK 125

Qy 125 LEI 127
Db 126 LEL 128

RESULT 11

US-11-107-028-28

; Sequence 28, Application US/11107028
; Publication No. US20050276803A1
; GENERAL INFORMATION:
; APPLICANT: CHAN, ANDREW C.
; APPLICANT: GONG, QIAN
; APPLICANT: MARTIN, FLAVIUS
; TITLE OF INVENTION: Method for Augmenting B Cell Depletion
; FILE REFERENCE: P2112R1
; CURRENT APPLICATION NUMBER: US/11/107,028
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/563,263
; PRIOR FILING DATE: 2004-04-16
; NUMBER OF SEQ ID NOS: 52
; SEQ ID NO 28
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Mus musculus

US-11-107-028-28

Query Match 71.6%; Score 470; DB 7; Length 106;
Best Local Similarity 87.6%; Pred. No. 4.2e-30;
Matches 92; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

Qy 23 QIVLSQSPAILSPGEGTVMTCRASSSVYMCWNOQKPGSSPKPWYIGTSTLASGVPTR 82
Db 1 QIVLSQSPAILSPGEGTVMTCRASSSVYMCWNOQKPGSSPKPWYIGTSTLASGVPAR 60

Qy 83 FSGSGGTYSYLTISRVEADAATYCCQWSSNPFTFGSGTKLEI 127
Db 61 FSGSGGTYSYLTISRVEADAATYCCQWSSNPFTFGAGTKLEL 105

RESULT 12

US-11-120-338-1

; Sequence 1, Application US/11120338
; Publication No. US20050271658A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G.
; APPLICANT: GREWAL, IQBAL S.
; APPLICANT: WALICKE, PATRICIA A.
; TITLE OF INVENTION: PREVENTING AUTOIMMUNE DISEASE
; FILE REFERENCE: P2079R2
; CURRENT APPLICATION NUMBER: US/11/120,338
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: US 60/568,460
; PRIOR FILING DATE: 2004-05-05
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 1
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus musculus

US-11-120-338-1

Query Match 71.6%; Score 470; DB 7; Length 107;
Best Local Similarity 87.6%; Pred. No. 4.2e-30;
Matches 92; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

Qy 23 QIVLSQSPAILSPGEGTVMTCRASSSVYMCWNOQKPGSSPKPWYIGTSTLASGVPTR 82
Db 1 QIVLSQSPAILSPGEGTVMTCRASSSVYMCWNOQKPGSSPKPWYIGTSTLASGVPAR 60

Qy 83 FSGSGGTYSYLTISRVEADAATYCCQWSSNPFTFGSGTKLEI 127
Db 61 FSGSGGTYSYLTISRVEADAATYCCQWSSNPFTFGAGTKLEL 105

RESULT 13

US-11-106-820-1

; Sequence 1, Application US/11106820
; Publication No. US20060002930A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G
; APPLICANT: SEWELL, KATHRYN L.
; TITLE OF INVENTION: Treatment of Disorders
; FILE REFERENCE: P2102R1
; CURRENT APPLICATION NUMBER: US/11/106,820
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/563,227
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/565,098
; PRIOR FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 45
; SEQ ID NO 1
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus musculus

US-11-106-820-1

Query Match 71.6%; Score 470; DB 7; Length 107;
Best Local Similarity 87.6%; Pred. No. 4.2e-30;
Matches 92; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

Qy	23	QIVLSQPAILFASPGETVTMTCRASSSVIYMCNQKQPGSSPKWIIYGTSTLASGVPTR	82
Db	1	QIVLSQPAILSASPGKVTMTCRASSSVYMHWTQKQPGSSPKWIIYAPNSLASGVPTAR	60
Qy	83	FSGSGSGTSYSLTISRVEAEDATYYCQOWSSNPPTFGSGTKLEI	127
Db	61	FSGSGSGTSYSLTISRVEAEDATYYCQOWSFNPPTFGAGTKLEL	105

```

RESULT 14
US-11-143-077-1
; Sequence 1, Application US/11143077
; Publication No. US2006004295A1
; GENERAL INFORMATION:
; APPLICANT: Brunetta, Paul G.
; TITLE OF INVENTION: METHOD FOR TREATING LUPUS
; FILE REFERENCE: P2133R1
; CURRENT APPLICATION NUMBER: US/11/143,077
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US 60/577,235
; PRIOR FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 60/617,997
; PRIOR FILING DATE: 2004-10-11
; NUMBER OF SEQ ID NOS: 24
; SEQ ID NO 1
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-143-077-1

```

```

RESULT 15
US-11-190-364-1
; Sequence 1, Application US/11190364
; Publication No. US20060024300A1
; GENERAL INFORMATION:
; APPLICANT: Adams ET AL.
; TITLE OF INVENTION: Immunoglobulin Variants and Uses Thereof
; FILE REFERENCE: P1990R3C1P1
; CURRENT APPLICATION NUMBER: US/11/190,364
; CURRENT FILING DATE: 2005-07-26
; PRIOR APPLICATION NUMBER: US 60/434,115
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: US 60/526,163
; PRIOR FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: PCT/US03/40426
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: US 11/147,780
; PRIOR FILING DATE: 2005-06-07
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 1
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-190-364-1

```

[illegible]

```

RESULT 16
US-11-147-780-1
; Sequence 1, Application US/11147780
; Publication No. US20060034835A1
; GENERAL INFORMATION:
; APPLICANT: Adams ET AL
; TITLE OF INVENTION: Immunoglobulin Variants and Uses Thereof
; FILE REFERENCE: P1990R3C1
; CURRENT APPLICATION NUMBER: US/11/147,780
; CURRENT FILING DATE: 2005-06-07
; PRIOR APPLICATION NUMBER: US 60/434,115
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: US 60/526,163
; PRIOR FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: PCT/US03/40426
; PRIOR FILING DATE: 2003-12-16
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 1
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-147-780-1

```

RESULT 17
US-11-143-386-1
; Sequence 1, Application US/11143386
; Publication No. US20060051345A1
; GENERAL INFORMATION:
; APPLICANT: FROHNA, PAUL A.
; TITLE OF INVENTION: METHOD FOR TREATING MULTIPLE SCLEROSIS
; FILE REFERENCE: P2134R1
; CURRENT APPLICATION NUMBER: US/11/143,386
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US 60/576,993
; PRIOR FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 1
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-143-386-1

	Query Match	71.6%;	Score 470;	DB 7;	Length 107;
	Best Local Similarity	87.6%;	Pred. No. 4.2e-30;		
	Matches 92;	Conservative 2;	Mismatches 11;	Indels 0;	Gaps 0
Qy	23	QIVLSQSPAILFASPGETVTWTCRASSSVIYMCWNQKPGSSKPEWYIGTSTLGSVQTR	82		
Db	1	QIVLSQSPAILFASPGKVTWTCRASSSVSYMHYQKPGSSKPEWYIAPNSLGSVQAR	60		
Qy	83	FSGSGSGTYSLTIISRVAEADAATYYCQWSSNPFPTFGSGTKLRI	127		

Db 61 FSGSGSGTSYSLTISRVEADATYYCQWSSNPPTFGAGTKLEI 105
|||||:|||||:
RESULT 18
US-11-193-440-89
; Sequence 89, Application US/11193440
; Publication No. US20060002939A1
; GENERAL INFORMATION:
; APPLICANT: Fischer, Gerald W.
; Schuman, Richard P.
; Wong, King
; Stinson, Jeffrey L.
TITLE OF INVENTION: OPSONIC AND PROTECTIVE MONOCLONAL AND
CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF GRAM
POSITIVE BACTERIA
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: FINNEGAN, HENDERSON, PARABOW, GARRETT &
DUNNER, LLP
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/193,440
FILING DATE: 01-Aug-2005
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/893,615
FILING DATE: 29-Jun-2001
ATTORNEY/AGENT INFORMATION:
NAME: Einaudi, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCES/DOCKET NUMBER: 04995.0041-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 89:
US-11-193-440-89
Query Match 71.2%; Score 467; DB 7; Length 106;
Best Local Similarity 88.8%; Pred. No. 7.1e-30;
Matches 93; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
QY 23 QIVLSQPAILFASPGETVMTTCRASSSVIYMCWNQKPGSSPKPKWIYGTSTLASGVPT 82
Db 1 QIVLSQPAILSASPGKVTMTTCRASSSVYHMYQKPGSSPKPKWISATSNLASGVPAR 60
QY 83 FSGSGSGTSYSLTISRVEADATYYCQWSSNPPTFGAGTKLEI 127
Db 61 FSGSGSGTSYSLTISRVEADATYYCQWSSNPPTFGAGTKLEI 105
RESULT 19
US-11-250-411-92
; Sequence 92, Application US/11250411
; Publication No. US20060034838A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: ITO, MIKITO
; APPLICANT: HANAI, NOBUO

APPLICANT: KAWADA, YOKO
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: SHIBUYA, MASABUMI
TITLE OF INVENTION: ANTI-HUMAN VEGF RECEPTOR FLT-1 MONOCLONAL ANTIBODY
FILE REFERENCE: 249-107
CURRENT APPLICATION NUMBER: US/11/250,411
CURRENT FILING DATE: 2005-10-17
PRIOR APPLICATION NUMBER: US/09/453,718
PRIOR FILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: 09/315,051
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/119,014
PRIOR FILING DATE: 1998-07-20
PRIOR APPLICATION NUMBER: PCT/JP97/04259
PRIOR FILING DATE: 1997-11-21
NUMBER OF SEQ ID NOS: 111
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 92
LENGTH: 128
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic protein
US-11-250-411-92
Query Match 70.4%; Score 462; DB 7; Length 128;
Best Local Similarity 72.4%; Pred. No. 2e-29;
Matches 92; Conservative 13; Mismatches 22; Indels 0; Gaps 0;
QY 1 MDPQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVMTTCRASSSVIYMCWNQK 60
Db 1 MDPQVQIFSFLLISASVIMSRGDIQMTQSPSLASVGRVITITCSASSSVYHMYQK 60
QY 61 PGSSPKPKWIYGTSTLASGVPTFRFSGSGTSYSLTISRVEADATYYCQWSSNPPTFG 120
Db 61 PKAPKLLIYDSKLPSPGVPRFSGSGSGTDFLLISSLPQDPFATYYCQWSSNPPTFG 120
QY 121 SGTGLEI 127
Db 121 QGTKEI 127
RESULT 20
US-11-107-028-34
; Sequence 34, Application US/11107028
; Publication No. US20050276803A1
; GENERAL INFORMATION:
; APPLICANT: CHAN, ANDREW C.
; APPLICANT: GONG, QIAN
TITLE OF INVENTION: Method for Augmenting B Cell Depletion
FILE REFERENCE: P2112R1
CURRENT APPLICATION NUMBER: US/11/107,028
CURRENT FILING DATE: 2005-04-15
PRIOR APPLICATION NUMBER: US 60/563,263
PRIOR FILING DATE: 2004-04-16
NUMBER OF SEQ ID NOS: 52
SEQ ID NO 34
LENGTH: 106
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: sequence is synthesized
US-11-107-028-34
Query Match 70.3%; Score 461; DB 7; Length 106;
Best Local Similarity 86.5%; Pred. No. 2.1e-29;
Matches 90; Conservative 3; Mismatches 11; Indels 0; Gaps 0;
QY 24 IVLQSPAILFASPGETVMTTCRASSSVIYMCWNQKPGSSPKPKWIYGTSTLASGVPT 83
Db 2 IQLTQSPAILSASPGKVTMTTCRASSSVYHMYQKPGSSPKPKWIYATSNLASGVPT 61

Qy 84 SGSGGTSYSLTISRVEADATYCCQWSSNPPTGSGTKLEI 127
Db 62 SGSGGTSYSLTISRVEADATYCCQWTSNPPTFGGTKLEI 105

Search completed: March 20, 2006, 07:32:42
Job time : 3.37968 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 20, 2006, 07:31:52 ; Search time 22.5444 Seconds
(without alignments)
2353.772 Million cell updates/sec

Title: US-10-687-035-33

Perfect score: 656

Sequence: 1 MDPQVQIFSLISASVMS.....YCOQWSSNPFPGSGTKLEI 127

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 100 summaries

Database :

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:**
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:**
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:**
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:**
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:**
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	656	100.0	127	5	US-10-687-035-33
2	578	88.1	129	5	US-10-723-003-38
3	578	88.1	129	6	US-11-004-639-38
4	578	88.1	235	5	US-10-723-003-42
5	578	88.1	235	6	US-11-004-639-42
6	572	87.2	128	3	US-09-905-928-4
7	572	87.2	128	4	US-10-096-364-4
8	572	87.2	128	4	US-10-238-681-7
9	572	87.2	128	4	US-10-411-037-60
10	572	87.2	128	4	US-10-411-026-60
11	572	87.2	128	4	US-10-410-962-60
12	572	87.2	128	4	US-10-411-049-60
13	572	87.2	128	4	US-10-327-663-12
14	572	87.2	128	4	US-10-410-930-60
15	572	87.2	128	4	US-10-410-997-60
16	572	87.2	128	4	US-10-411-012-60
17	572	87.2	128	4	US-10-287-994-60
18	572	87.2	128	4	US-10-410-913-60
19	572	87.2	128	5	US-10-410-980-60
20	572	87.2	128	5	US-10-410-897-60
21	572	87.2	128	5	US-10-492-361-60
22	572	87.2	128	5	US-10-956-039-4
23	566	86.3	128	5	US-10-941-768A-46
24	566	86.3	266	4	US-10-207-655-11
25	566	86.3	266	4	US-10-053-530-11
26	566	86.3	266	6	US-11-089-511-11
27	566	86.3	266	6	US-11-089-190-11
28	566	86.3	266	6	US-11-088-570-11
29	566	86.3	266	6	US-11-088-737-11
30	566	86.3	266	6	US-11-088-569-11
31	566	86.3	266	6	US-11-088-693-11
32	566	86.3	266	6	US-11-089-367-11
33	566	86.3	266	6	US-11-089-368-11
34	566	86.3	267	5	US-10-627-556-214
35	566	86.3	268	5	US-10-627-556-212
36	566	86.3	268	5	US-10-627-556-244
37	566	86.3	422	4	US-10-207-655-34
38	566	86.3	422	4	US-10-207-655-152
39	566	86.3	422	4	US-10-053-530-34
40	566	86.3	422	5	US-10-627-556-693
41	566	86.3	422	6	US-11-089-511-34
42	566	86.3	422	6	US-11-089-190-34
43	566	86.3	422	6	US-11-088-737-34
44	566	86.3	422	6	US-11-088-569-34
45	566	86.3	422	6	US-11-088-693-34
46	566	86.3	422	6	US-11-089-367-34
47	566	86.3	422	6	US-11-089-368-34
48	566	86.3	422	6	US-10-207-655-33
49	566	86.3	482	4	US-10-207-655-150
50	566	86.3	482	4	US-10-053-530-33
51	566	86.3	482	5	US-10-627-556-691
52	566	86.3	482	6	US-11-089-511-33
53	566	86.3	482	6	US-11-089-190-33
54	566	86.3	482	6	US-11-088-570-33
55	566	86.3	482	6	US-11-088-737-33
56	566	86.3	482	6	US-11-088-693-33
57	566	86.3	482	6	US-11-089-367-33
58	566	86.3	482	6	US-11-088-569-33
59	566	86.3	482	6	US-11-089-368-33
60	566	86.3	482	6	US-11-089-368-33
61	566	86.3	498	4	US-10-207-655-235
62	566	86.3	498	5	US-10-627-556-22
63	566	86.3	499	4	US-10-207-655-15
64	566	86.3	499	4	US-10-207-655-16
65	566	86.3	499	4	US-10-207-655-17
66	566	86.3	499	4	US-10-207-655-148
67	566	86.3	499	4	US-10-053-530-15
68	566	86.3	499	4	US-10-053-530-16
69	566	86.3	499	4	US-10-053-530-17
70	566	86.3	499	5	US-10-627-556-689
71	566	86.3	499	6	US-11-089-511-15
72	566	86.3	499	6	US-11-089-511-16
73	566	86.3	499	6	US-11-089-511-17
74	566	86.3	499	6	US-11-089-190-15
75	566	86.3	499	6	US-11-089-190-16
76	566	86.3	499	6	US-11-089-190-17
77	566	86.3	499	6	US-11-088-570-15
78	566	86.3	499	6	US-11-088-570-16
79	566	86.3	499	6	US-11-088-570-17
80	566	86.3	499	6	US-11-088-737-15
81	566	86.3	499	6	US-11-088-737-16
82	566	86.3	499	6	US-11-088-737-17
83	566	86.3	499	6	US-11-088-569-15
84	566	86.3	499	6	US-11-088-569-16
85	566	86.3	499	6	US-11-088-569-17
86	566	86.3	499	6	US-11-088-693-15
87	566	86.3	499	6	US-11-088-693-16
88	566	86.3	499	6	US-11-088-693-17
89	566	86.3	499	6	US-11-089-367-15
90	566	86.3	499	6	US-11-089-367-16
91	566	86.3	499	6	US-11-089-367-17
92	566	86.3	499	6	US-11-089-368-15
93	566	86.3	499	6	US-11-089-368-16
94	566	86.3	499	6	US-11-089-368-17
95	566	86.3	500	4	US-10-207-655-240
96	566	86.3	500	4	US-10-207-655-274
97	566	86.3	500	4	US-10-207-655-352
98	566	86.3	500	4	US-10-207-655-385
99	566	86.3	500	4	US-10-207-655-386
100	566	86.3	500	4	US-10-207-655-387

ALIGNMENTS

```
RESULT 1
US-10-687-035-33
; Sequence 33, Application US/10687035
; Publication No. US20050064518A1
; GENERAL INFORMATION:
; APPLICANT: Albione, Earl F.
; TITLE OF INVENTION: ANTIBODIES THAT BIND CELL-ASSOCIATED
; TITLE OF INVENTION: CA 125/0772P AND METHODS OF USE THEREOF
; FILE REFERENCE: 6750-214-999
; CURRENT APPLICATION NUMBER: US/10/687,035
; CURRENT FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: 60/485,986
; PRIOR FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: 60/418,828
; PRIOR FILING DATE: 2003-10-12
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 776.1 light chain polypeptide variable region (776.1L)
US-10-687-035-33

Query Match      100.0%; Score 656; DB 5; Length 127;
Best Local Similarity 100.0%; Pred. No. 5.9e-49;
Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYCMNQOK 60
Db      1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYCMNQOK 60

Qy      61 PGSSPKPWYGTSTLASGVPTFRFGSGSGTSYSLTISRVEADAATYCCQWSSNPFTFG 120
Db      61 PGSSPKPWYGTSTLASGVPTFRFGSGSGTSYSLTISRVEADAATYCCQWSSNPFTFG 120

Qy      121 SGTKLEI 127
Db      121 SGTKLEI 127

RESULT 2
US-10-723-003-38
; Sequence 38, Application US/10723003
; Publication No. US20040254108A1
; GENERAL INFORMATION:
; APPLICANT: MA, Jing
; APPLICANT: GUO, Yajun
; TITLE OF INVENTION: PREPARATION AND APPLICATION OF
; TITLE OF INVENTION: ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS
; FILE REFERENCE: 54906200200
; CURRENT APPLICATION NUMBER: US/10/723,003
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: CN 2003101199300
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: CN 031292909
; PRIOR FILING DATE: 2003-06-13
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-723-003-38

Query Match      88.1%; Score 578; DB 5; Length 129;
Best Local Similarity 90.6%; Pred. No. 3.2e-42;
Matches 115; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

Qy      1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYCMNQOK 60
Db      1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYCMNQOK 60

Qy      61 PGSSPKPWYGTSTLASGVPTFRFGSGSGTSYSLTISRVEADAATYCCQWSSNPFTFG 120
Db      61 PGSSPKPWYGTSTLASGVPTFRFGSGSGTSYSLTISRVEADAATYCCQWSSNPFTFG 120

Qy      121 SGTKLEI 127
Db      121 SGTKLEI 127

RESULT 3
US-11-004-639-38
; Sequence 38, Application US/11004639
; Publication No. US20050232931A1
; GENERAL INFORMATION:
; APPLICANT: MA, Jing
; APPLICANT: GUO, Yajun
; TITLE OF INVENTION: PREPARATION AND APPLICATION OF
; TITLE OF INVENTION: ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS
; FILE REFERENCE: 54906200200
; CURRENT APPLICATION NUMBER: US/11/004,639
; CURRENT FILING DATE: 2004-12-02
; PRIOR APPLICATION NUMBER: US/10/723,003
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: CN 2003101199300
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: CN 031292909
; PRIOR FILING DATE: 2003-06-13
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-004-639-38

Query Match      88.1%; Score 578; DB 6; Length 129;
Best Local Similarity 90.6%; Pred. No. 3.2e-42;
Matches 115; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

Qy      1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYCMNQOK 60
Db      1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYCMNQOK 60

Qy      61 PGSSPKPWYGTSTLASGVPTFRFGSGSGTSYSLTISRVEADAATYCCQWSSNPFTFG 120
Db      61 PGSSPKPWYGTSTLASGVPTFRFGSGSGTSYSLTISRVEADAATYCCQWSSNPFTFG 120

Qy      121 SGTKLEI 127
Db      121 SGTKLEI 127

RESULT 4
US-10-723-003-42
; Sequence 42, Application US/10723003
; Publication No. US20040254108A1
; GENERAL INFORMATION:
; APPLICANT: MA, Jing
; APPLICANT: GUO, Yajun
; TITLE OF INVENTION: PREPARATION AND APPLICATION OF
; TITLE OF INVENTION: ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS
; FILE REFERENCE: 54906200200
; CURRENT APPLICATION NUMBER: US/10/723,003
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: CN 2003101199300
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: CN 031292909
; PRIOR FILING DATE: 2003-06-13
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-723-003-38

Query Match      88.1%; Score 578; DB 5; Length 129;
```

```
Best Local Similarity 90.6%; Pred. No. 3.2e-42;
Matches 115; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

Qy      1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYCMNQOK 60
Db      1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYCMNQOK 60

Qy      61 PGSSPKPWYGTSTLASGVPTFRFGSGSGTSYSLTISRVEADAATYCCQWSSNPFTFG 120
Db      61 PGSSPKPWYGTSTLASGVPTFRFGSGSGTSYSLTISRVEADAATYCCQWSSNPFTFG 120

Qy      121 SGTKLEI 127
Db      121 SGTKLEI 127

RESULT 3
US-11-004-639-38
; Sequence 38, Application US/11004639
; Publication No. US20050232931A1
; GENERAL INFORMATION:
; APPLICANT: MA, Jing
; APPLICANT: GUO, Yajun
; TITLE OF INVENTION: PREPARATION AND APPLICATION OF
; TITLE OF INVENTION: ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS
; FILE REFERENCE: 54906200200
; CURRENT APPLICATION NUMBER: US/11/004,639
; CURRENT FILING DATE: 2004-12-02
; PRIOR APPLICATION NUMBER: US/10/723,003
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: CN 2003101199300
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: CN 031292909
; PRIOR FILING DATE: 2003-06-13
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-004-639-38

Query Match      88.1%; Score 578; DB 6; Length 129;
Best Local Similarity 90.6%; Pred. No. 3.2e-42;
Matches 115; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

Qy      1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYCMNQOK 60
Db      1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYCMNQOK 60

Qy      61 PGSSPKPWYGTSTLASGVPTFRFGSGSGTSYSLTISRVEADAATYCCQWSSNPFTFG 120
Db      61 PGSSPKPWYGTSTLASGVPTFRFGSGSGTSYSLTISRVEADAATYCCQWSSNPFTFG 120

Qy      121 SGTKLEI 127
Db      121 SGTKLEI 127

RESULT 4
US-10-723-003-42
; Sequence 42, Application US/10723003
; Publication No. US20040254108A1
; GENERAL INFORMATION:
; APPLICANT: MA, Jing
; APPLICANT: GUO, Yajun
; TITLE OF INVENTION: PREPARATION AND APPLICATION OF
; TITLE OF INVENTION: ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS
; FILE REFERENCE: 54906200200
; CURRENT APPLICATION NUMBER: US/10/723,003
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: CN 2003101199300
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: CN 031292909
; PRIOR FILING DATE: 2003-11-25
```

PRIOR APPLICATION NUMBER: CN 031292909
PRIOR FILING DATE: 2003-06-13
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 42
LENGTH: 235
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Construct
US-10-723-003-42

Query Match 88.1%; Score 578; DB 5; Length 235;
Best Local Similarity 90.6%; Pred. No. 5.9e-42;
Matches 115; Conservative 2; Mismatches 10; Indels 0; Gaps 0;
QY 1 MDFQVQIFSPLLISASVIMSRGQIVLSQSPAILFASPGETVTWTCRASSSVIYMCWNQOK 60
DB 1 MDFQVQIFSPLLISASVIMSRGQIVLSQSPAILFASPGETVTWTCRASSSVIYHFWQOK 60
QY 61 PGSSPKPMIYGTSTLASGVPTFRSGSGSGTYSLSITSRVEADAATYCCQWSSNPFTFG 120
DB 61 PGSSPKPMIYATSNLASGVPTFRSGSGSGTYSLSITSRVEADAATYCCQWTSNPFTFG 120
QY 121 SGTKEI 127
DB 121 GGTKEI 127

RESULT 5

US-11-004-639-42
Sequence 42, Application US/11004639
Publication No. US20050232931A1
GENERAL INFORMATION:
APPLICANT: MA, Jing
APPLICANT: GUO, Yajun
TITLE OF INVENTION: PREPARATION AND APPLICATION OF
FILE REFERENCE: 54906200200
CURRENT APPLICATION NUMBER: US/11/004,639
CURRENT FILING DATE: 2004-12-02
PRIOR APPLICATION NUMBER: US/10/723,003
PRIOR FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: CN 2003101199300
PRIOR FILING DATE: 2003-11-25
PRIOR APPLICATION NUMBER: CN 031292909
PRIOR FILING DATE: 2003-06-13
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 42
LENGTH: 235
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Construct
US-11-004-639-42

Query Match 88.1%; Score 578; DB 6; Length 235;
Best Local Similarity 90.6%; Pred. No. 5.9e-42;
Matches 115; Conservative 2; Mismatches 10; Indels 0; Gaps 0;
QY 1 MDFQVQIFSPLLISASVIMSRGQIVLSQSPAILFASPGETVTWTCRASSSVIYMCWNQOK 60
DB 1 MDFQVQIFSPLLISASVIMSRGQIVLSQSPAILFASPGETVTWTCRASSSVIYHFWQOK 60
QY 61 PGSSPKPMIYGTSTLASGVPTFRSGSGSGTYSLSITSRVEADAATYCCQWSSNPFTFG 120
DB 61 PGSSPKPMIYATSNLASGVPTFRSGSGSGTYSLSITSRVEADAATYCCQWTSNPFTFG 120
QY 121 SGTKEI 127
DB 121 GGTKEI 127

RESULT 6

US-09-905-928-4
Sequence 4, Application US/09905928
Publication No. US20030021781A1
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
APPLICANT: Hanna, Nabil
APPLICANT: Leonard, John E.
APPLICANT: Newman, Roland A.
APPLICANT: Reff, Mitchell E.
APPLICANT: Rastetter, William H.
TITLE OF INVENTION: Therapeutic Application of Chimeric and
TITLE OF INVENTION: Radiolabeled Antibodies to Human B Lymphocyte Restricted
TITLE OF INVENTION: Differentiation Antigen for the Treatment of B-Cell Lymphoma
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince St.
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/905,928
FILING DATE: 17-JUL-2001
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/475,813
FILING DATE: 07-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/149,099
FILING DATE: 03-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,891
FILING DATE: 13-NOV-1992
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-158
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-905-928-4

Query Match 87.2%; Score 572; DB 3; Length 128;
Best Local Similarity 89.8%; Pred. No. 1e-41;
Matches 114; Conservative 2; Mismatches 11; Indels 0; Gaps 0;
QY 1 MDFQVQIFSPLLISASVIMSRGQIVLSQSPAILFASPGETVTWTCRASSSVIYMCWNQOK 60
DB 1 MDFQVQIFSPLLISASVIMSRGQIVLSQSPAILFASPGETVTWTCRASSSVIYHFWQOK 60
QY 61 PGSSPKPMIYGTSTLASGVPTFRSGSGSGTYSLSITSRVEADAATYCCQWSSNPFTFG 120
DB 61 PGSSPKPMIYATSNLASGVPTFRSGSGSGTYSLSITSRVEADAATYCCQWTSNPFTFG 120
QY 121 SGTKEI 127
DB 121 GGTKEI 127

RESULT 7
US-10-096-964-4
; Sequence 4, Application US/10096964
; Publication No. US20030082172A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; Hanna, Nabil
; Leonard, John E.
; Newman, Roland A.
; Reff, Mitchell E.
; Rastetter, William H.
; TITLE OF INVENTION: Therapeutic Application of Chimeric and
; Radiolabeled Antibodies to Human B Lymphocyte Restricted
; Differentiation Antigen for the Treatment of B-Cell Lymphoma
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/096,964
; FILING DATE: 14-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,813
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/149,099
; FILING DATE: 03-NOV-1993
; APPLICATION NUMBER: US 07/978,891
; FILING DATE: 13-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-158
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-096-964-4

Query Match 87.2%; Score 572; DB 4; Length 128;
Best Local Similarity 89.8%; Pred. No. 1e-41;
Matches 114; Conservative 2; Mismatches 11; Indels 0; Gaps 0;
Qy 1 MDFQVQIFPSLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQOK 60
Db 1 MDFQVQIIISFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYHWFQOK 60
Qy 61 PGSSPKPMIYGTSTLAGVPTFRFGSGSGTYSITISRVEADAATYYCQOWSNPPTFG 120
Db 61 PGSSPKPMIYATSNLASGVPVRFSGSGGTYSITISRVEADAATYYCQOWTSNPPTFG 120
Qy 121 SGTKLEI 127
Db 121 GGTKLEI 127

RESULT 8

US-10-238-681-7
; Sequence 7, Application US/10238681
; Publication No. US20030147885A1
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, DARRELL R.
; APPLICANT: HANNA, NABIL
; APPLICANT: LEONARD, JOHN E.
; APPLICANT: NEWMAN, ROLAND A.
; APPLICANT: REFF, MITCHELL E.
; APPLICANT: RASTETTER, WILLIAM H.
; TITLE OF INVENTION: THERAPEUTIC APPLICATION OF CHIMERIC AND RADIOLABELED
; ANTIBODIES TO HUMAN B LYMPHOCYTE RESTRICTED
; DIFFERENTIATION ANTIGEN FOR TREATMENT OF B CELL
; TITLE OF INVENTION: LYMPHOMA
; FILE REFERENCE: 37003/0291808
; CURRENT APPLICATION NUMBER: US/10/238,681
; CURRENT FILING DATE: 2002-09-11
; PRIOR APPLICATION NUMBER: 08/921,060
; PRIOR FILING DATE: 1997-08-29
; PRIOR APPLICATION NUMBER: 08/149,099
; PRIOR FILING DATE: 1993-11-03
; PRIOR APPLICATION NUMBER: 07/978,891
; PRIOR FILING DATE: 1992-11-13
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Murine sp.
US-10-238-681-7

Query Match 87.2%; Score 572; DB 4; Length 128;
Best Local Similarity 89.8%; Pred. No. 1e-41;
Matches 114; Conservative 2; Mismatches 11; Indels 0; Gaps 0;
Qy 1 MDFQVQIFPSLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQOK 60
Db 1 MDFQVQIIISFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYHWFQOK 60
Qy 61 PGSSPKPMIYGTSTLAGVPTFRFGSGSGTYSITISRVEADAATYYCQOWSNPPTFG 120
Db 61 PGSSPKPMIYATSNLASGVPVRFSGSGGTYSITISRVEADAATYYCQOWTSNPPTFG 120
Qy 121 SGTKLEI 127
Db 121 GGTKLEI 127

RESULT 9
US-10-411-037-60
; Sequence 60, Application US/10411037
; Publication No. US2004004346A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DePree, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bove, Caryn
; TITLE OF INVENTION: ALPHA GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA
; FILE REFERENCE: 040853-01-5082
; CURRENT APPLICATION NUMBER: US/10/411,037
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25


```
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 60
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-411-037-60

Query Match      87.2%; Score 572; DB 4; Length 128;
Best Local Similarity 89.8%; Pred. No. 1e-41;
Matches 114; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

QY 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILPASGETVVTWTCRASSSVIYMCWNQOK 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 MDFQVQIISFLLISASVIMSRGQIVLSQSPAILPASGPKVVTWTCRASSSVIYHWFQOK 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 PGSSPKPWYGTSTLASGVPTRPSGSGTSSYSLTISRVEADAATYCCQWSSNPPTFG 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 PGSSPKPWYATSNLASGVPRFSGSGTSSYSLTISRVEADAATYCCQWSSNPPTFG 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 121 SGTGLEI 127
   |||||
Db 121 GGTGLEI 127
   |||||

RESULT 11
US-10-410-962-60
; Sequence 60, Application US/10410962
; Publication No. US20040077836A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryn
; TITLE OF INVENTION: GRANULOCYTE COLONY STIMULATING FACTOR: REMODELING AND
; FILE REFERENCE: 040853-01-5054
; CURRENT APPLICATION NUMBER: US/10/410,962
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 60
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-410-962-60

Query Match      87.2%; Score 572; DB 4; Length 128;
Best Local Similarity 89.8%; Pred. No. 1e-41;
Matches 114; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

QY 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILPASGETVVTWTCRASSSVIYMCWNQOK 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 MDFQVQIISFLLISASVIMSRGQIVLSQSPAILPASGPKVVTWTCRASSSVIYHWFQOK 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 PGSSPKPWYGTSTLASGVPTRPSGSGTSSYSLTISRVEADAATYCCQWSSNPPTFG 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 PGSSPKPWYATSNLASGVPRFSGSGTSSYSLTISRVEADAATYCCQWSSNPPTFG 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 121 SGTGLEI 127
   |||||
Db 121 GGTGLEI 127
   |||||

RESULT 12
US-10-411-049-60
; Sequence 60, Application US/10411049
; Publication No. US20040082026A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DePrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bove, Caryn
; TITLE OF INVENTION: INTERFERON ALPHA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
; FILE REFERENCE: 040853-01-5055
; CURRENT APPLICATION NUMBER: US/10/411,049
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 60
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-411-049-60

Query Match      87.2%; Score 572; DB 4; Length 128;
Best Local Similarity 89.8%; Pred. No. 1e-41;
Matches 114; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

Qy 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQOK 60
Db 1 MDFQVQIISFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYHWFQOK 60
Qy 61 PGSSPKPWIIYGTSLASGVPTRFSGSGSGTSYSLTISRVEADAATYYCQWSSNPPTFG 120
Db 61 PGSSPKPWIIYATSLASGVPTRFSGSGSGTSYSLTISRVEADAATYYCQWTSNPPTFG 120
Qy 121 SGTKLEI 127
Db 121 GGTKLEI 127

RESULT 14
US-10-410-930-60
; Sequence 60, Application US/10410930
; Publication No. US20040115168A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DePrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bove, Caryn
; TITLE OF INVENTION: INTERFERON BETA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
; FILE REFERENCE: 040853-01-5056
; CURRENT APPLICATION NUMBER: US/10/410,930
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 60
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-410-930-60

Query Match      87.2%; Score 572; DB 4; Length 128;
Best Local Similarity 89.8%; Pred. No. 1e-41;
Matches 114; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

Qy 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQOK 60
Db 1 MDFQVQIISFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYHWFQOK 60
Qy 61 PGSSPKPWIIYGTSLASGVPTRFSGSGSGTSYSLTISRVEADAATYYCQWSSNPPTFG 120
Db 61 PGSSPKPWIIYATSLASGVPTRFSGSGSGTSYSLTISRVEADAATYYCQWTSNPPTFG 120
Qy 121 SGTKLEI 127
Db 121 GGTKLEI 127

RESULT 13
US-10-327-663-12
; Sequence 12, Application US/10327663
; Publication No. US20040093621A1
; GENERAL INFORMATION:
; APPLICANT: Kenya SHITARA
; APPLICANT: Mikiko SAKURADA
; APPLICANT: Kazuhisa UCHIDA
; APPLICANT: Toyohide SHINKAWA
; APPLICANT: Mitsuo SATOH
; APPLICANT: Ryosuke NAKANO
; TITLE OF INVENTION: ANTIBODY COMPOSITION WHICH SPECIFICALLY BINDS TO CD20
; FILE REFERENCE: 249-289
; CURRENT APPLICATION NUMBER: US/10/327,663
; CURRENT FILING DATE: 2002-12-24
; PRIOR APPLICATION NUMBER: JP 2001-392753
; PRIOR FILING DATE: 2001-12-25
; PRIOR APPLICATION NUMBER: JP 2002-106948
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: JP 2002-319975
; PRIOR FILING DATE: 2001-11-01

```

```

; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 12
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-327-663-12

Query Match      87.2%; Score 572; DB 4; Length 128;
Best Local Similarity 89.8%; Pred. No. 1e-41;
Matches 114; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

Qy 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQOK 60
Db 1 MDFQVQIISFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYHWFQOK 60
Qy 61 PGSSPKPWIIYGTSLASGVPTRFSGSGSGTSYSLTISRVEADAATYYCQWSSNPPTFG 120
Db 61 PGSSPKPWIIYATSLASGVPTRFSGSGSGTSYSLTISRVEADAATYYCQWTSNPPTFG 120
Qy 121 SGTKLEI 127
Db 121 GGTKLEI 127

RESULT 14
US-10-410-930-60
; Sequence 60, Application US/10410930
; Publication No. US20040115168A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DePrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bove, Caryn
; TITLE OF INVENTION: INTERFERON BETA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
; FILE REFERENCE: 040853-01-5056
; CURRENT APPLICATION NUMBER: US/10/410,930
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 60
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-410-930-60

Query Match      87.2%; Score 572; DB 4; Length 128;
Best Local Similarity 89.8%; Pred. No. 1e-41;
Matches 114; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

Qy 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQOK 60
Db 1 MDFQVQIISFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYHWFQOK 60
Qy 61 PGSSPKPWIIYGTSLASGVPTRFSGSGSGTSYSLTISRVEADAATYYCQWSSNPPTFG 120
Db 61 PGSSPKPWIIYATSLASGVPTRFSGSGSGTSYSLTISRVEADAATYYCQWTSNPPTFG 120
Qy 121 SGTKLEI 127
Db 121 GGTKLEI 127

```



```
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR FILING DATE: 2002-08-16
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-287-994-60

Query Match      87.2%; Score 572; DB 4; Length 128;
Best Local Similarity 89.8%; Pred. No. 1e-41;
Matches 114; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

Qy 1 MDFQVQIISFLLISASVIMSRGQIVLSQSPAILSPGKVTMTCRASSSVSYIHWFQOK 60
Db 1 MDFQVQIISFLLISASVIMSRGQIVLSQSPAILSPGKVTMTCRASSSVSYIHWFQOK 60
Qy 61 PGSSPKPMIYGTSTLASGVPTFRFSGSGSGTSYSLTISRVEADAATYYCQWSSNPPTFG 120
Db 61 PGSSPKPMIYATSNLASGVPTFRFSGSGSGTSYSLTISRVEADAATYYCQWSSNPPTFG 120
Qy 121 SGTGLEI 127
Db 121 GGTGLEI 127

RESULT 19
US-10-410-980-60
; Sequence 60, Application US/10410980
; Publication No. US20050031584A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bove, Caryn
; TITLE OF INVENTION: INTERLEUKIN-2: REMODELING AND GLYCOCONJUGATION OF IL-2
; FILE REFERENCE: 040853-01-5066
; CURRENT APPLICATION NUMBER: US/10/410,980
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 60
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-410-980-60

Query Match      87.2%; Score 572; DB 5; Length 128;
Best Local Similarity 89.8%; Pred. No. 1e-41;
Matches 114; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

Qy 1 MDFQVQIISFLLISASVIMSRGQIVLSQSPAILSPGKVTMTCRASSSVSYIHWFQOK 60
Db 1 MDFQVQIISFLLISASVIMSRGQIVLSQSPAILSPGKVTMTCRASSSVSYIHWFQOK 60
Qy 61 PGSSPKPMIYGTSTLASGVPTFRFSGSGSGTSYSLTISRVEADAATYYCQWSSNPPTFG 120
Db 61 PGSSPKPMIYATSNLASGVPTFRFSGSGSGTSYSLTISRVEADAATYYCQWSSNPPTFG 120
Qy 121 SGTGLEI 127
Db 121 GGTGLEI 127

RESULT 20
US-10-410-997-60
; Sequence 60, Application US/10410897
; Publication No. US20050100982A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
```

Search completed: March 20, 2006, 07:35:09
Job time : 23.5444 secs

THIS PAGE BLANK (USPTO)

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	572	87.2	128	1	US-08-476-275-4	Sequence 4, Appli
2	572	87.2	128	2	US-08-475-8158-7	Sequence 7, Appli
3	572	87.2	128	2	US-08-473-813-4	Sequence 4, Appli
4	566	86.3	128	2	US-09-720-138-46	Sequence 46, Appl
5	566	86.3	128	2	US-09-630-198-46	Sequence 46, Appl
6	559	85.2	129	1	US-08-449-287-2	Sequence 2, Appli
7	559	85.2	125	1	US-09-423-439-18	Sequence 18, Appl
8	559	85.2	235	2	US-09-423-433-58	Sequence 58, Appl
9	559	85.2	235	2	US-09-423-433-58	Sequence 23, Appl
10	558	85.1	235	2	US-09-011-769A-23	Sequence 2, Appli
11	548	83.5	128	2	US-09-238-741-2	Sequence 2, Appli
12	548	83.5	128	4	US-08-619-491-2	Sequence 2, Appli
13	543	82.8	128	1	PCT-US95-07302-2	Sequence 2, Appli
14	543	82.8	128	1	US-07-946-421-26	Sequence 26, Appl
15	543	82.8	235	1	US-08-303-569B-5	Sequence 5, Appli
16	543	82.8	235	1	US-08-116-247-5	Sequence 5, Appli
17	543	82.8	235	2	US-09-795-515-5	Sequence 5, Appli
18	543	82.8	235	2	US-09-348-224-5	Sequence 5, Appli
19	532	81.1	129	1	US-08-116-778B-2	Sequence 2, Appli
20	532	81.1	129	1	US-08-438-562-2	Sequence 2, Appli
21	531	80.9	128	1	US-08-483-528B-92	Sequence 92, Appl
22	524	79.9	128	1	US-07-634-278-31	Sequence 2, Appli
23	524	79.9	128	1	US-08-477-728-31	Sequence 31, Appl
24	524	79.9	128	1	US-08-477-728-31	Sequence 31, Appl
25	524	79.9	128	1	US-08-474-040-31	Sequence 31, Appl
26	524	79.9	128	1	US-08-487-200-31	Sequence 31, Appl
27	524	79.9	235	2	US-08-484-537-31	Sequence 31, Appl
28	524	79.9	235	2	US-09-910-059-17	Sequence 17, Appl

ALIGNMENTS

```
RESULT 1
US-08-476-275-4
; Sequence 4, Application US/08476275
; Patent No. 5776456
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; APPLICANT: Hanna, Nabil
; APPLICANT: Leonard, John E.
; APPLICANT: Newman, Roland A.
; APPLICANT: Reff, Mitchell E.
; APPLICANT: Rastetter, William H.
; TITLE OF INVENTION: Therapeutic Application of Chimeric and
; Radiolabeled Antibodies to Human B Lymphocyte Restricted
; Differentiation Antigen for the Treatment of B-Cell
; TITLE OF INVENTION: Lymphoma
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,275
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/149,099
; FILING DATE: 03-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/978,891
; FILING DATE: 13-NOV-1992
; NAME: Teskin, Robin L.
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-476-275-4

Query Match      87.2%; Score 572; DB 1; Length 128;
Best Local Similarity 89.8%; Pred. No. 3.2e-50;
Matches 114; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

Qy      1 MDFQVQVIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQOK 60
Db      1 MDFQVQVIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYHWFOOK 60

Qy      61 PGSSPKWIVGTSTLASGVPFRFGSGSGTYSITISRVEADAATYTCQOWSNPPTFG 120
Db      61 PGSSPKWIVATSNLASGVPFRFGSGSGTYSITISRVEADAATYTCQOWSNPPTFG 120

Qy      121 SGTKLEI 127
Db      121 GGTKLEI 127

RESULT 3
```

```
RESULT 2
US-08-475-815B-7
; Sequence 7, Application US/08475815B
; Patent No. 6399061
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, DARRELL R.
; APPLICANT: HANNA, NABIL
; APPLICANT: LEONARD, JOHN E.
; APPLICANT: NEWMAN, ROLAND A.
; APPLICANT: REFF, MITCHELL E.
; APPLICANT: RASTETTER, WILLIAM H.
; TITLE OF INVENTION: THERAPEUTIC APPLICATION OF CHIMERIC AND
; RADIOLABELED ANTIBODIES TO HUMAN B LYMPHOCYTE RESTRICTED
; DIFFERENTIATION ANTIGEN FOR THE TREATMENT OF B CELL
; TITLE OF INVENTION: LYMPHOMA
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY WINTHROP
; STREET: 1100 New York Avenue, N.W., Ninth FL.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,815B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/149,099
; FILING DATE: 03-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/978,891
; FILING DATE: 13-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 23522-0157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-475-815B-7

Query Match      87.2%; Score 572; DB 2; Length 128;
Best Local Similarity 89.8%; Pred. No. 3.2e-50;
Matches 114; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

Qy      1 MDFQVQVIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQOK 60
Db      1 MDFQVQVIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYHWFOOK 60

Qy      61 PGSSPKWIVGTSTLASGVPFRFGSGSGTYSITISRVEADAATYTCQOWSNPPTFG 120
Db      61 PGSSPKWIVATSNLASGVPFRFGSGSGTYSITISRVEADAATYTCQOWSNPPTFG 120

Qy      121 SGTKLEI 127
Db      121 GGTKLEI 127

RESULT 3
```

US-08-475-813-4
; Sequence 4, Application US/08475813
; Patent No. 6682734
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; APPLICANT: Hanna, Nabil
; APPLICANT: Leonard, John E.
; APPLICANT: Newman, Roland A.
; APPLICANT: Reff, Mitchell E.
; APPLICANT: Rastetter, William H.
; TITLE OF INVENTION: Therapeutic Application of Chimeric and
; Radiolabeled Antibodies to Human B Lymphocyte Restricted
; Differentiation Antigen for the Treatment of B-Cell Lymphoma
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,813
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/149,099
; FILING DATE: 03-NOV-1993
; APPLICATION NUMBER: US 07/978,891
; FILING DATE: 13-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-158
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-475-813-4

Query Match 87.2%; Score 572; DB 2; Length 128;
Best Local Similarity 89.8%; Pred. No. 3.2e-50;
Matches 114; Conservative 2; Mismatches 11; Indels 0; Gaps 0;
QY 1 MDFQVOIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTTTCRASSSVIYMCWNQOK 60
Db 1 MDFQVOIIFSLISASVIMSRGQIVLSQSPAILFASPGEKVTTCRASSSVYIHFQOK 60
QY 61 PGSSPKPWIYGTSLASGVPTFRFSGSGSGTSYSLTISRVEAEADAATYCCQWSSNPFTFG 120
Db 61 PGSSPKPWIYATSNLGSVPFRFSGSGSGTSYSLTISRVEAEADAATYCCQWTSNPFTFG 120
QY 121 SGTGLEI 127
Db 121 GGTGLEI 127

RESULT 4
US-09-724-138-46
; Sequence 46, Application US/09724138
; Patent No. 6652852
; GENERAL INFORMATION:

; APPLICANT: Robinson, Randy
; APPLICANT: Liu, Alvin
; APPLICANT: Ledbetter, Jeffrey
; TITLE OF INVENTION: Chimeric Antibody with Specificity to Human B Cell Surface Anti-
; FILE REFERENCE: PPL-001CN2
; CURRENT APPLICATION NUMBER: US/09/724,138
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/630198
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: US 09/021934
; PRIOR FILING DATE: 1998-02-12
; PRIOR APPLICATION NUMBER: US 08/471984
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 07/665939
; PRIOR FILING DATE: 1991-03-05
; PRIOR APPLICATION NUMBER: US 07/195961
; PRIOR FILING DATE: 1988-05-13
; PRIOR APPLICATION NUMBER: US 07/016202
; PRIOR FILING DATE: 1987-01-08
; PRIOR APPLICATION NUMBER: PCT/US86/02269
; PRIOR FILING DATE: 1986-10-27
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 46
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-724-138-46
Query Match 86.3%; Score 566; DB 2; Length 128;
Best Local Similarity 88.2%; Pred. No. 1.3e-49;
Matches 112; Conservative 4; Mismatches 11; Indels 0; Gaps 0;
QY 1 MDFQVOIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTTTCRASSSVIYMCWNQOK 60
Db 1 MDFQVOIFSFLLISASVIMSRGQIVLSQSPAILFASPGEKVTTCRASSSVIYMHQOK 60
QY 61 PGSSPKPWIYGTSLASGVPTFRFSGSGSGTSYSLTISRVEAEADAATYCCQWSSNPFTFG 120
Db 61 PGSSPKPWIYATSNLGSVPFRFSGSGSGTSYSLTISRVEAEADAATYCCQWTSNPFTFG 120
QY 121 SGTGLEI 127
Db 121 AGTKLEI 127
RESULT 5
US-09-630-198-46
; Sequence 46, Application US/09630198
; Patent No. 6893625
; GENERAL INFORMATION:
; APPLICANT: Robinson, Randy
; APPLICANT: Liu, Alvin
; APPLICANT: Ledbetter, Jeffrey
; TITLE OF INVENTION: Chimeric Antibody with Specificity to Human B Cell Surface Anti-
; FILE REFERENCE: PPL-001CN
; CURRENT APPLICATION NUMBER: US/09/630,198
; CURRENT FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: US 09/021934
; PRIOR FILING DATE: 1998-02-12
; PRIOR APPLICATION NUMBER: US 08/471984
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 07/665939
; PRIOR FILING DATE: 1991-03-05
; PRIOR APPLICATION NUMBER: US 07/195961
; PRIOR FILING DATE: 1988-05-13
; PRIOR APPLICATION NUMBER: US 07/016202
; PRIOR FILING DATE: 1987-01-08
; PRIOR APPLICATION NUMBER: PCT/US86/02269
; PRIOR FILING DATE: 1986-10-27
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 46

```
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-630-198-46

Query Match      86.3%; Score 566; DB 2; Length 128;
Best Local Similarity 88.2%; Pred. No. 1.3e-49;
Matches 112; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQOK 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQOK 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 PGSSPKPWIVGTSTLASGVPTFRSGSGSGTSYSLTISRVEADAATYCCQWSSNPPTFG 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 PGSSPKPWIVGTSTLASGVPTFRSGSGSGTSYSLTISRVEADAATYCCQWSSNPPTFG 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 SGTKLEI 127
   |||||:
Db 121 AGTKLEL 127

RESULT 6
US-08-449-287-2
; Sequence 2, Application US/08449287
; Patent No. 5877293
; GENERAL INFORMATION:
; APPLICANT: ADAIR, John Robert
; APPLICANT: BODMER, Mark William
; APPLICANT: MOUNTAIN, Andrew
; APPLICANT: OWENS, Raymond John
; TITLE OF INVENTION: CDR Grafted Anti-CEA Antibodies and
; TITLE OF INVENTION: Their Production
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,287
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/154,389
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT GB91/01108
; FILING DATE: 05-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9014932.9
; FILING DATE: 05-JUL-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT GB90/02017
; FILING DATE: 21-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 40283/110 CARA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid

; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-449-287-2

Query Match      85.2%; Score 559; DB 1; Length 129;
Best Local Similarity 88.2%; Pred. No. 6.6e-49;
Matches 112; Conservative 1; Mismatches 14; Indels 0; Gaps 0;

QY 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQOK 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQOK 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 PGSSPKPWIVGTSTLASGVPTFRSGSGSGTSYSLTISRVEADAATYCCQWSSNPPTFG 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 PGSSPKPWIVGTSTLASGVPTFRSGSGSGTSYSLTISRVEADAATYCCQWSSNPPTFG 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 SGTKLEI 127
   |||||:
Db 121 GGTKLEI 127

RESULT 7
US-09-423-439-18
; Sequence 18, Application US/09423439
; Patent No. 6339070
; GENERAL INFORMATION:
; APPLICANT: EMERY, Stephen Charles
; APPLICANT: BLAKEY, David Charles
; TITLE OF INVENTION: CHEMICAL COMPOUNDS
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Winthrop, L.L.P.
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/423 439
; FILING DATE: 09-No. 6339070-1599
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB98/01294
; FILING DATE: 05-MAY-1998
; APPLICATION NUMBER: GB 9709421.3
; FILING DATE: 10-MAY-1997
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-423-439-18

Query Match      85.2%; Score 559; DB 2; Length 235;
Best Local Similarity 88.2%; Pred. No. 1.4e-48;
Matches 112; Conservative 1; Mismatches 14; Indels 0; Gaps 0;

QY 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQOK 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQOK 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 PGSSPKPWIVGTSTLASGVPTFRSGSGSGTSYSLTISRVEADAATYCCQWSSNPPTFG 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 PGSSPKPWIVGTSTLASGVPTFRSGSGSGTSYSLTISRVEADAATYCCQWSSNPPTFG 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

Qy 121 SGTKEI 127
Db 121 GGTKEI 127

RESULT 8

US-09-423-439-58
; Sequence 58, Application US/09423439
; Patent No. 6339070
; GENERAL INFORMATION:
; APPLICANT: EMERY, Stephen Charles
; TITLE OF INVENTION: CHEMICAL COMPOUNDS
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Winthrop, L.L.P.
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/423.439
; FILING DATE: 09-May-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB98/01294
; FILING DATE: 05-MAY-1998
; APPLICATION NUMBER: GB 9709421.3
; FILING DATE: 10-MAY-1997
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 58:
US-09-423-439-58

Query Match 85.2%; Score 559; DB 2; Length 235;
Best Local Similarity 88.2%; Pred. No. 1.4e-48;
Matches 112; Conservative 1; Mismatches 14; Indels 0; Gaps 0;
Qy 1 MDPQVQIFSPLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQK 60
Db 1 MDPQVQIFSPLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYHWYQK 60
Qy 61 PGSSPKRWIYGTSLASGVTPRFGSGSGTSYSLTISRVEAEDAATYCCQWSSNPFTFG 120
Db 61 PGSSPKRWIYATNSLASGVTPRFGSGSGTSYSLTISRVEAEDAATYCCQWSSKPFTFG 120
Qy 121 SGTKEI 127
Db 121 GGTKEI 127

RESULT 9

US-09-011-769A-23
; Sequence 23, Application US/09011769A
; Patent No. 6436691
; GENERAL INFORMATION:
; APPLICANT: SLATER, Anthony M.
; BLAKEY, David C.
; DAVIES, David H.
; HENNAM, John F.
; HENNEQUIN, Laurent F.A.
; MARSHAW, Peter R.
; DOWELL, Robert I.

; TITLE OF INVENTION: Chemical Compounds
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Madison & Sutro, LLP
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 Mb disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/011.769A
; FILING DATE: 13-Feb-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB96/01975
; FILING DATE: 13-AUG-1996
; APPLICATION NUMBER: GB 9612295.7
; FILING DATE: 12-JUN-1996
; APPLICATION NUMBER: GB 9611019.2
; FILING DATE: 25-MAY-1996
; APPLICATION NUMBER: GB 9516810.0
; FILING DATE: 16-AUG-1995
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-011-769A-23

Query Match 85.2%; Score 559; DB 2; Length 235;
Best Local Similarity 88.2%; Pred. No. 1.4e-48;
Matches 112; Conservative 1; Mismatches 14; Indels 0; Gaps 0;
Qy 1 MDPQVQIFSPLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQK 60
Db 1 MDPQVQIFSPLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYHWYQK 60
Qy 61 PGSSPKRWIYGTSLASGVTPRFGSGSGTSYSLTISRVEAEDAATYCCQWSSNPFTFG 120
Db 61 PGSSPKRWIYATNSLASGVTPRFGSGSGTSYSLTISRVEAEDAATYCCQWSSKPFTFG 120
Qy 121 SGTKEI 127
Db 121 GGTKEI 127
RESULT 10
US-09-238-741-2
; Sequence 2, Application US/09238741
; Patent No. 6897044
; GENERAL INFORMATION:
; APPLICANT: BRASLAWSKY, GARY R.
; APPLICANT: HANNA, NABIL
; APPLICANT: HARIHARAN, KANDASAMY
; APPLICANT: LABAREE, MICHAEL J.
; APPLICANT: HUYNH, TRI B.
; TITLE OF INVENTION: PRODUCTION OF TETRAVALENT ANTIBODIES
; FILE REFERENCE: 23522.0584
; CURRENT APPLICATION NUMBER: US/09/238.741
; CURRENT FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Artificial Sequence

```
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: "Dimeric" Anti-CD20 Light Chain (Version 1)
US-09-238-741-2

Query Match      85.1%; Score 558; DB 2; Length 235;
Best Local Similarity 88.2%; Pred. No. 1.7e-48;
Matches 112; Conservative 2; Mismatches 13; Indels 0; Gaps 0;

Qy 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILPASPGETVTMTCRASSSVIYMCWNQOK 60
Db 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILPASPGETVTMTCRASSSVIYHWFQOK 60

Qy 61 PGSPKPMIYGTSTLASGVTRFSGSGSGTSYSLTISRVEADAATYCCQWSSNPFTFG 120
Db 61 PGSPKPMIYATSNLASGVTRFSGSGSGTSYSLTISRVEADAATYCCQWTSNPFTFG 120

Qy 121 SGTKLEI 127
Db 121 GGAKLEI 127

RESULT 11
US-08-619-491-2
; Sequence 2, Application US/08619491
; Patent No. 6210670
; GENERAL INFORMATION:
; APPLICANT: Berg, Ellen L.
; TITLE OF INVENTION: Cross-Reacting Monoclonal Antibodies
; TITLE OF INVENTION: Specific for E-Selectin and P-Selectin
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/619,491
; FILING DATE: 26-MAR-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION NUMBER: WO PCT/US95/07302
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/259,963
; FILING DATE: 14-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 011823-005810US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-619-491-2

Query Match      83.5%; Score 548; DB 2; Length 128;
Best Local Similarity 85.8%; Pred. No. 8.4e-48;
Matches 109; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

Qy 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILPASPGETVTMTCRASSSVIYMCWNQOK 60
Db 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILPASPGETVTMTCRASSSVIYHWFQOK 60

Qy 61 PGSPKPMIYGTSTLASGVTRFSGSGSGTSYSLTISRVEADAATYCCQWSSNPFTFG 120
Db 61 PGSPKPMIYATSNLASGVTRFSGSGSGTSYSLTISRVEADAATYCCQWTSNPFTFG 120

Qy 121 SGTKLEI 127
Db 121 GGAKLEI 127

RESULT 12
PCT-US95-07302-2
; Sequence 2, Application PC/TUS9507302
; GENERAL INFORMATION:
; APPLICANT: Berg, Ellen L.
; TITLE OF INVENTION: Cross-Reacting Monoclonal Antibodies
; TITLE OF INVENTION: Specific for E-Selectin and P-Selectin
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: PCT/US95/07302
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: 08/259,963
; FILING DATE: 14-JUNE-94
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-005810PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-07302-2

Query Match      83.5%; Score 548; DB 4; Length 128;
Best Local Similarity 85.8%; Pred. No. 8.4e-48;
Matches 109; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

Qy 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILPASPGETVTMTCRASSSVIYMCWNQOK 60
Db 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILPASPGETVTMTCRASSSVIYHWFQOK 60

Qy 61 PGSPKPMIYGTSTLASGVTRFSGSGSGTSYSLTISRVEADAATYCCQWSSNPFTFG 120
Db 61 PGSPKPMIYATSNLASGVTRFSGSGSGTSYSLTISRVEADAATYCCQWSSNPFTFG 120

Qy 121 SGTKLEI 127
Db 121 SGTKLEI 127

RESULT 13
US-07-946-421-26
```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5859205ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,569B
FILING DATE: 07-SEP-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Yanko
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CARP-0032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-303-569B-5

Query Match 82.8%; Score 543; DB 1; Length 235;
Best Local Similarity 85.0%; Pred. No. 5.7e-47;
Matches 108; Conservative 5; Mismatches 14; Indels 0; Gaps 0

Qy	1	MDPQVQIFSFLLISASVIMSRGQIVLSQSPAILFPASGETVTMTCRASSSVIYMCWNOOK	60
Db	1	MDPQVQIFSFLLISASVIMSRGQIVLSQSPAILFPASGETVTMTCSASSSVYMNWYQOK	60
Qy	61	PGSSPKPKWIVGTSTLASGVPTFGSGSGSYSLTISRVEADAATYCCQWSSNPFTFG	120
Db	61	SGTSPKRWIVDTSLKSLASGVPAHFRGSGSGSYSLTISGMEADAATYCCQWSSNPFTFG	120
Qy	121	SGTKLEI 127	
Db	121	SGTKLEI 127	

RESULT 15
US-08-116-247-5
Sequence 5, Application US/08116247
Patent No. 5929212
GENERAL INFORMATION:
APPLICANT: Jolliffe, Linda K.
APPLICANT: Zivin, Robert A.
APPLICANT: Adair, John R.
APPLICANT: Athwal, Diljeet S.
TITLE OF INVENTION: CD3 Specific Recombinant Antibody
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5929212ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/116,247

```
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/743,377
; FILING DATE: 10-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Paintin, Francis A.
; REGISTRATION NUMBER: 19,386
; REFERENCE/DOCKET NUMBER: CARP-0011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-116-247-5

Query Match      82.8%; Score 543; DB 1; Length 235;
Best Local Similarity 85.0%; Pred. No. 5.7e-47;
Matches 108; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

Qy      1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQOK 60
Db      1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCSASSSVYNNWYQOK 60
Qy      61 PGSPKPMIYGTSTLASGVPTFRFGSGSGTYSYLSITISRVEADAATYCCQWSSNPPTFG 120
Db      61 SGTSPKRWIYDTSKLAGVPAHFRGSGSGTYSYLSITISGMEADAATYCCQWSSNPPTFG 120
Qy      121 SGTKLEI 127
Db      121 SGTKLEI 127

RESULT 16
US-09-795-515-5
; Sequence 5, Application US/09795515
; Patent No. 6632927
; GENERAL INFORMATION:
; APPLICANT: Adair, John R.
; APPLICANT: Athwal, Diljeet S.
; APPLICANT: Emtege, John S.
; TITLE OF INVENTION: Humanised Antibodies
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6632927ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/795,515
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/846,658
; FILING DATE: 01-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yanko
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
```

```
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-795-515-5

Query Match      82.8%; Score 543; DB 2; Length 235;
Best Local Similarity 85.0%; Pred. No. 5.7e-47;
Matches 108; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

Qy      1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQOK 60
Db      1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCSASSSVYNNWYQOK 60
Qy      61 PGSPKPMIYGTSTLASGVPTFRFGSGSGTYSYLSITISRVEADAATYCCQWSSNPPTFG 120
Db      61 SGTSPKRWIYDTSKLAGVPAHFRGSGSGTYSYLSITISGMEADAATYCCQWSSNPPTFG 120
Qy      121 SGTKLEI 127
Db      121 SGTKLEI 127

RESULT 17
US-09-348-224-5
; Sequence 5, Application US/09348224
; Patent No. 6750325
; GENERAL INFORMATION:
; APPLICANT: Jollieffe, Linda Kay
; APPLICANT: Zivin, Robert Allan
; APPLICANT: Adair, John Robert
; APPLICANT: Athwal, Diljeet Singh
; TITLE OF INVENTION: CD3 Specific Recombinant Antibody
; FILE REFERENCE: CARP0066
; CURRENT APPLICATION NUMBER: US/09/348,224
; CURRENT FILING DATE: 1999-07-06
; EARLIER APPLICATION NUMBER: 08/116,247
; EARLIER FILING DATE: 1993-09-03
; EARLIER APPLICATION NUMBER: 07/743,377
; EARLIER FILING DATE: 1991-10-04
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Mouse
; US-09-348-224-5

Query Match      82.8%; Score 543; DB 2; Length 235;
Best Local Similarity 85.0%; Pred. No. 5.7e-47;
Matches 108; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

Qy      1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQOK 60
Db      1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCSASSSVYNNWYQOK 60
Qy      61 PGSPKPMIYGTSTLASGVPTFRFGSGSGTYSYLSITISRVEADAATYCCQWSSNPPTFG 120
Db      61 SGTSPKRWIYDTSKLAGVPAHFRGSGSGTYSYLSITISGMEADAATYCCQWSSNPPTFG 120
Qy      121 SGTKLEI 127
Db      121 SGTKLEI 127

RESULT 18
US-08-116-778B-2
; Sequence 2, Application US/08116778E
; Patent No. 5830470
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, KAZUYASU
```



```
; IDENTIFICATION METHOD: CONSENSUS
; OTHER INFORMATION: /product= "HYPERVARIABLE REGION 2"
; FEATURE:
; NAME/KEY: domain
; LOCATION: 88..96
; IDENTIFICATION METHOD: BY SIMILARITY
; IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
; IDENTIFICATION METHOD: CONSENSUS
; OTHER INFORMATION: /product= "HYPERVARIABLE REGION 3"
; OTHER INFORMATION: /product= "HYPERVARIABLE REGION 3"
; US-08-438-562-2

Query Match      81.1%; Score 532; DB 1; Length 129;
Best Local Similarity 84.3%; Pred. No. 3.5e-46;
Matches 107; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

Qy 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQOK 60
Db 1 MHFQVQIFSFLLISASVIMSRGQIVLTQSPAIMASPGKVTITCSASSSVYMHWFQOK 60
Qy 61 PGSSPKWIVGTSTLASGVPTFRFSGSGSGTSYSLTISRVEAEDAATYCCQWSSNPFTFG 120
Db 61 PGTSPLKIWIYSTNLASGVTPARFSGSGSGTSYSLTISRMEADAATYCCQRSSYPYTFG 120
Qy 121 SGTKLEI 127
Db 121 GGTKLEI 127

RESULT 20
US-08-483-528B-92
; Sequence 92, Application US/08483528B
; Patent No. 5939532
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: KOIKE, MASAMICHI
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: KUWANA, YOSHIHISA
; APPLICANT: HASEGAWA, NAMORU
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,528B
; FILING DATE: 07-JUN-95
; CLASSIFICATION: 536
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4000
; TELEFAX: (703)816-4100
; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: -22..-1
; IDENTIFICATION METHOD: BY SIMILARITY WITH KNOWN SEQUENCE TO TO AN
; IDENTIFICATION METHOD: ESTABLISHED CONSENSUS
; FEATURE:
```

```
; NAME/KEY: domain
; LOCATION: 24..33
; IDENTIFICATION METHOD: BY SIMILARITY
; IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
; IDENTIFICATION METHOD: CONSENSUS
; OTHER INFORMATION: /product= "HYPERVARIABLE REGION 1"
; FEATURE:
; NAME/KEY: domain
; LOCATION: 49..55
; IDENTIFICATION METHOD: BY SIMILARITY
; IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
; IDENTIFICATION METHOD: CONSENSUS
; OTHER INFORMATION: /product= "HYPERVARIABLE REGION 2"
; FEATURE:
; NAME/KEY: domain
; LOCATION: 88..96
; IDENTIFICATION METHOD: BY SIMILARITY
; IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
; IDENTIFICATION METHOD: CONSENSUS
; OTHER INFORMATION: /product= "HYPERVARIABLE REGION 3"
; US-08-483-528B-92

Query Match      81.1%; Score 532; DB 1; Length 129;
Best Local Similarity 84.3%; Pred. No. 3.5e-46;
Matches 107; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

Qy 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQOK 60
Db 1 MHFQVQIFSFLLISASVIMSRGQIVLTQSPAIMASPGKVTITCSASSSVYMHWFQOK 60
Qy 61 PGSSPKWIVGTSTLASGVPTFRFSGSGSGTSYSLTISRVEAEDAATYCCQWSSNPFTFG 120
Db 61 PGTSPLKIWIYSTNLASGVTPARFSGSGSGTSYSLTISRMEADAATYCCQRSSYPYTFG 120
Qy 121 SGTKLEI 127
Db 121 GGTKLEI 127

Search completed: March 20, 2006, 07:31:34
Job time : 7.76331 secs
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 20, 2006, 07:28:19 ; Search time 45.9655 Seconds

(without alignments)
1213.978 Million cell updates/sec

Title: US-10-687-035-33

Perfect score: 656

Sequence: 1 MDPQVQIFSPFLISASVIMS.....YCOQWSNPFTFGSGTKLEI 127

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

A Geneseq_21.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	656	100.0	127	ADS94334	Ads94334 Antibody
2	579	88.3	145	AAR15323	Aar15323 IL-2 chim
3	579	88.3	145	AAR32127	Aar32127 Anti-IL2R
4	578	88.1	129	ADV2494	Adv2494 2B8 light
5	578	88.1	129	ADV98557	Adv98557 Novel chi
6	578	88.1	235	ADV92498	Adv92498 Anti-CD20
7	578	88.1	235	ADV98561	Adv98561 Novel chi
8	572	87.2	128	AAR55214	Aar55214 Murine va
9	572	87.2	128	ABR55872	Abr55872 Anti-CD20
10	572	87.2	128	ABU08393	Abu08393 Murine an
11	572	87.2	128	ADC66268	Adc66268 Mouse ant
12	572	87.2	128	ADB85686	Adb85686 Murine im
13	572	87.2	128	ADP73083	Adp73083 Murine fu
14	572	87.2	128	ADF60660	Adf60660 Protein r
15	572	87.2	128	ADN49732	Adn49732 Mature va
16	572	87.2	128	ADU74408	Adu74408 Mouse ant
17	572	87.2	128	ADZ59908	Adz59908 Fucosyltr
18	572	87.2	235	AAE27925	Aae27925 Human C2B
19	572	87.2	235	ABB82834	Abb82834 Antibody
20	567	86.4	500	ADY21925	Ady21925 Antibody
21	566	86.3	128	AAp70628	Aap70628 Sequence
22	566	86.3	128	AAp94781	Aap94781 2 H7 VL g
23	566	86.3	128	AAW10243	Aaw10243 Light cha
24	566	86.3	128	AAW10589	Aaw10589 2H7 antib

25	566	86.3	128	AAW16344	Aaw16344 2H7 light
26	566	86.3	128	AAW41071	Aaw41071 Mouse 2H7
27	566	86.3	128	AAW47514	Aaw47514 Mouse 2H7
28	566	86.3	128	AAW47521	Aaw47521 Mouse 2H7
29	566	86.3	128	AAW89541	Aaw89541 Mouse ant
30	566	86.3	128	AAW98093	Aaw98093 2H7 light
31	566	86.3	128	ADC65029	Adc65029 Immunoglo
32	566	86.3	266	ABG31021	Abg31021 Mouse sin
33	566	86.3	266	ADD25450	Add25450 Binding d
34	566	86.3	266	ADM42725	Adm42725 Synthetic
35	566	86.3	266	AEBS95393	Aeb95393 Mouse 2H7
36	566	86.3	266	AEBS94427	Aeb94427 Mouse ant
37	566	86.3	267	ADY21839	Ady21839 Human ant
38	566	86.3	268	ADY21869	Ady21869 Human ant
39	566	86.3	268	ADY21837	Ady21837 Human ant
40	566	86.3	422	ABG31032	Abg31032 Synthetic
41	566	86.3	422	ADD25591	Add25591 Binding d
42	566	86.3	422	ADD25473	Add25473 Binding d
43	566	86.3	422	ADM42748	Adm42748 2H7scfv-C
44	566	86.3	422	AEBS95416	Aeb95416 Mouse 2H7
45	566	86.3	422	AEBS94450	Aeb94450 Mouse ant
46	566	86.3	426	ADY22144	Ady22144 Antibody
47	566	86.3	426	AEBS95423	Aeb95423 Mouse 2H7
48	566	86.3	426	AEBS94457	Aeb94457 Mouse ant
49	566	86.3	482	ABG31031	Abg31031 Synthetic
50	566	86.3	482	ADD25472	Add25472 Binding d
51	566	86.3	482	ADD25589	Add25589 Binding d
52	566	86.3	482	ADM42747	Adm42747 2H7-CD154
53	566	86.3	482	AEBS95415	Aeb95415 Mouse 2H7
54	566	86.3	482	AEBS94449	Aeb94449 Mouse ant
55	566	86.3	486	ADY22142	Ady22142 Antibody
56	566	86.3	486	AEBS94425	Aeb95425 Mouse 2H7
57	566	86.3	486	AEBS94456	Aeb94456 Mouse ant
58	566	86.3	498	ADD25674	Add25674 Binding d
59	566	86.3	498	ADY21647	Ady21647 Antibody
60	566	86.3	499	ABG31026	Abg31026 Synthetic
61	566	86.3	499	ABG31027	Abg31027 Synthetic
62	566	86.3	499	ABG31025	Abg31025 Synthetic
63	566	86.3	499	ADD25587	Add25587 Binding d
64	566	86.3	499	ADD25454	Add25454 Binding d
65	566	86.3	499	ADD25456	Add25456 Binding d
66	566	86.3	499	ADD25455	Add25455 Binding d
67	566	86.3	499	ADM42731	Adm42731 2H7scfv-I
68	566	86.3	499	ADM42729	Adm42729 2H7scfv-I
69	566	86.3	499	ADM42730	Adm42730 2H7scfv-I
70	566	86.3	499	AEBS95397	Aeb95397 Mouse hum
71	566	86.3	499	AEBS95398	Aeb95398 Mouse hum
72	566	86.3	499	AEBS95399	Aeb95399 Mouse hum
73	566	86.3	499	AEBS94431	Aeb94431 Mouse-ant
74	566	86.3	499	AEBS94433	Aeb94433 Mouse ant
75	566	86.3	499	AEBS94432	Aeb94432 Mouse ant
76	566	86.3	500	ADD25826	Add25826 Binding d
77	566	86.3	500	ADD25827	Add25827 Binding d
78	566	86.3	500	ADD25837	Add25837 Binding d
79	566	86.3	500	ADD25713	Add25713 Binding d
80	566	86.3	500	ADD25836	Add25836 Binding d
81	566	86.3	500	ADD25824	Add25824 Binding d
82	566	86.3	500	ADD25827	Add25827 Binding d
83	566	86.3	500	ADD25835	Add25835 Binding d
84	566	86.3	500	ADD25828	Add25828 Binding d
85	566	86.3	500	ADD25679	Add25679 Binding d
86	566	86.3	500	ADD25791	Add25791 Binding d
87	566	86.3	500	ADY21783	Ady21783 Antibody
88	566	86.3	500	ADY21891	Ady21891 Antibody
89	566	86.3	500	ADY21764	Ady21764 Antibody
90	566	86.3	500	ADY21793	Ady21793 Antibody
91	566	86.3	500	ADY21915	Ady21915 Antibody
92	566	86.3	500	ADY21997	Ady21997 Antibody
93	566	86.3	500	ADY21787	Ady21787 Antibody
94	566	86.3	500	ADY21931	Ady21931 Antibody
95	566	86.3	500	ADY21993	Ady21993 Antibody
96	566	86.3	500	ADY21683	Ady21683 Antibody
97	566	86.3	500	ADY21785	Ady21785 Antibody

DR N-PSDB; AAQ15115.
XX New recombinant DNA encoding chimeric antibody - with human constant and
PT non-human variable regions, esp. directed against interleukin 2 receptor.
PT
XX Disclosure; Page 12; 24pp; German.
XX
CC The sequence is that of the interleukin-2 (IL-2) chimeric antibody light
CC chain, coded by clone 215. Antibodies against IL-2 receptors are useful
CC as immunosuppressants, and are much less immunogenic than mouse or rat
CC antibodies. See also AAR15321-R15326. (Updated on 25-MAR-2003 to correct
CC PI field.) (Updated on 24-OCT-2003 to standardise OS field)
XX
SQ Sequence 145 AA;
Query Match 88.3%; Score 579; DB 2; Length 145;
Best Local Similarity 89.8%; Pred. No. 6.2e-35;
Matches 114; Conservative 4; Mismatches 9; Indels 0; Gaps 0;
QY 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNOOK 60
DB 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNOOK 60
QY 61 PGSSPKPWYGTSTLASGVPTFRFSGSGTSYSLTISRVEAEDATYYCOQWSSNPFTFG 120
DB 61 PGSSPKPWIQATSNLAFGVPSRFSGSGTSYSLTISRVEAEDATYYCOQWSSNPFTFG 120
QY 121 SGTKLEI 127
DB 121 SGTKLEI 127
RESULT 3
AAR32127
ID AAR32127 standard; protein; 145 AA.
AC AAR32127;
XX
XX 25-MAR-2003 (revised)
DT 10-MAR-2003 (revised)
DT 02-JUN-1993 (first entry)
XX
XX Anti-IL2R-alpha antibody M-215 light chain variable region.
XX immunosuppression; tissue transplantation; graft; L chain; V region;
KW T-helper cell inhibition; transplant rejection; Mab;
KW interleukin-2 receptor.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FT Peptide 1..22
FT Region /label= signal
FT Region 23..116
FT Region /label= Variable-region
FT Region 117..128
FT Region /label= J4-region
FT Region 129..145
FT /label= start_of_constant_region
XX
XX DE4143214-A1.
PN
XX
XX 28-JAN-1993.
XX
XX 30-DEC-1991; 91DE-04143214.
XX
XX 25-JUL-1991; 91DE-04124759.
XX
XX (BOEP) BOEHRINGER MANNHEIM GMBH.
PA
XX Weidle U, Scheuer W, Kaluza B, Riethmüller G;
PI
XX WPI; 1993-037582/05.
DR

DR N-PSDB; AAQ36613.
XX Synergistic antibody compsn. for use as immunosuppressant - comprises
PT monoclonal anti-CD4 antibodies and monoclonal anti-IL2R alpha- or anti-
PT IL2R beta antibodies.
XX
XX Example 1; Page 15; 18pp; German.
XX
CC This sequence is from the light chain variable region of an anti-IL2R
CC alpha monoclonal antibody. The antibody is only weakly inhibitory on its
CC own. When anti-IL2R alpha antibodies which are strongly inhibitory on
CC their own are used with anti-CD4 antibodies which are also strongly
CC inhibitory, their immunosuppressive properties are improved; they
CC synergistically inhibit T-helper cell proliferation to effectively
CC inhibit transplant rejection at low doses without significantly reducing
CC the general immune response. No such synergistic effect is observed with
CC the weakly inhibitory Mab M-215. See AAQ36607-Q36616. (Updated on 10-MAR-
CC 2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 145 AA;
Query Match 88.3%; Score 579; DB 2; Length 145;
Best Local Similarity 89.8%; Pred. No. 6.2e-35;
Matches 114; Conservative 4; Mismatches 9; Indels 0; Gaps 0;
QY 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNOOK 60
DB 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNOOK 60
QY 61 PGSSPKPWYGTSTLASGVPTFRFSGSGTSYSLTISRVEAEDATYYCOQWSSNPFTFG 120
DB 61 PGSSPKPWIQATSNLAFGVPSRFSGSGTSYSLTISRVEAEDATYYCOQWSSNPFTFG 120
QY 121 SGTKLEI 127
DB 121 SGTKLEI 127
RESULT 4
ADV92494
ID ADV92494 standard; protein; 129 AA.
AC ADV92494;
XX
XX 10-MAR-2005 (first entry)
DT
XX
XX 2B8 light chain variable region protein.
XX
XX Antibody engineering; chimeric antibody; cytostatic; gene therapy;
KW vaccine; gastrointestinal disease; immune response; melanoma; malignancy;
KW breast cancer; hepatocellular carcinoma.
XX
XX Mus sp.
XX
XX Key Location/Qualifiers
FT Peptide 1..22
FT Region /label= Signal peptide
FT Region 23..129
FT /note= "Light chain variable region gene (VL)"
FT Protein 23..129
FT /note= "Mature 2B8 light chain variable region protein"
XX
XX US2004254108-A1.
XX
XX 16-DEC-2004.
PD
XX
XX 26-NOV-2003; 2003US-00723003.
XX
XX 13-JUN-2003; 2003CN-00129290.
PR
XX 25-NOV-2003; 2003CN-01119930.
XX
XX (MAJ/J) MA J.
PA

PA (GUOY/) GUO Y.
 XX Ma J, Guo Y;
 PI WPI; 2005-030218/03.
 XX DR N-PSDB; ADV92493.
 XX
 PT New chimeric protein comprises an Flt3 ligand and a proteinous or
 PT peptidyl tumoricidal agent, useful for treating malignancy or neoplasm,
 PT e.g. melanoma, breast cancer, or hepatocellular carcinoma.
 XX
 XX Claim 23; SEQ ID NO 38; 158pp; English.
 PS
 CC The present invention relates to a chimeric protein having a Flt3 ligand
 CC (FL) or its biologically active fragment and a proteinous or peptidyl
 CC tumoricidal agent. The invention is useful for treating malignancy,
 CC neoplasm e.g. melanoma, breast cancer, hepatocellular carcinoma and as a
 CC vaccine for eliciting an immune response. The invention is also useful in
 CC gene therapy. The present sequence is the 2B8 light chain variable region
 CC protein.
 XX
 SQ Sequence 129 AA;

Query Match 88.1%; Score 578; DB 9; Length 129;
 Best Local Similarity 90.6%; Pred. No. 6.5e-35;
 Matches 115; Conservative 2; Mismatches 10; Indels 0; Gaps 0;
 QY 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFPASGETVTWTCRASSSVIYMCNQOK 60
 DB 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFPASGETVTWTCRASSSVIYHWFQOK 60
 QY 61 PGSSPKPMIYGTSTLASGVPTFRFSGSGTYSYLSITSRVEADAATYCCQWSNPPTFG 120
 DB 61 PGSSPKPMIYATNSLASGVPTFRFSGSGTYSYLSITSRVEADAATYCCQWTSNPPTFG 120
 QY 121 SGTKLEI 127
 DB 121 GGTKLEI 127

RESULT 5
 ADV98557
 ID ADV98557 standard; protein; 129 AA.
 XX
 AC ADV98557;
 XX
 DT 24-MAR-2005 (first entry)
 XX
 DE Novel chimeric protein-related 2B8 light chain protein SeqID38.
 XX
 KW protein engineering; pharmaceutical; cytostatic; vaccine; cancer;
 KW neoplasm; melanoma; breast tumor; hepatocellular carcinoma.
 XX
 OS Homo sapiens.
 OS Mus sp.
 OS Synthetic.
 XX
 XX W02005001048-A2.
 XX
 XX 06-JAN-2005.
 XX
 XX 04-JUN-2004; 2004WO-US017765.
 XX
 XX 13-JUN-2003; 2003CN-00129290.
 XX
 XX 25-NOV-2003; 2003CN-01119930.
 XX
 XX 26-NOV-2003; 2003US-00723003.
 XX
 XX 28-NOV-2003; 2003TW-00133577.
 XX
 XX (SYMB-) SYMBIGENE ACQUISITION CO INC.
 XX
 XX Ma J, Guo Y;
 XX WPI; 2005-075540/08.
 XX

DR N-PSDB; ADV98556.
 XX
 PT New chimeric protein for preventing or treating neoplastic conditions,
 PT e.g. melanoma, breast cancer or hepatocellular carcinoma, comprises an
 PT Flt3 ligand or its fragment, and a proteinous or peptidyl tumoricidal
 PT agent.
 XX
 XX Example 5; SEQ ID NO 38; 147pp; English.
 PS
 CC This invention relates to a novel chimeric protein comprising an Flt3
 CC ligand, or its biological fragment, and a proteinous or peptidyl
 CC tumoricidal agent. The invention may be useful for the production of
 CC compounds with a cytostatic activity or a vaccine. The composition and
 CC methods are useful for preventing or treating neoplastic conditions, such
 CC as melanoma, breast cancer or hepatocellular carcinoma. The present
 CC sequence is that of a protein which is related to the chimeric proteins
 CC of the invention.
 XX
 SQ Sequence 129 AA;

Query Match 88.1%; Score 578; DB 9; Length 129;
 Best Local Similarity 90.6%; Pred. No. 6.5e-35;
 Matches 115; Conservative 2; Mismatches 10; Indels 0; Gaps 0;
 QY 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFPASGETVTWTCRASSSVIYMCNQOK 60
 DB 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFPASGETVTWTCRASSSVIYHWFQOK 60
 QY 61 PGSSPKPMIYGTSTLASGVPTFRFSGSGTYSYLSITSRVEADAATYCCQWSNPPTFG 120
 DB 61 PGSSPKPMIYATNSLASGVPTFRFSGSGTYSYLSITSRVEADAATYCCQWTSNPPTFG 120
 QY 121 SGTKLEI 127
 DB 121 GGTKLEI 127

RESULT 6
 ADV92498
 ID ADV92498 standard; protein; 235 AA.
 XX
 AC ADV92498;
 XX
 DT 10-MAR-2005 (first entry)
 XX
 DE Anti-CD20 chimeric antibody light chain protein.
 XX
 KW Antibody engineering; chimeric antibody; cytostatic; gene therapy;
 KW vaccine; gastrointestinal disease; immune response; melanoma; malignancy;
 KW breast cancer; hepatocellular carcinoma.
 XX
 OS Mus sp.
 XX
 XX Key Location/Qualifiers
 XX Peptide 1..22
 XX Region /label= Signal peptide
 XX Region 23..129
 XX Region /note= "Light chain variable region gene (VL)"
 XX Region 130..235
 XX Region /note= "Human kappa chain constant cdna (CL)"
 XX
 XX US2004254108-A1.
 XX
 XX 16-DEC-2004.
 XX
 XX 26-NOV-2003; 2003US-00723003.
 XX
 XX 13-JUN-2003; 2003CN-00129290.
 XX
 XX 25-NOV-2003; 2003CN-01119930.
 XX
 XX (MAJJ/) MA J.
 XX (GUOY/) GUO Y.
 XX

PI Ma J, Guo Y;
 XX WPI; 2005-030218/03.
 DR N-PSDB; ADV92497.
 XX
 XX New chimeric protein comprises an Flt3 ligand and a proteinous or
 PT peptidyl tumoricidal agent, useful for treating malignancy or neoplasm,
 PT e.g. melanoma, breast cancer, or hepatocellular carcinoma.
 XX
 XX Claim 23; SEQ ID NO 42; 158pp; English.
 XX
 XX The present invention relates to a chimeric protein having a Flt3 ligand
 CC (FL) or its biologically active fragment and a proteinous or peptidyl
 CC tumoricidal agent. The invention is useful for treating malignancy,
 CC neoplasm e.g. melanoma, breast cancer, hepatocellular carcinoma and as a
 CC vaccine for eliciting an immune response. The invention is also useful in
 CC gene therapy. The present sequence is the anti-CD20 chimeric antibody
 CC light chain protein.
 XX
 XX Sequence 235 AA;
 SQ
 Query Match 88.1%; Score 578; DB 9; Length 235;
 Best Local Similarity 90.6%; Pred. No. 1.2e-34;
 Matches 115; Conservative 2; Mismatches 10; Indels 0; Gaps 0;
 QY 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCNQK 60
 DB 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYHWFQK 60
 QY 61 PGSSPKPWIYGTSTLASGVTPFRSGSGSGTYSLTISRVEAEADAATYCCQWSSNPPTFG 120
 DB 61 PGSSPKPWIYATNLASGVTPFRSGSGSGTYSLTISRVEAEADAATYCCQWTSNPPTFG 120
 QY 121 SGTKLEI 127
 DB 121 GGTKLEI 127
 RESULT 7
 ADV98561
 ID ADV98561 standard; protein; 235 AA.
 XX
 AC ADV98561;
 XX
 XX 24-MAR-2005 (first entry)
 DT
 DE Novel chimeric protein-related anti-CD20 light chain protein SeqID42.
 XX
 XX protein engineering; pharmaceutical; cytostatic; vaccine; cancer;
 KW neoplasm; melanoma; breast tumor; hepatocellular carcinoma.
 XX
 OS Homo sapiens.
 XX
 PN WO2005001048-A2.
 XX
 XX 06-JAN-2005.
 PD
 XX 04-JUN-2004; 2004WO-US017765.
 PF
 XX 13-JUN-2003; 2003CN-00129290.
 PR 25-NOV-2003; 2003CN-01119930.
 PR 26-NOV-2003; 2003US-00723003.
 PR 28-NOV-2003; 2003TW-00133577.
 XX
 PA (SYMB-) SYMBIGENE ACQUISITION CO INC.
 XX
 XX Ma J, Guo Y;
 PI WPI; 2005-075540/08.
 DR N-PSDB; ADV98560.
 XX
 XX New chimeric protein for preventing or treating neoplastic conditions,
 PT e.g. melanoma, breast cancer or hepatocellular carcinoma, comprises an

PT Flt3 ligand or its fragment, and a proteinous or peptidyl tumoricidal
 PT agent.
 XX
 PS Example 5; SEQ ID NO 42; 147pp; English.
 XX
 CC This invention relates to a novel chimeric protein comprising an Flt3
 CC ligand, or its biological fragment, and a proteinous or peptidyl
 CC tumoricidal agent. The invention may be useful for the production of
 CC compounds with a cytostatic activity or a vaccine. The composition and
 CC methods are useful for preventing or treating neoplastic conditions, such
 CC as melanoma, breast cancer or hepatocellular carcinoma. The present
 CC sequence is that of a protein which is related to the chimeric proteins
 CC of the invention.
 XX
 SQ Sequence 235 AA;
 Query Match 88.1%; Score 578; DB 9; Length 235;
 Best Local Similarity 90.6%; Pred. No. 1.2e-34;
 Matches 115; Conservative 2; Mismatches 10; Indels 0; Gaps 0;
 QY 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCNQK 60
 DB 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYHWFQK 60
 QY 61 PGSSPKPWIYGTSTLASGVTPFRSGSGSGTYSLTISRVEAEADAATYCCQWSSNPPTFG 120
 DB 61 PGSSPKPWIYATNLASGVTPFRSGSGSGTYSLTISRVEAEADAATYCCQWTSNPPTFG 120
 QY 121 SGTKLEI 127
 DB 121 GGTKLEI 127
 RESULT 8
 AAR55214
 ID AAR55214 standard; protein; 128 AA.
 XX
 AC AAR55214;
 XX
 XX 25-MAR-2003 (revised)
 DT
 DT 01-FEB-1995 (first entry)
 XX
 DE Murine variable region light chain from 2B8.
 XX
 KW B cell lymphoma chimeric antibody; CD20; peripheral blood cells;
 KW cell lysis.
 XX
 OS Mus musculus.
 XX
 PN WO9411026-A2.
 XX
 PD 26-MAY-1994.
 XX
 PF 12-NOV-1993; 93WO-US010953.
 XX
 PR 13-NOV-1992; 92US-00978891.
 PR 03-NOV-1993; 93US-00149099.
 XX
 PA (IDEC-) IDEC PHARM CORP.
 XX
 PI Anderson DR, Rastetter WH, Hanna N, Leonard JB, Newman RA;
 PI Reff ME;
 XX
 XX WPI; 1994-183162/22.
 DR N-PSDB; AAQ65630.
 XX
 XX Treating B cell lymphoma with chimeric antibody - against CD20, causing
 PT rapid depletion of peripheral B cells, also new antibodies and
 PT hybridomas.
 XX
 PS Disclosure; Fig 4; 101pp; English.
 XX
 XX The sequence is the murine variable region light chain derived from

CC murine anti-CD20 monoclonal antibody 2B5. See also AA065629-35. (Updated
 CC on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct
 CC PI field.)

XX Sequence 128 AA;

Query Match 87.2%; Score 572; DB 2; Length 128;
 Best Local Similarity 89.8%; Pred. No. 1.8e-34;
 Matches 114; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

QY 1 MDFQVQIFSPILLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQOK 60

DB 1 MDFQVQIISPELLISASVIMSRGQIVLSQSPAILFASPGKVMTTCRASSSVSIHWFQOK 60

QY 61 PGSSPKPWIYGTSLASGVPTFRFSGSGSGTSYSLTISRVEADAATYCCOWSNPPTFG 120

DB 61 PGSSPKPWIYATNLASGVPTFRFSGSGSGTSYSLTISRVEADAATYCCOWTSNPPTFG 120

QY 121 SGTKLEI 127

DB 121 GGTKLEI 127

RESULT 9

ABR55872

ID ABR55872 standard; protein; 128 AA.

XX AC ABR55872;

XX 02-SEP-2003 (first entry)

XX Anti-CD20 antibody light chain variable region.

XX Peptide remodeling; glycoconjugation; glycosyltransferase; glycan; CD20;

XX antibody; mouse.

XX Mus musculus.

XX W02003031464-A2.

XX 17-APR-2003.

XX 09-OCT-2002; 2002WO-US032263.

XX 10-OCT-2001; 2001US-0328523P.

XX 19-OCT-2001; 2001US-0344692P.

XX 28-NOV-2001; 2001US-0334233P.

XX 28-NOV-2001; 2001US-0334301P.

XX 07-JUN-2002; 2002US-0387292P.

XX 25-JUN-2002; 2002US-0391777P.

XX 17-JUL-2002; 2002US-0396594P.

XX 16-AUG-2002; 2002US-0404249P.

XX 28-AUG-2002; 2002US-0407527P.

XX (NEOS-) NEOSE TECHNOLOGIES INC.

XX De Frees S, Zopf D, Bayer R, Bowe C, Hakes D, Chen X;

XX WPI; 2003-449162/42.

XX N-PSDB; ACC78894.

XX Remodeling a peptide, by removing a saccharyl subunit from the peptide to

XX form truncated glycan, and adding or deleting glycosyl groups to a

XX peptide and/or adding modifying group of a peptide to remodel the

XX peptide.

XX Example; Fig 82B; 900pp; English.

XX The invention relates to a cell-free, in vitro method of remodeling a

XX peptide. The method involves removing a saccharyl subunit from the

XX peptide, thus forming a truncated glycan, and contacting the truncated

XX glycan with at least one glycosyltransferase and at least one glycosyl

XX donor under conditions suitable to transfer at least one glycosyl donor

XX

CC

CC

CC

CC

CC

CC

CC

CC

CC to the truncated glycan, thus remodeling the peptide. Conjugates can be
 CC formed between a granulocyte colony stimulating factor (G-CSF) peptide,
 CC interferon alpha peptide, interferon beta peptide, Factor VIIa peptide,
 CC Factor IX peptide, follicle stimulating hormone peptide, erythropoietin
 CC (EPO) peptide, granulocyte macrophage colony stimulating factor (GM-CSF)
 CC peptide, interferon-gamma peptide, alpha-1-protease inhibitor (A-1-PI)
 CC peptide, beta-glucosidase peptide, tissue plasminogen activator (TPA)
 CC peptide, interleukin-2 (IL-2) peptide, Factor VIII peptide, TNFalpha
 CC receptor/immunoglobulin (Ig) G fusion peptide, urokinase peptide, anti-
 CC glycoprotein IIb/IIIa monoclonal antibody peptide, chimeric anti HER2
 CC antibody peptide, anti-respiratory syncytial virus (RSV) F peptide, anti-
 CC CD20 antibody peptide, recombinant DNase peptide, anti-TNF alpha peptide,
 CC insulin peptide, hepatitis B surface antigen (HBeAg), human growth
 CC hormone (HGH) peptide, and a modifying group, where the modifying group
 CC is covalently attached to the peptide through an intact glycosyl linking
 CC group. The method is useful for a cell-free, in vitro method of
 CC remodeling the above mentioned peptides. The present sequence represents
 CC the murine anti-CD20 antibody light chain mature variable region

XX Sequence 128 AA;

QY Query Match 87.2%; Score 572; DB 6; Length 128;

Best Local Similarity 89.8%; Pred. No. 1.8e-34;

Matches 114; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

QY 1 MDFQVQIFSPILLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQOK 60

DB 1 MDFQVQIISPELLISASVIMSRGQIVLSQSPAILFASPGKVMTTCRASSSVSIHWFQOK 60

QY 61 PGSSPKPWIYGTSLASGVPTFRFSGSGSGTSYSLTISRVEADAATYCCOWSNPPTFG 120

DB 61 PGSSPKPWIYATNLASGVPTFRFSGSGSGTSYSLTISRVEADAATYCCOWTSNPPTFG 120

QY 121 SGTKLEI 127

DB 121 GGTKLEI 127

RESULT 10

ABU08393

ID ABU08393 standard; protein; 128 AA.

XX AC ABU08393;

XX 11-JUN-2003 (first entry)

XX Murine anti-CD20 antibody light chain variable region.

XX B cell lymphoma; chimeric anti-CD20 antibody; cytostatic; mouse; VL;

XX expression vector; murine; light chain; variable region.

XX Mus sp.

XX Key Location/Qualifiers

XX Peptide 1..22

XX Protein /label= signal_peptide

XX 23..128

XX /label= Mature_anti-CD20_antibody_VL_region

XX US2002197255-A1.

XX 26-DEC-2002.

XX 25-JUL-2001; 2001US-00911703.

XX 07-JUN-1995; 95US-00475813.

XX (IDEC-) IDEC PHARM CORP.

XX Anderson DR, Hanna N, Leonard JE, Newman RA, Reff ME;

XX Rastetter WH;

XX WPI; 2003-352746/33.

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

DR N-PSDB; ABX94206.
 XX Treating B cell lymphoma in humans, comprises administering
 PT immunologically active, chimeric anti-CD20 antibodies and/or radiolabeled
 PT anti-CD20 antibodies to the human.
 XX Example; Fig 4; 51pp; English.
 XX The present invention relates to a method for treating B cell lymphoma.
 CC The method comprises administering at a first administration period, an
 CC immunologically active, mouse/human chimeric anti-CD20 antibody and/or
 CC administering, at a second administration period, a radiolabelled anti-
 CC CD20 antibody, to the human subject. The invention also discloses
 CC expression vectors that may be used in the method of the present
 CC invention. The method is useful for treating B cell lymphoma in humans.
 CC The present sequence represents murine anti-CD20 antibody light chain
 CC variable region
 XX Sequence 128 AA;
 SQ Query Match 87.2%; Score 572; DB 6; Length 128;
 Best Local Similarity 89.8%; Pred. No. 1.8e-34;
 Matches 114; Conservative 2; Mismatches 11; Indels 0; Gaps 0;
 QY 1 MDFQVQIFPFLILISASVIMSRGQIVLSQSPAILFASPGETVTWTCRASSSVIYHWNQOK 60
 DB 1 MDFQVQIISFLILISASVIMSRGQIVLSQSPAILFASPGETVTWTCRASSSVIYHWNQOK 60
 QY 61 PGSSPKPWYIGTSTLASGVPTFRSGSGSGTSYSLTISRVEAEDAATYCCQWSSNPPTFG 120
 DB 61 PGSSPKPWYIATNLASGVPTFRSGSGSGTSYSLTISRVEAEDAATYCCQWTSNPPTFG 120
 QY 121 SGTKLEI 127
 DB 121 GGTKLEI 127
 RESULT 11
 ADC66268
 ID ADC66268 standard; protein; 128 AA.
 XX AC ADC66268;
 XX 19-DEC-2003 (first entry)
 DT Mouse anti-CD20 antibody light chain variable region.
 DE immunosuppressant; cytostatic; antibody; CD20;
 KW N-glycoside bond complex sugar chain; fucose; N-acetylglucosamine;
 KW sugar chain; cancer; immune disorder.
 XX Mus musculus.
 OS WC2003055993-A1.
 XX PN 10-JUL-2003.
 XX PD 25-DEC-2002; 2002WO-JP013534.
 XX PF 25-DEC-2001; 2001JP-00392753.
 PR 09-APR-2002; 2002JP-00106948.
 PR 01-NOV-2002; 2002JP-00319975.
 XX (KYOW) KYOWA HAKKO KOGYO KK.
 XX Shitara K, Sakurada M, Uchida K, Shinkawa T, Satoh M, Nakano R;
 PI WPI; 2003-559274/52.
 DR N-PSDB; ADC66267.
 XX Antibody binding to CD20 and having Fc-bound sugar chains of low fucose
 PT content for treatment of cancer and immune disorders.
 XX

PS Claim 31; SEQ ID NO 12; 200pp; Japanese.
 XX The invention relates to cells producing an antibody molecule
 CC specifically binding to CD20 are new, in which the antibody contains N-
 CC glycoside bond complex sugar chains bonded to the Fc region of the
 CC antibody peptide chains, of which less than 20% have a fucose residue
 CC bonded to the N-acetylglucosamine residue at the reducing end of the
 CC sugar chain. The cells are used in the treatment and prevention of cancer
 CC and immune disorders. This sequence corresponds to a protein used in the
 CC method of the invention.
 XX Sequence 128 AA;
 SQ Query Match 87.2%; Score 572; DB 7; Length 128;
 Best Local Similarity 89.8%; Pred. No. 1.8e-34;
 Matches 114; Conservative 2; Mismatches 11; Indels 0; Gaps 0;
 QY 1 MDFQVQIFPFLILISASVIMSRGQIVLSQSPAILFASPGETVTWTCRASSSVIYHWNQOK 60
 DB 1 MDFQVQIISFLILISASVIMSRGQIVLSQSPAILFASPGETVTWTCRASSSVIYHWNQOK 60
 QY 61 PGSSPKPWYIGTSTLASGVPTFRSGSGSGTSYSLTISRVEAEDAATYCCQWSSNPPTFG 120
 DB 61 PGSSPKPWYIATNLASGVPTFRSGSGSGTSYSLTISRVEAEDAATYCCQWTSNPPTFG 120
 QY 121 SGTKLEI 127
 DB 121 GGTKLEI 127
 RESULT 12
 ADE85686
 ID ADE85686 standard; protein; 128 AA.
 XX AC ADE85686;
 XX 29-JAN-2004 (first entry)
 DT Murine immunoglobulin light chain variable region.
 DE B cell lymphoma; anti-CD20; peripheral B cell; C2B8;
 KW immunoglobulin light chain variable region; mouse; antibody.
 XX Mus sp.
 OS US2003147885-A1.
 XX PN 07-AUG-2003.
 XX PD 11-SEP-2002; 2002US-00238681.
 XX PF 13-NOV-1992; 92US-00978891.
 PR 03-NOV-1993; 93US-00149099.
 PR 29-AUG-1997; 97US-00921060.
 XX (IDEC-) IDEC PHARM CORP.
 XX Anderson DR, Hanna N, Leonard JE, Newman RA, Reff ME;
 PI Rastetter WH;
 PI WPI; 2003-897520/82.
 DR N-PSDB; ADE85696.
 XX Treating B cell lymphoma by administering an anti-CD20 antibody and at
 PT least one chemotherapeutic agent.
 XX Example; SEQ ID NO 7; 52pp; English.
 XX The invention relates to an improved method for treating B cell lymphoma
 CC comprising administering an anti-CD20 antibody. The improvement comprises
 CC administering at least one chemotherapeutic agent. The antibody causes a
 CC substantial depletion of peripheral B cells. The antibody is chimeric
 CC anti-CD20 or C2B8. The method is useful for treating B cell lymphoma.

CC This sequence represents a murine immunoglobulin light chain variable
 CC region used in the method of the invention.

XX
 SQ Sequence 128 AA;

Query Match 87.2%; Score 572; DB 7; Length 128;
 Best Local Similarity 89.8%; Pred. No. 1.8e-34;
 Matches 114; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

QY 1 MDFQVQIFSPFLISASVIMSRGQIVLSQSPAILFASPGETVMTTCRASSSVIYMCWNQOK 60
 |||||
 DB 1 MDFQVQIIISFLLISASVIMSRGQIVLSQSPAILFASPGETVMTTCRASSSVIYHWFQOK 60
 |||||

QY 61 PGSSPKPWYCTSLASGVPTRESGSGTYSYSLTISRVEADAATYCCQWSSNPPTFG 120
 |||||
 DB 61 PGSSPKPWYATNLASGVPTRESGSGTYSYSLTISRVEADAATYCCQWTSNPPTFG 120
 |||||

QY 121 SGTKLEI 127
 |||||
 DB 121 GGTKLEI 127
 |||||

RESULT 13

AD73083
 ID ADE73083 standard; protein; 128 AA.

XX AC ADE73083;

XX DT 29-JAN-2004 (first entry)

XX DE Murine FUT8-related sequence.

XX KW Antiallergic; Anti-inflammatory; Immunosuppressive; Antibacterial;
 KW Antiviral; Cytostatic; enzyme; alpha 1,6-fucosyltransferase; tumour;
 KW allergy; inflammation; autoimmune disease; circulatory disorder;
 KW viral infection; bacterial infection; murine.

XX OS Mus musculus.

XX PN WO2003085107-A1.

XX PD 16-OCT-2003.

XX PF 09-APR-2003; 2003WO-JP004507.

XX PR 09-APR-2002; 2002JP-00106953.

XX PA (KYOW) KYOWA HAKKO KOGYO KK.

XX PI Yamane N, Satoh M, Mori K, Yamano K;

XX DR WPI; 2003-833570/77.

XX DR N-PSDB; ADE73068.

XX PT Cells with reduced or absent alpha 1,6-fucosyltransferase activity for
 PT treatment of tumors, allergy, inflammation, autoimmune disease,
 PT circulatory disorders, and viral and bacterial infection.

XX PS Example 6; Page 164-165; 187pp; Japanese.

XX CC The present invention relates to cells with modified sugar chain
 CC modifying enzyme activity. The enzyme activity of binding the 1-position
 CC of fucose to the 6-position of an N-acetylglucosamine at the reducing end
 CC of a complex N-glycoside linked sugar chain via an alpha-bond is absent
 CC or less than in the parent cell. The sugar chain modifying enzyme is
 CC preferably alpha 1,6-fucosyltransferase (ADE73052-ADE73053 and ADE73055-
 CC ADE73056). The invention is useful for the treatment and prevention of
 CC tumours, allergy, inflammation, autoimmune disease, circulatory
 CC disorders, and viral and bacterial infection. The present sequence was
 CC used in an example from the invention.

XX SQ Sequence 128 AA;

Query Match 87.2%; Score 572; DB 7; Length 128;
 Best Local Similarity 89.8%; Pred. No. 1.8e-34;
 Matches 114; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

QY 1 MDFQVQIFSPFLISASVIMSRGQIVLSQSPAILFASPGETVMTTCRASSSVIYMCWNQOK 60
 |||||
 DB 1 MDFQVQIIISFLLISASVIMSRGQIVLSQSPAILFASPGETVMTTCRASSSVIYHWFQOK 60
 |||||

QY 61 PGSSPKPWYCTSLASGVPTRESGSGTYSYSLTISRVEADAATYCCQWSSNPPTFG 120
 |||||
 DB 61 PGSSPKPWYATNLASGVPTRESGSGTYSYSLTISRVEADAATYCCQWTSNPPTFG 120
 |||||

QY 121 SGTKLEI 127
 |||||
 DB 121 GGTKLEI 127
 |||||

RESULT 14

AD73083
 ID ADF60660 standard; protein; 128 AA.

XX AC ADF60660;

XX DT 12-FEB-2004 (first entry)

XX DE Protein related to the invention #1.

XX KW Cytostatic; antiallergic; immunomodulator; cardiant; virucide;
 KW antibacterial; drug; antibody; lectin; N-acetylglucosamine; fucose;
 KW tumour; allergy; inflammation; autoimmune disease; circulatory system;
 KW viral; bacterial; infection; CCR4.

XX OS Mus musculus.

XX PN WO2003084569-A1.

XX PD 16-OCT-2003.

XX PF 09-APR-2003; 2003WO-JP004503.

XX PR 09-APR-2002; 2002JP-00106949.

XX PA (KYOW) KYOWA HAKKO KOGYO KK.

XX PI Niwa R, Shitara K;

XX DR WPI; 2003-812676/76.

XX DR N-PSDB; ADF60645.

XX PT Drugs containing antibody compositions produced by cells tolerant to
 PT lectin recognizing specific sugar-chain structure, useful in screening
 PT and treating patients not suitable for drugs not derived from these
 PT cells.

XX PS Example 2; SEQ ID NO 6; 157pp; Japanese.

XX CC The invention relates to a drug containing as the active ingredient, an
 CC antibody composition produced by cells tolerant to a lectin recognising a
 CC sugar-chain structure in which an alpha-bond is formed between the 6-
 CC position of N-acetylglucosamine at the reducing end of an N-glycoside
 CC bond-type complex sugar chain and the 1-position of fucose. The drugs are
 CC useful in screening and treating patients not suitable for drugs not
 CC derived from these cells. They are particularly useful as diagnostics,
 CC preventives or remedies for diseases accompanying tumour, allergy or
 CC inflammation, autoimmune diseases, diseases of the circulatory system,
 CC and viral or bacterial infections. In a method from the invention, a CCR4
 CC gene was used for constructing a vector (CAG-CCR4/pcDNA3) for producing a
 CC transfectant EL-4 cell (ATCC TIB-39) to express chimeric CCR4. Antibody-
 CC dependent cytotoxicity of the thus produced antibody composition was
 CC confirmed. The current sequence represents a protein related to the
 CC invention.

XX SQ Sequence 128 AA;

```
Query Match      87.2%; Score 572; DB 7; Length 128;
Best Local Similarity 89.8%; Pred. No. 1.8e-34;
Matches 114; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

QY 1 MDFQVQIFPSLLISASVIMSRGQIVLSQSPAILFASPGETVTWTCRASSSVIYMCWNQOK 60
DB 1 MDFQVQIISFLLISASVIMSRGQIVLSQSPAILFASPGETVTWTCRASSSVIYHWFQOK 60
QY 61 PGSSPKPWYIGTSLASGVPTFRSGSGSGTYSLTISRVEADAATYCCOWSSNPPTFG 120
DB 61 PGSSPKPWYIATSNLASGVPTFRSGSGSGTYSLTISRVEADAATYCCOWTSNPPTFG 120
QY 121 SGTKLEI 127
DB 121 GGTKLEI 127

RESULT 15
ADN49732
ID ADN49732 standard; protein; 128 AA.
XX
AC ADN49732;
XX
DT 15-JUL-2004 (first entry)
XX
DE Mature variable light chain anti-CD20 murine antibody protein SeqID 60.
XX
KW mouse; murine; antibody; erythropoietin; EPO; glycoconjugation;
KW glycoPEGylated EPO peptide; anaemia; antianaemic; haematocrit level;
KW kidney dialysis; haematology; CD20.
XX
OS Mus musculus.
XX
PN WO2004033651-A2.
XX
PD 22-APR-2004.
XX
PF 08-OCT-2003; 2003WO-US031974.
XX
PR 09-OCT-2002; 2002WO-US032263.
XX
PR 05-NOV-2002; 2002US-00287994.
XX
PR 06-JAN-2003; 2003US-00360770.
XX
PR 19-FEB-2003; 2003US-00360779.
XX
PR 09-APR-2003; 2003US-00410945.
XX
PA (NEOS-) NEOSE TECHNOLOGIES INC.
XX
PI De Frees S, Zopf D, Bayer R, Bowe C, Hakes D, Chen X;
XX
DR WPI; 2004-399848/37.
XX
DR N-PSDB; ADN49731.
XX
PT Novel erythropoietin peptide comprising one or more glycans, having
PT glycoconjugate molecule covalently attached to peptide, useful for
PT treating anemia in mammal such as human.
XX
PS Disclosure; SEQ ID NO 60; 1018pp; English.
XX
CC This invention relates to novel erythropoietin (EPO) peptides and the
CC remodelling and glycoconjugation of these naturally occurring peptides
CC thereof. Specifically, each EPO peptide comprises one or more glycans and
CC has a glycoconjugate molecule such as polyethylene glycol (PEG) attached
CC to it. Accordingly, the present invention provides glycoPEGylated EPO
CC peptides that have either monoantennary, biantennary or triantennary
CC glycans covalently attached thereto. As such, these peptides are useful
CC for the treatment of anaemia, and hence exhibit antianaemic activities
CC working to increase haematocrit levels in mammals, in particular in
CC humans i.e. increasing the relative volume of blood occupied by
CC erythrocytes. Furthermore, EPO therapy can be used to treat kidney
CC dialysis patients. This polypeptide is a human protein sequence related
CC to the field of haematology, given in an exemplification of the
CC invention.
```

```
XX
SQ Sequence 128 AA;
Query Match      87.2%; Score 572; DB 8; Length 128;
Best Local Similarity 89.8%; Pred. No. 1.8e-34;
Matches 114; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

QY 1 MDFQVQIFPSLLISASVIMSRGQIVLSQSPAILFASPGETVTWTCRASSSVIYMCWNQOK 60
DB 1 MDFQVQIISFLLISASVIMSRGQIVLSQSPAILFASPGETVTWTCRASSSVIYHWFQOK 60
QY 61 PGSSPKPWYIGTSLASGVPTFRSGSGSGTYSLTISRVEADAATYCCOWSSNPPTFG 120
DB 61 PGSSPKPWYIATSNLASGVPTFRSGSGSGTYSLTISRVEADAATYCCOWTSNPPTFG 120
QY 121 SGTKLEI 127
DB 121 GGTKLEI 127

RESULT 16
ADU74408
ID ADU74408 standard; protein; 128 AA.
XX
AC ADU74408;
XX
DT 10-FEB-2005 (first entry)
XX
DE Mouse anti-CD20 light chain variable region.
XX
KW Hemostatic; Hepatotropic; Antianemic; Cytostatic; Osteopathic;
KW Antibacterial; Respiratory-Gen.; Antiinflammatory; Nephrotropic;
KW Antiinfertility; Antitubercular; Tuberculostatic; protein engineering;
KW bleeding; factor VIII deficiency; factor IX deficiency; liver cirrhosis;
KW infertility; anemia; end-stage renal disease; acute myelogenous leukemia;
KW osteoporosis; pulmonary fibrosis; tuberculosis.
XX
OS Mus musculus.
XX
PN WO2004099231-A2.
XX
PD 18-NOV-2004.
XX
PF 09-APR-2004; 2004WO-US011494.
XX
PR 09-APR-2003; 2003US-00410897.
XX
PR 09-APR-2003; 2003US-00410913.
XX
PR 09-APR-2003; 2003US-00410930.
XX
PR 09-APR-2003; 2003US-00410945.
XX
PR 09-APR-2003; 2003US-00410962.
XX
PR 09-APR-2003; 2003US-00410980.
XX
PR 09-APR-2003; 2003US-00410997.
XX
PR 09-APR-2003; 2003US-00411012.
XX
PR 09-APR-2003; 2003US-00411026.
XX
PR 09-APR-2003; 2003US-00411037.
XX
PR 09-APR-2003; 2003US-00411043.
XX
PR 09-APR-2003; 2003US-00411044.
XX
PR 09-APR-2003; 2003US-00411049.
XX
PA (NEOS-) NEOSE TECHNOLOGIES INC.
XX
PI De Frees S, Zopf D, Bayer R, Bowe C, Hakes D, Chen X;
XX
DR WPI; 2004-833698/82.
XX
DR N-PSDB; ADU74407.
XX
CC Cell-free in vitro method of remodeling peptide comprising poly(ethylene
CC glycol) useful for generating glycopeptide suitable for therapeutic uses
CC in mammal, involves addition or deletion of glycosyl groups to peptide.
XX
PS Disclosure; SEQ ID NO 60; 1024pp; English.
XX
CC The invention relates to a cell-free in vitro method (M1) of remodeling a
```

CC peptide comprising poly(ethylene glycol). (M1) is useful for remodeling
CC protein to generate glycopeptide having desired glycosylation pattern
CC suitable for therapeutic use in mammal. (M1) is useful for remodeling
CC peptides chosen from immunoglobulin, erythropoietin, tissue-type
CC activator peptide, etc. (M1) is useful for remodeling (a) G-CSF which is
CC useful for treating acute myeloid leukemia (AML), non-myeloid cancer
CC patient receiving bone marrow transplant, (b) factor VII for treating
CC bleeding episode, factor VIII deficiency, factor IX deficiency, liver
CC cirrhosis, (c) FSH for patients undergoing intrauterine insemination, in
CC vitro fertilization and for infertile patient, (d) EPO for treating
CC anemia, anemic patients having chronic renal insufficiency and end stage
CC renal disease, anemic patient undergoing dialysis, (e) GM-CSF for
CC treating acute myelogenous leukemia, (f) IFN-gamma for treating malignant
CC osteoporosis, pulmonary fibrosis, tuberculosis, cryptococcal meningitis,
CC etc. The glycopeptide produced using (M1) has specific customized or
CC desired glycosylation pattern. (M1) allows efficient production of
CC improved therapeutic moiety. The present sequence represents the amino
CC acid sequence of a protein remodelled in the present invention
XX
SQ Sequence 128 AA;
Query Match 87.2%; Score 572; DB 8; Length 128;
Best Local Similarity 89.8%; Pred. No. 1.8e-34;
Matches 114; Conservative 2; Mismatches 11; Indels 0; Gaps 0;
QY 1 MDFQVQIIFSLISASVIMSRGQIVLSQSPAILFASPGETVTWTCRASSSVIYMCWNOOK 60
DB 1 MDFQVQIIFSLISASVIMSRGQIVLSQSPAILFASPGETVTWTCRASSSVIYHFWQOK 60
QY 61 PGSSPKPWIIYGTSTLASGVPTFRFSGSGGTSYSLTISRVEADAATYCCQWSSNPPTFG 120
DB 61 PGSSPKPWIIYATSNLASGVPTFRFSGSGGTSYSLTISRVEADAATYCCQWTSNPPTFG 120
QY 121 SGTKLEI 127
DB 121 GGTKLEI 127
RESULT 17
ADZ59908
ID ADZ59908 standard; protein; 128 AA.
XX
XX ADZ59908;
AC ADZ59908;
XX
XX 30-JUN-2005 (first entry)
DE Fucosyltransferase 8 (alpha (1,6) fucosyltransferase.
XX cytosolic; antiinflammatory; immunosuppressive; vasotropic; virucide;
XX antibacterial; drug discovery; cell culture; immune disorder; cancer;
XX neoplasm; inflammation; autoimmune disease; allergy; antiallergic;
XX viral infection; infection; bacterial infection;
XX Fucosyltransferase 8 (alpha (1,6) fucosyltransferase.
XX
XX Mus musculus.
XX WO2005035740-A1.
XX
XX 21-APR-2005.
XX
XX 08-OCT-2004; 2004WO-JP015315.
XX
XX 09-OCT-2003; 2003JP-00350166.
XX
XX (KYOWA) KYOWA HAKKO KOGYO KK.
XX Nakano R, Satoh M, Iida S, Urakubo M, Kusunoki M, Kinoshita S;
XX Ohnuki N;
XX WPI; 2005-346214/35.
XX
XX Novel cell that is neutralized to serum-free medium and carrying knockout
XX of gene encoding enzyme involved in carbohydrate modification, useful for

PT manufacturing glycoprotein composition useful in treating, e.g. cancer.
XX
XX Disclosure; Page 122-123; 135pp; Japanese.
XX
CC The invention describes a cell (I) that is neutralized to a serum-free
CC medium and carrying a knockout genome gene encoding an enzyme which
CC participates in a sugar chain modification, where fucose is linked by an
CC alpha linkage at the 1-position to the 6-position of N-acetylglucosamine
CC at the reducing end of an N-glycoside-binding complex sugar chain. Also
CC described are: a neutralization (M1) method of cell to the serum free
CC medium; cloning, after making neutralizing cell to the serum free medium
CC by (M1); a cell having a knockout genome gene encoding the enzyme
CC which is involved in the carbohydrate modification that is neutralized to
CC the serum free medium; and a cloned cell strain, comprising having a
CC knocked out genome gene encoding the enzyme which is involved in the
CC carbohydrate modification that is neutralized to the serum free medium.
CC (I) is useful for manufacturing a glycoprotein composition, which
CC involves culturing (I) in a culture medium and collecting the accumulated
CC glycoprotein composition from the culture medium. The glycoprotein
CC composition is useful in drug discovery and for treating immunological
CC disease such as cancer, inflammatory disease, autoimmune disease, is the
CC allergy, circulatory disorder, virus or bacterial infection. This is the
CC amino acid sequence of a polypeptide used in the creation of host cells
CC capable of producing glycoprotein compositions useful in drug discovery.
XX
SQ Sequence 128 AA;
Query Match 87.2%; Score 572; DB 9; Length 128;
Best Local Similarity 89.8%; Pred. No. 1.8e-34;
Matches 114; Conservative 2; Mismatches 11; Indels 0; Gaps 0;
QY 1 MDFQVQIIFSLISASVIMSRGQIVLSQSPAILFASPGETVTWTCRASSSVIYMCWNOOK 60
DB 1 MDFQVQIIFSLISASVIMSRGQIVLSQSPAILFASPGETVTWTCRASSSVIYHFWQOK 60
QY 61 PGSSPKPWIIYGTSTLASGVPTFRFSGSGGTSYSLTISRVEADAATYCCQWSSNPPTFG 120
DB 61 PGSSPKPWIIYATSNLASGVPTFRFSGSGGTSYSLTISRVEADAATYCCQWTSNPPTFG 120
QY 121 SGTKLEI 127
DB 121 GGTKLEI 127
RESULT 18
AAE27925
ID AAE27925 standard; protein; 235 AA.
XX
XX AAE27925;
XX
XX 27-DEC-2002 (first entry)
XX
XX Human C2B8 antibody light chain protein.
XX
XX Human; CC49 antibody; C2B8 antibody; tumour associated antigen; TAG-72;
XX neoplasm; neoplastic disorder; haematologic neoplasm; colon cancer;
XX non-Hodgkin's lymphoma; haematologic malignancy; tumour.
XX
XX Homo sapiens.
XX WO200260955-A2.
XX
XX 08-AUG-2002.
XX
XX 29-JAN-2002; 2002WO-US002373.
XX
XX 29-JAN-2001; 2001US-0264318P.
XX
XX 16-NOV-2001; 2001US-0331481P.
XX
XX (IDEC-) IDEC PHARM CORP.
XX
XX Braslawsky GR, Hanna N, Chinn P;
XX

DR WPI; 2002-698547/75.
 DR N-PSDB; AAD45754.
 XX
 PT Novel domain deleted CC49 antibody reactive with tumor associated antigen
 PT -72, or C2B8 antibody reactive with CD20, useful for treating
 PT myelosuppressed patient suffering from a neoplastic disorder.
 XX
 PS Example 1; Fig 3B; 74pp; English.
 XX
 CC The present invention relates to domain deleted CC49 or C2B8 antibodies.
 CC Domain deleted CC49 antibodies comprise a heavy chain human CC49 domain
 CC deleted sequence in which CH2 domain has been deleted and are reactive
 CC with tumor associated antigen (TAG)-72. The C2B8 antibodies are reactive
 CC with CD20 and comprise a heavy chain having a sequence of a derived
 CC domain deleted C2B8 construct where the CH2 domain has been deleted.
 CC Sequences of the invention are useful for imaging a neoplasm. They are
 CC also useful for treating myelosuppressed patients suffering from
 CC neoplastic disorder such as haematologic neoplasm, preferably non-
 CC Hodgkin's lymphoma. Antibodies of the invention are also used to treat
 CC neoplastic disorder, colon cancer and haematologic malignancy. They are
 CC useful for reducing tumour size, inhibiting tumour growth and/or
 CC prolonging the survival time of tumour-bearing animals and for treating
 CC tumours. The present sequence is human C2B8 light chain protein. This
 CC sequence is used in the exemplification of the invention
 XX
 SQ Sequence 235 AA;
 Query Match 87.2%; Score 572; DB 5; Length 235;
 Best Local Similarity 89.8%; Pred. No. 3.2e-34;
 Matches 114; Conservative 2; Mismatches 11; Indels 0; Gaps 0;
 QY 1 MDPQVQIFSLISASVIMSRGQIVLSQSPAILFASPGETVTWTCRASSSVIYMCNQOK 60
 DB 1 MDPQVQIIIFSLISASVIMSRGQIVLSQSPAILSASGKVTWTCRASSSVIYHFWQOK 60
 QY 61 PGSSPKPWYIGTSLASGVPTFRSGSGSGTYSYSLTISRVEADAATYTCQWSSNPPTFG 120
 DB 61 PGSSPKPWYATNSLASGVPTFRSGSGSGTYSYSLTISRVEADAATYTCQWTSNPPTFG 120
 QY 121 SGTKLEI 127
 DB 121 GGTKLEI 127
 RESULT 19
 ABB82834
 ID ABB82834 standard; protein; 235 AA.
 AC ABB82834;
 XX
 DT 31-MAR-2003 (first entry)
 XX
 DE Antibody C2B8 light chain.
 XX
 CC C2B8; antibody; cytostatic; antiallergic; antianemic; antiasthmatic;
 KW vscotropic; immunomodulator; protozoacide; antidiabetic; nephrotropic;
 KW thyromimetic; hepatotropic; haemostatic; antileprotic; antibacterial;
 KW neuroprotective; antipsoriatic; antirheumatic; antiarthritic; antiulcer;
 KW dermatological; immunosuppressive; antiinflammatory.
 XX
 OS Homo sapiens.
 XX
 PN WO200296948-A2.
 XX
 PD 05-DEC-2002.
 XX
 XX 29-JAN-2002; 2002WO-US0002374.
 XX
 PR 29-JAN-2001; 2001US-0264318P.
 PR 16-NOV-2001; 2001US-0331481P.
 PR 21-DEC-2001; 2001US-0341858P.
 XX
 PA (IDEC-) IDEC PHARM CORP.

XX Braslawsky GR, Hanna N, Chinn P, Hariharan K;
 XX WPI; 2003-140446/13.
 DR N-PSDB; ABZ24018.
 XX
 PT Novel dimeric antibody useful for treating immune disorder and neoplastic
 PT disorder, has several non-covalently associated monomeric subunits.
 XX
 PS Example 1; Fig 3B; 78pp; English.
 XX
 CC The invention relates to a dimeric antibody (I) comprising several
 CC monomeric subunits, where the monomeric subunits are non-covalently
 CC associated. (I) is useful for treating a disorder, especially immune
 CC disorder, and neoplastic disorder such as relapsed Hodgkin's disease,
 CC resistant Hodgkin's disease high grade, low grade and intermediate grade
 CC non-Hodgkin's lymphomas, B cell chronic lymphocytic leukemia (B-CLL),
 CC lymphoplasmacytoid lymphoma (LPL), mantle cell lymphoma (MCL), follicular
 CC lymphoma (FL), diffuse large cell lymphoma (DLCL), Burkitt's lymphoma,
 CC AIDS-related lymphomas, monocytic B cell lymphoma, angioimmunoblastic
 CC lymphadenopathy, small lymphocytic, follicular, diffuse large cell,
 CC diffuse small cleaved cell, large cell immunoblastic lymphoblastoma,
 CC small, non-cleaved, Burkitt's and non-Burkitt's, follicular, mixed small
 CC cleaved and large cell lymphomas, in a mammal (see ABZ24017 for a
 CC detailed description of the various uses of (I)). The present sequence
 CC represents the antibody C2B8 light chain
 XX
 SQ Sequence 235 AA;
 Query Match 87.2%; Score 572; DB 6; Length 235;
 Best Local Similarity 89.8%; Pred. No. 3.2e-34;
 Matches 114; Conservative 2; Mismatches 11; Indels 0; Gaps 0;
 QY 1 MDPQVQIFSLISASVIMSRGQIVLSQSPAILFASPGETVTWTCRASSSVIYMCNQOK 60
 DB 1 MDPQVQIIIFSLISASVIMSRGQIVLSQSPAILSASGKVTWTCRASSSVIYHFWQOK 60
 QY 61 PGSSPKPWYIGTSLASGVPTFRSGSGSGTYSYSLTISRVEADAATYTCQWSSNPPTFG 120
 DB 61 PGSSPKPWYATNSLASGVPTFRSGSGSGTYSYSLTISRVEADAATYTCQWTSNPPTFG 120
 QY 121 SGTKLEI 127
 DB 121 GGTKLEI 127
 RESULT 20
 ADY21925
 ID ADY21925 standard; protein; 500 AA.
 AC ADY21925;
 XX
 DT 05-MAY-2005 (first entry)
 XX
 DE Antibody fusion 2H7 VH L1LS-IgG1 (CSSS-S)H-K290QCH2-CH3.
 XX
 CC Antibacterial; Virucide; Antiparasitic; Fungicide; Immunotherapy;
 KW antibody engineering; cancer; neoplasm; cytostatic; immune disorder;
 KW graves disease; antithyroid; endocrine disease; hashimoto's disease;
 KW immunosuppressive; rheumatoid arthritis; antiarthritic; antirheumatic;
 KW inflammation; musculoskeletal disease; systemic lupus erythematosus;
 KW antiinflammatory; dermatological; dermatological disease;
 KW metabolic disorder; sjogrens syndrome; ocular disease;
 KW thrombocytopenic purpura; hemostatic; hematological disease;
 KW multiple sclerosis; neuroprotective; neurological disease;
 KW myasthenia gravis; muscular-gen.; bacterial infection; fungal infection;
 KW fungicide; viral infection; virucide; parasitic infection; antiparasitic;
 KW fusion protein.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO2005017148-A1.

XX PD 24-FEB-2005.
XX PF 24-DEC-2003; 2003WO-US041600.
XX PR 26-JUL-2003; 2003US-00627556.
XX PA (TRUB-) TRUBION PHARM INC.
XX PI Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;
XX WT: 2005-182370/19.
XX N-PSDB; ADY21924.
XX New non-naturally occurring single chain protein comprising polypeptides
PT with binding domain, connecting regions and N-terminally truncated
PT immunoglobulin, having immunological activity, useful for neutralizing
PT infectious agent.
XX Disclosure; Page 383; 590pp; English.
XX The invention relates to a non-naturally occurring single chain protein
CC (1) comprising a first polypeptide having a binding domain polypeptide
CC capable of binding to a target molecule, the binding domain polypeptide
CC comprising a heavy chain variable region, which comprises an amino acid
CC substitution or deletion at one or more amino acid residues, a second
CC polypeptide comprising a connecting region attached to the first
CC polypeptide, and a third polypeptide comprising an N-terminally truncated
CC immunoglobulin heavy chain constant region polypeptide attached to the
CC second polypeptide, where the non-naturally occurring single-chain
CC protein is capable of an immunological activity. Also included are
CC reducing a target cell population in a subject (involving administering
CC to the subject a protein that is less than 150 kD, which involves
CC treating the target cell population with a first protein or peptide that
CC binds to cells within the target cell population, and treating the target
CC cell population with a second protein or peptide that capable of at least
CC one of binding an Fc receptor, inducing target cell apoptosis, or fix
CC complements, where the first protein or peptide molecule is directly
CC connected to the second protein or peptide molecule or, optionally, the
CC first protein or peptide molecule and the second protein or peptide
CC molecule are linked by a third protein or peptide molecule, and where the
CC protein molecule is not an antibody, a member of the TNF family or the
CC TNF receptor family, and is not conjugated with a bacterial toxin, a
CC cytotoxic drug, or a radioisotope), depleting cells in an animal
CC (involving administering a modified IgE protein into the blood stream of
CC an animal), a polynucleotide that encodes the polypeptide of the
CC invention, a cell containing the polynucleotide, a recombinant vector
CC capable of expressing the polypeptide, expressing the polypeptide, a
CC composition comprising the polypeptide) in combination with one or more
CC additional therapeutic compounds, displaying recombinant molecules (which
CC molecules include a native or engineered immunoglobulin heavy chain
CC variable region, the improvement comprising an immunoglobulin heavy chain
CC region that includes one or more mutation, substitution, alteration,
CC and/or deletion at one or more amino acid residue corresponding to
CC positions 9, 10, 11, 12, 108, 110, and 112 in the heavy chain variable
CC region) and a non-naturally occurring single chain antigen-binding
CC protein comprising protein having a mutation chosen from a list given in
CC the specification. The polypeptides of the invention comprise single
CC chain antibodies (scFv, with or without mutated residues) linked via an
CC immunoglobulin hinge region (wild-type or mutants where the cysteines are
CC changed to serines/prolines and denoted (SSS-P/H), (CSC-S/H) etc) to an
CC immunoglobulin (IgG, IgE or IgA) heavy chain constant region (CH) which
CC may also have mutations in CH2 (e.g. T256N) or a truncated CH3 (e.g. T4
CC CH3, a 4 amino acid deletion). The polypeptide may be further linked to a
CC non-antibody protein such as the transmembrane and cytoplasmic tail
CC (TW/CT) of caspase-3, caspase-8 or CD80. The fusion polypeptides are
CC useful for neutralization of an infectious agent (where the infectious
CC agent is a bacterium, a virus, a parasite, or a fungus) and also for
CC treatment of cancer, immune disorders, Grave's disease, Hashimoto's
CC disease, rheumatoid arthritis, systemic lupus erythematosus, Sjogren's
CC syndrome, thrombocytopenic purpura, multiple sclerosis and myasthenia
CC gravis. The present sequence represents a fusion protein of the
CC invention.

Search completed: March 20, 2006, 07:35:40
Job time : 48.9655 secs

XX SQ Sequence 500 AA;
Query Match 86.4%; Score 567; DB 9; Length 500;
Best Local Similarity 88.2%; Pred. No. 1.6e-33;
Matches 112; Conservative 4; Mismatches 11; Indels 0; Gaps 0;
QY 1 MDFQVQIFSLISASVIMSRGOVLVSQSPAILFASPGETVTMTCRASSSVIYMCWNOOK 60
DB 1 MDFQVQIFSLISASVILARGOVLVSQSPAILFASPGETVTMTCRASSSVIYMCWNOOK 60
QY 61 PGSSPKPWIYGTSTLASGVPTREFSGSGSGTYSLSLTISRVEADAATYYCQWSSNPPTFG 120
DB 61 PGSSPKPWIYAPENLASGVPTREFSGSGSGTYSLSLTISRVEADAATYYCQWSSNPPTFG 120
QY 121 SGTKEI 127
DB 121 AGTKLEL 127